

683

701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP
 51 WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCAR REVEKAMSYR AVRVMPEFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFP	AFRRYSAFQPT	TIFPKPADT	PWHRVRRFKSN	
a294	MRITCAPMSLLSAAVWSIRV	VRTSSNRFP	AFRRYSAFRPT	TIFPKPAGT	PWHRVRRFKSN	
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGG	CRRAWTALSHNIAERARES	PRRCGKRYADIGGDS	DTIRI		
a294	RRTRGGKPLKKTYRPRRAEC	RCRRARTALSHNIAERARES	PRRYGKRYADIGGDS	DTIRI		
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVH	LYCAIAFVGGV	FFEVLVLSVLHTGRVS	REARREVEKAMSYR		
a294	RVFRLEYRMSIYAVAHIVH	LYCAIAFVGGV	FFEVLVLSVLHTGRVS	CEARREVEKAMSYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMPEFVVGLLFASGIV	MAANRYLSILGEPFATS	SFGTMLTLKILLAFSV	LAHFAIAVVK		
a294	AVRVMPEFVVGLLFASGIV	MAANRYLSILGEPFATS	SFGTMLTLKILLAFSV	LAHFAIAVVK		
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVV	FTHMLLIVFLAKAMFYIS	WX			
a294	MARSTLTVGWSKYIHTVV	FTHMLLIVFLAKAMFYIS	WX			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcgga tggcgcgga cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gttttcaaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgcgcgc ccaatttcgc caaccgcgcc
 251 gcacccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctcgggg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca
 351 gccgcgcatt cgcaaaaaac agcggcacac ccgctcgccg gcattccttc
 401 atcagatttg gccagatttc ggtttccatc aaaatgccga acatcgggcg
 451 gtgttcgcgc aaaaactgcc gtacccacgt tttttgtca tacggaagat
 501 agcggcattg cgcaccgga aacagaactt gcgcggttc ccgtcccgtc
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcgcaa
 601 ctcgcgtatc aagggttgg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgccggtg acgggattcg gatgcggctt gccgaacgc
 701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgcctaa
 751 ataacgcgt atccatatcg gcgaagcag ccacaatata tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep

```

1  MLGMARHDDQ QGIAAILLPR RQQFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVF RQVVFVGIAA HLHGCRAQFR QPRRIRLRLR QTARQMSGCG
101 TDQAADFQIT VQREFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

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1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGTATGATG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGCGGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
401 ATCAGTTTGG GCCAGATTTC GGTTCCTATC AAAATGCCGA ACATCGGGCG
451 GTGTTTCGCGC AAAAAGTGGC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATG CCGATCGGGA AACAGAACTT CGCGGGTTTC CCGCCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAAAC GCCGCCGCAA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTCT GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTCCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

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1  MLGMARHDDQ QRIAAILLPR RQQFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHLEF RYDVVFVGIAA HLHGCRAQFR QPRRIRLCLR QTARQMSGGR
101 TDQAADFQIT VQREFFRQPRI RQKQRHTRAP AFPHQVGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL RIGKQNLRGF PPRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS*

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m295/g295 93.9% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMARHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRFHLEF
g295	10	20	30	40	50	60
	MLGMARHDDQ	QGIAAILLPR	RQQFFRLVFA	PINARAAAHG	NRPASDAFFK	LPRQRFHVF
m295.pep	70	80	90	100	110	120
	RYDVVFVGIAA	HLHGCRAQFR	QPRRIRLCLR	QTARQMSGGR	TDQAADFQIT	VQREFFRQPRI
g295	70	80	90	100	110	120
	RHQVVFVGIAA	HLHGCRAQFR	QPRRIRLRLR	QTARQMSGCG	TDQAADFQIT	VQREFFRQPRI
m295.pep	130	140	150	160	170	180
	RQKQRHTRAP	AFPHQVGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
g295	130	140	150	160	170	180
	RQKQRHTRSP	AFHLQIGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
m295.pep	190	200	210	220	230	240
	PPRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRIRL	AETLVPMRPI
g295	190	200	210	220	230	240
	PSRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRMRL	AETLVPMRPV
m295.pep	250	260	270	280	290	
	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
g295	250	260	270	280	290	
	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	RTVRTAFRQR	NQIS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1   ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTTCAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTCCG GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCCGACC GAAACGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1   MLGMARHDDQ QGIAAILLPR RQQFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGIAA HLHGCRAQFR QPRRIRLRLC QTARQSGGR
101 TDQAADFQIT V*REFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NRNPASDAFFK	LPRQRFHLFR
a295	MLGMARHDDQ	QGIAAILLPR	RQQFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRFHLFR
	70	80	90	100	110	120
m295.pep	RYDVVFGIAA	HLHGCRAQFR	QPRRIRLRLC	QTPRQSGGR	TDQAADFQIT	VQRFFRQPRI
a295	RHQQVFGIAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSGGR	TDQAADFQIT	VXREFRQPRI
	130	140	150	160	170	180
m295.pep	RQKQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQK	LPYPRFFV	IRKIAALRIGKQNLRGF
a295	RQKQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQK	LPYPRFFV	IRKIAALCIRKQNLRGF
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETLVPMRPI
a295	PSRRGHLRHQ	QRRIGKTP	PQLAYQRL	GGTRFPDR	NGVYPNR	RAGNGIRIRLAETLVPMRPI
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTA	FRQRNQISX
a295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTA	FRQRNQISX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1   ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
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51  GCTTGCCGTT TCGATTATTC TGGTGtcgGC GGCATACATT Gcttcgacag
101 aggggaccga gcgcgtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTTGGg gcggcaacg9 CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagcc9 ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTCGC TTTGGAAAAA AAAGCGCGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGCGCGG GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCGACG CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTG GTTTCGACAGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

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1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51  LSWGNGVQT AYWVQEAVQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGS REVQFTDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHQQQVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYVDEGDRV LQEKGGFNIE PLVYTRISSP FGVRMHPILH TWRLHTGIDY
301 AAPQGTFPVR SADGVITFKG RKGGYGNVAVM IRHANGVELL YAHLSAFSQA
351 QGNVRGGEVI GFVVGSTGRST GPHLHYEARI NGQPNVPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

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1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAAGCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TCGGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGCGGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGCGCA
401 ATCTGTGTCG TTTGGAAAAG AAAGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGCGCGG TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTG GTTTCGACCGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

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This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PQRVEQNLP
51  LSWGSGVQT AYWVQEAVQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGA REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGRHQAFY YRSDKEGGGG
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTpvra SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

m297.pep	10	20	30	40	50	60
	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQRVEQNLPLPSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQRVEQKLPLPSWGGNGVQT					
	10	20	30	40	50	60
m297.pep	70	80	90	100	110	120
	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
m297.pep	130	140	150	160	170	180
	REVQFFTDDEGGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEPV					
g297	REVQFFTDDEGGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEPV					
	130	140	150	160	170	180
m297.pep	190	200	210	220	230	240
	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGGRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQQAAGDILAAEVVKGGRTHQAFY					
	190	200	210	220	230	240
m297.pep	250	260	270	280	290	300
	YRSDKEGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
m297.pep	310	320	330	340	350	360
	AAPQGTpvRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTpvRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
m297.pep	370	380	390	400	410	420
	GFVGSTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
m297.pep	430					
	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTGCGC	GGCATACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTCAAGCG	GATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTTGG	TCGGCGGCGA
351	CGGCGGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTTCG	TTTGGAAAAA	AAAGGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTTT	GCCGACGCTG	CGTTCCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GGCCTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTCT GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV R PQRVEQKLPP
51  LSWGGSGVQT AYWVQEA VQPGDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGD GGA REVQFFTEDED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TLRSVVV KTSAR GSLARAEV PV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQ QVA AGDILAEV V KGGTRHQAFY YRSDKEGGGG
251 GNYYDE DGRV LQEKGGF NIE PLVYTRIS SPFGYRMHP ILHTWRLHTG IDY
301 AAPQGT PVRASADGVIT FKG RKG GYGNAVMIRHANGVETLYAHL S AFSQAEGNVRGGEVI
351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAAFAAQKQ KADALLARLR GIPVTVSQSD *

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m297/a297 99.3% identity in 430 aa overlap

```

          10      20      30      40      50      60
m297.pep  MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV R PQRVEQNL PPLSWGGSGVQT
          |||||||
a297      MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV R PQRVEQKL PPLSWGGSGVQT
          10      20      30      40      50      60

          70      80      90     100     110     120
m297.pep  AYWVQEA VQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGD GGA
          |||||||
a297      AYWVQEA VQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGD GGA
          70      80      90     100     110     120

          130     140     150     160     170     180
m297.pep  REVQFFTEDEDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVV KTSARGSLARAEV PV
          |||||||
a297      REVQFFTEDEDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVV KTSARGSLARAEV PV
          130     140     150     160     170     180

          190     200     210     220     230     240
m297.pep  EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSL YFHGQQVAAGDILAEVVKGGTRHQAFY
          |||||||
a297      EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSL YFHGQQVAAGDILAEVVKGGTRHQAFY
          190     200     210     220     230     240

          250     260     270     280     290     300
m297.pep  YRSDKEGGGGGNYYDE DGV LQEKGGF NIE PLVYTRIS SPFGYRMHP ILHTWRLHTG IDY
          |||||||
a297      YRSDKEGGGGGNYYDE DGRV LQEKGGF NIE PLVYTRIS SPFGYRMHP ILHTWRLHTG IDY
          250     260     270     280     290     300

          310     320     330     340     350     360
m297.pep  AAPQGT PVRASADGVIT FKG RKG GYGNAVMIRHANGVETLYAHL S AFSQAEGNVRGGEVI
          |||||||
a297      AAPQGT PVRASADGVIT FKG RKG GYGNAVMIRHANGVETLYAHL S AFSQAEGNVRGGEVI
          310     320     330     340     350     360

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	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

1	ATGAAAAACT	TTCTTTCCCT	TTTCGCCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	AGCGGAGCGG	CGTTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
201	AACCTTCCTG	TCCGGCGAAA	cgccccccac	ggCTCAAGAC	GGCGTTTCGG
251	CAGATATGCC	GCCTGAAGCC	GCCGCATCCG	AAGCCGCCCC	GCCGGCCGGC
301	GGAACAGAAT	GGAAACAAGG	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAAGTCTTT	TTCGCCGGAG	ATTCGCTGAT	GCAGGGCGTT	GCGCCTTTCG
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TCGAATCCGC	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTTTC	CTATCCCTCA	TTCTTCGACT	GGCCGAAAAC
501	GATTGAAGAA	ACCTTGAAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGCCC	GAACGACCCG	TGGGATTTC	CCGTCGGCAA	ACGTACCTC
601	AAATTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GCGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACC CGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCCTACAT	GAAAAAAGTC	AAGCTCGACG	GTCAGATGCG	CTACCTCGAC
751	AAACTGCTTT	CGGAACACTT	GAAAGGCAAA	ATCATCCTGA	TTCCCACCGC
801	GCAAACTAG	AGCGGCGGGA	AAGgcccGCTA	CACCGATTCC	GTCAACGTCA
851	ACGGCAAACC	CGTCCGCTAC	CGCAGTAAGG	ACGGCATACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGAAAAATA	ATGGAAAAA	TCGTTTTTGA
951	ACCGAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

1	MKNFLSLFAS	ILMSALIAVW	FSQNPINAYW	QQTYHRNSPL	EPLAAYGWWR
51	SGAALQENAY	ALSDGIKTFI	SGETPPTAQD	GGSadMPPEA	AASEAAPPAG
101	GTEWKQGETA	AAVRSGDKVF	FAGDSLMQGV	APFVQKSLKQ	QYGIESANLS
151	KQSTGLSYPS	FFDWPKTIEE	TLKKHPEISV	LAVFLGPNDP	WDFPVGKRYL
201	KFASDEWAQE	YlKRVDRIle	AAHThRVQVv	WLGIPYMKKV	KLDGQMRYLD
251	KLLSEHLK GK	ILlPTAQTL	SGGKGRYTDS	VNVNGKPVRY	RSKdGIHfTA
301	EGQKLLAEKI	MEKIVFEPST	QPSSTQP*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

1	ATGAAAAACT	TTCTTTCCCT	TTTCTCCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	AGCGGTGCGG	CGTTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
201	AGCCTTCCTG	TCCGGCGAAA	CGCCGCGGAC	GGCTCAAGAC	GGCGTTTCGG
251	CAGATATGCC	GTCTGAAGCC	GCCGCATCCG	AAGCCGTCCC	TCAAACCGGT
301	GAAACAGAAT	GGAAACAAGA	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAAGTCTTT	TTTGTCGGCG	ACTCGCTGAT	GCAGGGCGTT	GCCCCCTTCG
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TCGAATCCGT	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTGTC	CTACCCCTCA	TTCTTCGACT	GGCCGAAAAC
501	GATTGAAGAA	ACCCTGCAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGACC	GAACGACCCG	TGGGATTTC	CCGTCGGCAA	ACTCTATCTC
601	AAATTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GTGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACC CGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCCTACAT	GAAAAAAGCC	AAGCTCGACG	GACAGATGCG	CTACCTAGAC
751	AAACTGCTTT	CGGAACATTT	GAAAGGCAAA	ATCATCCTGA	TTCCCACCAC
801	GCACACCCTG	AGCGGCGGGA	AAGACC GCTA	CACCGACTCC	GTCAACGTCA
851	ACGGCAAACC	CGTCCGCTAC	CGCAGCAAGG	ACGGCATACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGCAAAAATA	ATGGAAAAA	TCGTTTTTGA
951	ACCAAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1  MKNFLSLFSS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGI PYMKKA KLDGQMYRLD
251 KLLSEHLKGK IILIPTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKTFISGETPPTAQDGGSDMPPEAAASEAAPPAGGETEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
m298.pep	FVGDSLMOGVAPFVQKSLKQYQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQYQYGIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGI PYMKKA					
g298	LAVFLGPNDPWFDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGI PYMKKV					
	190	200	210	220	230	240
m298.pep	KLDGQMYRLDKLLSEHLKGKIILIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMYRLDKLLSEHLKGKIILIPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTGCGCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCCG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC
301 GAAACAGAAAT GGAAACAAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTCC CCGTTGGCAA ACGCTACCTC
601 AATTCGCTT CCGCAAGATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751  AAAGTCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCCACCGC
801  GCACACCCTG  AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
  1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
 51  SGAALQENAY  ALSDGIKAF  LSGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101  ETEWKQNTA  AAVRTGDKV  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNLS
151  KQSTGLSYPS  FFDWPKTIE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201  KFASDEWAQ  EYLKRVDR  ILEAAHTRYV  QVWLGIPIY  MKKAKLDGQ  MRYLD
251  KLLSEYLGK  GIIPIAHT  LSGGKDRYTD  SVNVNGKPV  RYRSKDG  IHF
301  EGQKLLAAK  IMEKIVFE  PSTQPSSTQ  PX

```

m298/a298 96.3% identity in 327 aa overlap

```

              10      20      30      40      50      60
m298.pep      MKNFLSLFSSILMSALIAVWFSSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
              |||||:|||||
a298           MKNFLSLFASILMSALIAVWFSSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
              10      20      30      40      50      60

              70      80      90     100     110     120
m298.pep      ALSDGIKAFSLGETPPTAQDGGADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
              |||||:|||||
a298           ALSDGIKAFSLGETPPTAQDGGADMPSEAAAPETAPQTGETEWKQNTAEEAVRTGDKVF
              70      80      90     100     110     120

              130     140     150     160     170     180
m298.pep      FVGDSLMOGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV
              |:|||||
a298           FAGDSLMOGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV
              130     140     150     160     170     180

              190     200     210     220     230     240
m298.pep      LAVFLGPNDPWDFPVGKLYLKFADEWAQEYLKRVDRILEAAHTRVQVWLGIPIYMKKA
              |||||:|||||
a298           LAVFLGPNDPWDFPVGKRYLKFADEWAQEYLKRVDRILEAAHTRYVQVWLGIPIYMKKA
              190     200     210     220     230     240

              250     260     270     280     290     300
m298.pep      KLDGQMRYLDKLLSEHLKGKIIPIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA
              |||||:|||||
a298           KLDGQMRYLDKLLSEYLGKIIPIPTAHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA
              250     260     270     280     290     300

              310     320
m298.pep      EGQKLLAAKIMEKIVFEPSTQPSSTQPX
              |||||:|||||
a298           EGQKLLAAKIMEKIVFEPSTQPSSTQPX
              310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
  1  ATGAACCCCA  AACACTTCAT  CGCATTTCCT  GCCCTGTTTC  CCGCCACGCA
 51  GGCAGAAGCC  CTGCCCGTCG  CCTCCGTCAG  CCCCACACCC  GTTACCGTTT
101  CCCCCTCCGC  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151  AACGCCGCCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAGG
201  CAGCGGCGAG  GCCTTCCGCA  TCCTGCAAAT  CGGCGACTCG  CATACGCGCG
251  GCGACTTCTT  TACCGACGCC  CTGCGCAAAC  GCCTGCAAAA  AACATGGGGC
301  GACGGCGGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351  GGCGGCCGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401  ATACCGGAGA  TTTCCCGCTC  GCGGCGATCC  TCGCCCAAAC  CGGCAGCGGC
451  GGCGGCATGA  CCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

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501	TTCCCTGTTT	GCCAAACCGC	TGCTCGCCGA	ACAAACCCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGGCCAT	ACAGACCGAA	ATGCCGTGGG	ACATCGCGCTT
651	CTACAACATC	GAAAATCCCG	CGCGGCGGCT	TACCGTTTCC	CGCATGGGCA
701	TCAACGGCGC	ACAATTGACC	CAGTGGTCTGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCGGATTG	GTTATCCTTT	CCTACGGCAC
801	CAACGAAGCC	TTCAACAACA	ACATCGACAT	TGCCGATACC	GAACAAAAAT
851	GGCTGGATAC	CGTCGCCCAA	ATCCGCGACA	GCCTCGCCCG	CGCCGGCATC
901	CTCATCATCG	CGCGCGCCGA	ATCCCTGAAA	AACACGCTCG	CGGTATGCGG
951	CACGCGCCCC	GTCTCTCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCGTCG
1001	CCCGTCAGGG	GCAGACGATG	TTTTGTGCTT	GGCAAAACCG	AATGGGCGGC
1051	ATATGTCAGCA	TGAAAAACTG	GCTCAACCAA	GGATGGGCGC	CCAAAGACGG
1101	CGTACACTTC	TCCGCCCAAG	GCTACCGCGC	CGCGCGGGAA	ATGCTTGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCGCGCGCG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pap

1	<u>MNP</u> KHFIAFS	<u>ALFAATQ</u> AEA	LPVASVSPDT	VTVSPSPAPYT	DTNGLLLTDYG
51	NAAASVPMWK	LRSAVQQSGE	AFRILQIGDS	HTAGDFFDTA	LRKRLQKWTWG
101	DGGIGWVYPA	NVKGQRMVAV	RHSGNWSQFTS	SRNNTGDFPL	GGILAQTGSG
151	GGMTLTASDG	KTGKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGWQVLDTG
201	AALPLAQITE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQITGADL	VILSYGTNEA	FNNNIDIAET	EQKWLDTQGT	IRDSLPAAGI
301	LIIGAPESLK	NLTGVCGRTP	VLLTEVQQQV	RRVARQGGQM	FWSWQNAMGG
351	ICSMKNWLNQ	GWAAKDGVHF	SAQGYRRAAE	MLADSLEELV	RAAAIRQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTCC	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTGC	CCTCCGTGAG	CCTCGACACC	GTTACCGTTC
101	CCCCGTCCGC	CCCCTACACC	GATACAAAGC	GGCTGCTGAC	CGCATACGGC
151	AACGCCTCCG	CCTCGCTTTG	GATGAAAAAA	TCTCAATCCG	TCGCACAAGG
201	CAGCGCGGAG	ACCTTCCGTA	TCTGTCAAAT	CGGCGACTCG	CATACCCGCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAAC	GCCTGCAAAA	AACTTGGGGC
301	GACGGCGGGA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCGGTC	CGGCACAACG	GTAACCTGGCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	TCTCCGCTC	GGCGGCATCC	TCGCCCAAC	CGGACGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCATGTC	CCCTGACCAT	ACACACCGAA	ATGCGGTGGG	ACATCGGGTT
651	CATCAACATC	GAAATATCCG	CGGGCGGCAT	TACCGTTTCC	CGGATGGGCA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTCG	CCCAAACCGG	CGCCGATTGT	GTTATCCTTT	CCTACGGCAC
801	CAACGAAGCT	TTCAACAACA	ACATGCACAT	TGCCGACACC	GAACAAAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTGCCTGC	CGCCGGGCATC
901	CTCATCATCG	CGGCACCCGA	TATCCTGAAA	AACACGCTCG	CGGTATGCGG
951	CACACGCCCC	GTCGCGCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCGTGC
1001	CCCGTCAGGG	GCAGACGATG	TTCTGTGCTT	GGCAAAACGC	CATGGGCGGC
1051	ATATGCAAGG	TGAAAAACTG	GCTCAACCAA	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTC	TCCGCGCAAG	GCTACCGGGT	CGCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pap

1	MNPKHLIAFS	ALFAATQAEA	LPVASVSLDT	VTVSPSAPYT	DTNGLLTDYG
51	NASASPWMKK	LQSVAQSGE	TFRILQIGDS	HTAGDFFTDS	LRKRLQKTWG
101	DGGIGWVYPA	NVKGQRMMAV	RHNGNWQSLT	SRNNTGDFPL	GGILAHTGSG
151	GSMTLTASDG	IASKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGWQVLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NLDLAQTGADL	VILSYGTNEA	FNNNIDIAMT	EQKWLDTVRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGTRP	VRLTEVQQDQ	RRVARQQQTM	FWSQWNAAGG
351	ICSMKNWLNQ	GWAAKDGVHF	SAKGYRRAE	MLADSLEELV	PSAAIRO*

m299/g299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSAPSAPYTDTNGLLTDYGNASASPWMKK
||||| : |||||

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDVTVTSPSPAPYTDNGLLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
g299	LRSVAQSGSEAFRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNN TGDFPLGGILAHTGSGGSMILTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFTSRNN TGDFPLGGILAQTGSGGSMILTASDGKTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAA LPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAA LPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKN TLGVCGTRPVRLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKN TLGVCGTRPVLLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDG VHFSAKGYRRAAEMLADSLEELVRSAAIRQX
	370 380 390
g299	GWAAKDG VHFSAQGYRRAAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTTCG CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCTG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGTCTGAC CGACTACGGC
151 AACGCCCTCG CCTCGCCTTG GATGAAAAA CTCCAATCCG TCGCACAAAG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCCGTC CGGCACAACG GTAAC TGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGCTC GGCGGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAACG
551 GCAACACCGT CTCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTGCAGCA TGAAAACTG GCTCAACCAC GGATGGGCCG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCTCGA AGA ACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

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This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQRM AAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNWLNH GWAAKDGVHF SAKGYQRSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTD	DTNGLLTDYGNASASPWMKK				
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTD	DTNGLLTDYGNASASPWMKK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m299.pep	LQSV AQSGETFRILQIGDSHTAGDFFTDSL	LRKRLQKTWGDGGIGWVYPANVKGQRM AAV				
a299	LQSV AQSGETFRILQIGDSHTAGDFFTDSL	LRKRLQKTWGDGGIGWVYPANVKGQRM AAV				
	70	80	90	100	110	120
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGI	ASKQRVSLFAKPLLAEQTL				
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGI	ASKQRVSLFAKPLLAEQTL				
	130	140	150	160	170	180
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINI	ENPAGGITVSAMGINGAQLT				
a299	TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINI	ENPAGGITVSAMGINGAQLT				
	190	200	210	220	230	240
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTE	QKWLDTVRQIRDSLPAAGI				
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTE	QKWLDTVRQIRDSLPAAGI				
	250	260	270	280	290	300
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRPVR	LTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ				
a299	LIIGAPESLKNTLGVCGRPVR	LTEVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNWLNH				
	310	320	330	340	350	360
	370	380	390			
m299.pep	GWAAKDGVHFS	SAKGYRRAAEM	LADSLEELVRSAAIRQX			
a299	GWAAKDGVHFS	SAKGYQRSAEM	LADSLEELVRSAAIRQX			
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCCGACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTAC GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGTTTCTT TATTGGGCGT
```

```

351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTGTG
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTGCGA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTAAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGGTATTGTG
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILHTVKN
101 FTGFAPLGTV LVSLLVGVIA EKSGLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMEE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGAFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIIPTMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTTACGCTT TTTATTATT TTATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGTTGTCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCGT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGTTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTTATTT TCTTGTGTG TGCATGyCG GGcmTTGTTT
1001 ATGGMCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGGCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTTCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAA TGCGCCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCG CTTTCTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTTGT TTGGGCGCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

```

m302.pep
1  MHSIYFFKEK QMSQTDQTD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRVGA KGRADDGLIY IVSLLNADGF IKILHTVKN
101 FTGFAPLGTV LVSL LGVIA EKSG LISALM RLLLT KSPRK LTTFM VVFTG
151 ILSNTASELG YVVL IPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFM VAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIFFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIFGILIC AFINLMIGSA SAQWAVTAPI FVPMLMLAGY APEVIQAAAYR
451 IGDVSTNIIT PMMSYFGLIM ATVIKYKKDA GVGTLISMML PYSAFFLIAW
501 IALFCIWVFW LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	: :					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGA KGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSL LGVIA					
	: :					
g302	SVPDPRPVGA KGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSL LGVIA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSG LISALMRLLLT KSPRKLTTFMVVFTGILSNTASELGYVVL IPLSAI IFHSLGRHPL					
	: :					
g302	EKSG LISALMRLLLT KSPRKLTTFMVVFTGILSNTASELGYVVL IPLSAV IFHSLGRHPL					
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
	: :					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW					
g302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep    SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
             |||||:|||||:|||||:|||||:|||||
g302         SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
             310      320      330      340      350      360

             360      370      380      390      400      410
m302.pep    SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
             |||||:|||||:|||||:|||||:|||||
g302         SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVGAVFLKEVGLGGSVLFIFIGFILICAFI
             370      380      390      400      410      420

             420      430      440      450      460      470
m302.pep    NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIAQAYRIGDSVTNIITPMSYFGLIMATV
             |||||:|||||:|||||:|||||:|||||
g302         NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIAQAYRIGDSVTNIITPMSYFGLIMATV
             430      440      450      460      470      480

             480      490      500      510      520
m302.pep    IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWFVVLGLPVGPGAPTFYPAPX
             |||||:|||||:|||||:|||||:|||||
g302         IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWFVVLGLPVGPGTPTFYVPVX
             490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1   ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGCGTGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGCGCTT TCGGGCGGTT ATTCGGCCAA TCTGTCTTAA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGACATFCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTGCGT CATCCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTGTG
1001 TTGCACTGCC GGGCATGTG TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGCAATAT ATTGCCGTTA AAGGGCGCAC GTTCTTAAAA
1201 GAAGTCGGCT TGGCGGCGAG CGTGTGTTT ATCGGTTTAA TTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAATACA
1451 AAAAAAGATG GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTGTT
1551 TTTGGGCCTG CCCGTCGGTC CCGCGCGGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1   MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLTKSPRK LTTFMVVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFIILCAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

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m302/a302 96.1% identity in 533 aa overlap

```

      10      20      30      40      50      60
m302.pep MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNNMLPHPVTLFIIIFIVLLLIASAVGAYFGL
          |||||
a302     MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNNMLPHPVTLFIIIFIVLLLIASAGAYFGL
      10      20      30      40      50      60

      70      80      90     100     110     120
m302.pep SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVGIA
          |||||
a302     SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLGVGIA
      70      80      90     100     110     120

      130     140     150     160     170     180
m302.pep EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL
          |||||
a302     EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL
      130     140     150     160     170     180

      190     200     210     220     230
m302.pep AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI
          |||||
a302     AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI
      190     200     210     220     230     240

      240     250     260     270     280     290
m302.pep ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW
          |||||
a302     ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW
      250     260     270     280     290     300

      300     310     320     330     340     350
m302.pep SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||
a302     SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE
      310     320     330     340     350     360

      360     370     380     390     400     410
m302.pep SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFIILCAFI
          |||||
a302     SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFIILCAFI
      370     380     390     400     410     420

      420     430     440     450     460     470
m302.pep NLMIGSASAOAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||
a302     NLMIGSASAOAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
      430     440     450     460     470     480

      480     490     500     510     520
m302.pep IKYKKGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
          |||||
a302     IKYKKGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
      490     500     510     520     530

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

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```

151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIIPTMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

```

              10      20      30      40      50      60
m302.pep      MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNMPLPHVTLFIIIFIVLLLIASAVGAYFGL
              |||||||
a302          MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNMPLPHVTLFIIIFIVLLLIASAAGAYFGL
              10      20      30      40      50      60

              70      80      90      100     110     120
m302.pep      SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLGVGIA
              |||||||
a302          SVPDPRPVGAKGRADDGLIHVSVLLDADGLIKILTHTVKNFTGFAPLGTVLVSLGVGIA
              70      80      90      100     110     120

              130     140     150     160     170     180
m302.pep      EKSGLISALMRLLLTKSPRKLTFMVVFTGILSNTASELG YVVLIPLSAI IFHSLGRHPL
              |||||||
a302          EKSGLISALMRLLLTKSPRKLTFMVVFTGILSNTASELG YVVLIPLSAI IFHSLGRHPL
              130     140     150     160     170     180

              190     200     210     220     230
m302.pep      AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI
              |||||||
a302          AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI
              190     200     210     220     230     240

              240     250     260     270     280     290
m302.pep      ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVV FVALSALLAW
              |||||||
a302          ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVV FVALSALLAW
              250     260     270     280     290     300

              300     310     320     330     340     350
m302.pep      SIVPADGILRHPETGLVSGSPFLKSIVVFI FLLFALGXGVYGRVTRSLRGEQEVVNAMAE
              |||||||
a302          SIVPADGILRHPETGLVSGSPFLKSIVVFI FLLFALPGIVYGRVTRSLRGEQEVVNAMAE
              310     320     330     340     350     360

              360     370     380     390     400     410
m302.pep      SMSTLXLXLIFFAAQFVAFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
              |||||||
a302          SMSTLGLYLVIIFFAAQFVAFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
              370     380     390     400     410     420

              420     430     440     450     460     470
m302.pep      NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIIPTMMSYFGLIMATV
              |||||||
a302          NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIIPTMMSYFGLIMATV
              430     440     450     460     470     480

              480     490     500     510     520
m302.pep      IKYKKGAGVGT LISMMLPYS AFFLIAWIAL FCIWVFLGLPVGPGAPTFY PAPX
              |||||||
a302          IKYKKGAGVGT LISMMLPYS AFFLIAWIAL FCIWVFLGLPVGPGAPTFY PAPX
              490     500     510     520     530

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq

```

1  ATGGATTTT  TGATTGTCCT  GAAAGCCCTG  ATGATGGGCT  TGGTAGAAGG
51  TTTTACCGAA  TTTTACCGA  TTTCCAGCAC  CGGACATTG  ATTGTGTTG
101 GCAATCTGAT  TGGTTTTTAC  AGCAATCACA  AGGTTTTTGA  AATTGCCATC
151 CAGCTCGGTG  CGGTTTTTGG  GGTAGTGTTT  GAATACCGGC  AGCGTTTCAG
201 CAATGTGTTG  CATGGCGTGG  GAAAAGACCG  GAAAGCCAAC  CGTTTCGTCC
251 TCAATCTTGC  CATTGCTTTT  ATACCTGCCG  CCGTGATGGG  GCTGTTGTTT
301 GACAAACAAA  TCAAAGAGTA  TCTGTTTAAC  CCCTTGAGTG  TTGCAGTCAT
351 GCTGGTTTTG  GCGGTTTTTT  TTATTTTGTG  GGTGGAGAAA  CGCCAAAGCC
401 GAGCAGAGCC  TAAAATTGCC  GATGTTGATG  CATTGCGTCC  GATTGATGCG
451 TTGATGATCG  GTGTTGCCCA  AGTGTGTTGCA  CTGGTTCCGG  GTACGTCCCG
501 TTCGGGCAGT  ACGGTTATGG  GCGGGATGCT  TTGGGGAATC  GAGCGGAAAA
551 CGGCAACGGA  GTTTTCATTT  TTCTTGCCCG  TTCCGATGAT  GGTGTCAGCA
601 ACGGCTTATG  ATGTCCTGAA  ACATTACCGA  TTTTTCACCC  TGCATGATGT
651 CGGTTTGATT  TTGATAGGCT  TTATTGCCGC  TTTGTTTCC  GGTGTTGGTAG
701 CGGTAAAGC  ACTGCTGAAG  TTTGTTTCCA  AGAAAACTA  TATCCCGTTT
751 GCCTATTACC  GCATTGTTTT  CGGCATTGTC  ATCATAATAT  TGTGGTTGTC
801 GGGCTGGATA  AGTTGGGAAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLIAIF IPAAVMGLLF
101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFLHLDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1  AtGGATTTTC  TGATTGTCCT  GAAAGCCCTG  ATGATGGGCT  TGGTAGAAGG
51  TTTTACCGAA  TTTTACCGA  TTTCCAGCAC  CGGACATTG  ATTGTGTTG
101 GCAATCTGAT  TGGTTTTTAC  AGCAATCACA  AGGTTTTTGA  AATTGCCATC
151 CAGCTCGGTG  CAGTTTTTGG  GGTAGTGTTT  GAATACCGGC  AACGTTTCAG
201 CAATGTGTTG  CACGGCTTGG  GAAAAGACCG  GAAAGCCAAC  CGCTTCGTCC
251 TTAATCTTGC  CATTGCTTTT  ATACCTGCCG  CCGTGATGGG  GCTGTTGTTT
301 GGCAwACAAA  TCAAAGAGyA  TCTGTTTAAC  CCCTTGAGTG  TTGCAGTCAT
351 GCTGGTtyTG  GrCGGTTTTT  yTATTTTGTG  GGTGGAGAAA  CGCCAAAGCC
401 GAGCAGAGCC  TAAAATTGCC  GATGTTGATG  CATTGCGTCC  GATTGATGCC
451 TTGATGATCG  GCGTTGCCCA  AGTGTGTTGCA  CTGGTTCCGG  GTACGTCCCG
501 TTCGGGCAGT  ACGATTATGG  GCGGGATGCT  TTGGGGCATC  GAACGGAAAA
551 CTGCGACAGA  ATTCTCGTTT  TTCTTGCTG  TGCCGATGAT  GGTGCGCGCA
601 ACGGCTTATG  ATGTCCTGAA  ACATTACCGA  TTTTTCACCC  TGCATGATGT
651 CGGTTTGATT  CTGATAGGCT  TTATTGCTGC  CTTTGTTC  GGCTTGTTAG
701 CGGTAAAAGC  GTTGCTGAGG  TTTGTTTCGG  GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLIAIF IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFLHLDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSN HKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSN HKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRSRAEPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGGMLWGI					
m305	XGFXILWVEKRSRAEPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1   ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTG GAATACCGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAA CCGTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCG TTCCGATGAT GGTTGCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTC A GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1   MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVALAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEITAIQLGAVLAVVF					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQGLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
a305	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	130	140	150	160	170	180
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTTCGGTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAAG
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KGLSGFFFGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  QQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGawCC  GGCCGATCAA  AACGCCTTGT  CCGAACCAGG
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAaw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)
 1 ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

	10	20	30	40
m306.pep	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX			
g306	MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
g306	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRICKWARMPTNPARGKSGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPWRSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq
 1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
 51 CTTCGGTTTG ATACTGGCGA CGGTCAATTAT TGCCGGTATT TTGTTTTATC
 101 TGAACCAGAG CGGTCAAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCTTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TGCACAAGAA AGCACTGACG GAAGAGCGTG
 401 AACAAACCGT CCGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

703

```

601 GAAGTGCAGA AAATGAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCGGTTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
  1 MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
 51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                   GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                   |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              MFMNKFSQSGKGLSGFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                   10      20      30      40      50      60

m306.pep          50      60      70      80      90      100
                   NQXKEDIQXPADQNALSEPDAAEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEDP
                   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              NQPKEDIQPEPADQNALSEPDAAEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                   70      80      90      100     110     120

m306.pep          110     120     130     140     150     160
                   GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
                   130     140     150     160     170     180

m306.pep          170     180     190     200     210     220
                   TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
                   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                   190     200     210     220     230     240

m306.pep          230     240     250
                   LPRWSVIRRDIKFTGCKAAICLPMRX
                   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              LPRWSVIRRDIKFTGCKAAICLPMRX
                   250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
  1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
 51 cgcagcctgc ggcgggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcatctggc gagggcgagt tggacatcaa cgtcttccaa
301 cacaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gaccgcgtca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaactc aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaatcgc tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataagc agcggcatga agctgaccga agcctgttc caagagccga

```

g307.pcp

m307.seq (partial)

m307.pep (partial)

m307/g307

a307.seq

a307.pcp

1 MKTFEKTLSA AALALILAAC GGQKDSAPAA SASAAAADNGA AKKXIVFGTT

705

```

51  VGDFGDMVKE QIQPELEKKG YTVKLVEFTD YVRPNLALAE GEXDINVFQH
101 KPYLDDFKKE HNLDITEVFQ VPTAPLGLYP GKLSLEEVK DGSTVSAPND
151 PSNFARVLVM LDELGWIKLK XGINPLTASK ADIAENLKNI KIVELEAAQL
201 PRSRADVDFX VVNGXYAISS GMKLTEALFQ EPSFAYVNWS AVKTADKDSQ
251 WLKDVTEAYN SDAFKAYAHK RFEGYKSPAA WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAXX
          |||||
a307      AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTTCGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RRMVRRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPPL NLAHLNLMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFID TPDLAEQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTTCGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGcT GACGCgTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GwAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTT GCACACGCtT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCArgGAATG gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

```

m308.pep (partial)

```

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  XTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSFLGID  TPDSAEWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSAEWQGM					
g308	VTEMGGVVFPVPAMYRKQPQTADDIVAHSLAHTLSLFGIDTPDLAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACGCGAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMXR  VTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSFLGID  TPDSAEWQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

m308.pep	10	20	30	40	50	60
	MLNRVYFIRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
a308	MLNRIFIRILGVADNLYPYLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
m308.pep	70	80	90	100	110	120
	GVKALELLRQADVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
a308	GVKALXLLRQADIETHLVVSKGAEMARSETXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308.pep	130	140	150	160	170	180
	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDMNKR					
a308	KTDGMLVAPCSMRTLASVVHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDMNKR					
	130	140	150	160	170	180
m308.pep	190	200	210	220	230	
	XTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSAEWQGMMA					
a308	VTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

1	ATGTTAAATC	GGGTATTTTA	TCGGATATTG	GGTGTGCGC	ACAATTTGTA
51	TCCGTGTTTA	TCGGATTTC	GTTTTTTCAC	TATAATAGCC	GGTTTGCCGT
101	TGCAGGCGGT	TTTATGGGAA	AGGCGGATGA	TGGTACGGCG	TTTGATAATC
151	GGCATCAGCG	GGGCGAGCGG	TTTCCAATAC	GGCGTGAAGG	CTTTGGAATC
201	TTTGCGCGCG	CAAGATGTGC	AAACGCACTT	TGTGGTATCG	AAAGGCGCGG
251	AGATGGCGCG	CGCTTCGGAA	ACGGATTATA	CGAAAGACGA	AGTATATGCC
301	TGGGCTGATT	TCGTCATCC	GATCGGCAAT	ATCGGGGCGT	GATTGCGGAC
351	CGGTACGTTT	AAAACGGACG	GGATGCTGGT	CGCACCCCTGT	TCGATGCGGA
401	CGCTTGCGCT	TGTCGCGCAC	GGCTTCGGCG	ACAACTCTCT	GACGCGTGGC
451	CGGGATGTGG	TTTTGAAGGA	AAGGCGGCGG	CTGTGTCTGA	TGTGTCGCGG
501	AACGCCGCTG	AACCTTGCCC	ATTTGGACAA	TATGAAGCGG	GTAACGGAAA
551	TGGGGCGGCT	GGTGTPTCCC	CCTGATCTCG	CGATGTACCG	CAAGCCGACG
601	ACGGCGGACG	ACATAGTGGC	GCACAGTACT	GCACACACGC	TTCGCTGGT
651	CGGAATTCAT	ACGCCGGATT	TGGCGGAATG	GCAGGGAATG	GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pwp

1	MLNRVFYRIL	GVADNLYPCL	SDFCFTTIIA	GLPLQAVLWE	RRMMVRRLLI
51	GISGASGFQY	GVKALELLRA	QDVETHLVVS	KGAEARASE	TDYTKDEVYA
101	LADFVHPIGN	IGACIASRGT	KDGLMLVACP	SMRTLASVAH	GFGDNLltra
151	ADVVLKERRH	LVLMIARETF	NLAHLDNMKR	VMTGGGVFP	PVPAMYRRKPQ
201	TADDIVAHSI	AHTLSLFQID	TPDLAEWQGM	AD*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

1	ATGTTAAATC	GGGTATTTTA	TCGGATATTG	GGTGTGCCG	ACAATTTGTA
51	TCCGCGTTTA	TCGGATTCT	ATTTTTCAC	TATAATAGCC	GGTTTGCCGT
101	TGCAGTGGT	TTTATGGGA	GGTCCGATGA	TGGTAGCGG	TTTGATAATC
151	GCGACACGCG	GGGCGAGCGG	TTTCCAATAC	GGCGTGAAGG	CTTTGGAATC
201	TTTGCGCGCG	CAAGATGTCG	AAACGCGACCT	TGTGGTATCG	AAAGGTGCGG
251	AGATGGCGCG	CGCTTCGGAA	ACGCGTTATG	CGAGAGACGA	GGTATATGCC
301	TTGGCGGACT	TCGTGCATCC	CATCGGCAAT	ATCGGGGCGT	GCATTGCCAC
351	CGGTACGTTT	AAAACGGATG	GGATGCTGGT	CGCCCCCTGT	TCGATGCGGA
401	CGCTTGCCCT	TGTCGCGCAC	GGCTTCGGCG	ACAATCTGCT	GACGCGCTGC
451	CGGATGTGG	TTTGAAGGA	AAGGCGGCGG	CTGCTGCTGA	TGTGCGCGCA
501	AACGCCGCTG	AACCTTGCCC	ATTTGGACAA	TATGAAGCGG	GTAAACGGAAA
551	TGGCGGCGCT	GGTGTTTCCC	CCTGTTCCCTG	CGATGTACCG	CAAACCTGAT
601	ACGGCGGAGC	ACATAGTGGC	GCACAGTGTT	GCACACGCTT	TGTCGCTGTT
651	CGGAATCGAT	ACGCCGGATT	CGGCCGGAAT	GCAGGGAATG	CGGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.ppt

1 MLNRFVYRIL GVADNLYPRL SDFCFFTHIA GLPLOAVLWE RRMVVRRLII

708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
 151 ADVVLKERRR LVLMVRETPL NLAHLNMXR VTEMGGVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFGID TPDSA EWQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRVYRILGVADNLYPRLSDFCFFTI	IAGLPLQAVLWERRMMVRRLI	IGISGASGFQY			
g308-1	MLNRVYRILGVADNLYPRLSDFCFFTI	IAGLPLQAVLWERRMMVRRLI	IGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADFVHPIGNIGACIASGTF				
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFNDLLTRAAD	VVLKERRRLVLMVRETPLNLAHLNMXR				
g308-1	KTDGMLVAPCSMRTLASVAHGFNDLLTRAAD	VVLKERRRLVLMVRETPLNLAHLNMXR				
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVFPVPVPAMYRKPO	TADDIVAHSAHLSFGIDTPDSA EWQGMADX				
g308-1	VTEMGGVFPVPVPAMYRKPO	TADDIVAHSAHLSFGIDTPDLA EWQGMADX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTGCGC ACAATTTGTA
 51 TCCGTATTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTGCGCT
 101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGC TTTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCCTGAAGG CTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
 401 CGCTTCGCTC GGTCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
 451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
 501 AACGCGCGTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
 551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTG CGATGTACCG CAAACCGCAG
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTI GLPLQAVLWE RRMVRRLLI
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA
 151 ADVVLKERRR LVLMVRETPL NLAHLNMXR VTEMGGVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFGID TPDSA EWQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFFTI	IAGLPLQAVLWERRMMVRRLI	IGISGASGFQY			
m308-1	MLNRVYRILGVADNLYPRLSDFCFFTI	IAGLPLQAVLWERRMMVRRLI	IGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADXVHPIGNIGACIASGTF				
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGFNDLLTRAAD	VVLKERRRLVLMVRETPLNLAHLNMXR				

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTLRAADVVLKERRRLVLMVRETPLNLHLNDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPVPAMYRKPQTADDIVAHSAHALSLFGIDTPDSA EWQGMADX
              |||||
m308-1      VTEMGGVVFPVPAMYRKPQTADDIVAHSAHALSLFGIDTPDSA EWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1   atgttcagtt tcggttgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgctgcccg gcgcgctttg ggggtgtttgg
101 gtttggaacac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattggggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggt
201 tgccgtgggtc ggtatcggca tcaatttcgt gctgcccagg gaagtggaaa
251 acgcccgttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttggaac acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgcgtgttga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccc taccgcgatt
701 tgcgcctttt gggcgcggaag tggcggaaga aggcggatgg aaatgtccgc
751 atcgtcgggt gcgcgctgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgca caggctttgg
851 gcatacgcaa ccaactaccg caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cagggccgtt tgaaagaaaa aaacggcgcg
1201 ggaagcctg tcgatgtcat cattaccggc ggcggcgcgg cgaaagtgcg
1251 cgaagccctg ccgcctgcat ttttggcgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILITV RAGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVHLHE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKAWVEN GTFATVGSAP YRDLSPLGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNAVASGMM DAVCGSIMMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCTT GTTGCGGCAG TGGCGTGTG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATATTAAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGCTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGTTTC CTGnCGAAG CCGCGGGATT

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710

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401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAG ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGC GGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGGTTCAG CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCCG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGT GCGGAAAATA CCGTGCAGCT
1101 GGCGGACAAC CTCGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
  51 KLGGILITV RTGGKTVAVV GIGINFVLPX EVENAASVQS LFQTASRRGN
 101 ADAAVLLXXX XXXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
 151 WVENGTATV GSAPYRDLSP LGAWEAEKAD GNVRIVGCAV CGEFKKAQVQ
 201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
 251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
 301 PFPTTTGNAV ASGMDAVCG SVMMMHGRLK EKTGAGKPD VIITGGGAAG
 351 VAEALPPAFL AENTVRVADN LVIYGLNMI AAEGREYEH...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILITV
          |||||:|||||||||||||||:|||||: |||:|||||||||||||||||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILITV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLXXX-----
          |:||||||||||||||| ||||||||||||||||||||| :
g311      RAGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLLETLLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXX
          :
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAVVENGTFATVGSAPYRDLSP LGAE
          ||||| || ||| |||:||||||||||||||| |||||||||||||||||
g311      GEISLRPDNRSVSPKRPDSEFLLLEGGNSRLKWAVVENGTFATVGSAPYRDLSP LGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          ||||| ||||| |||||:||||||||||||||| |||||||||||||||||
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIIITGGGAAKVAEA					
g311	PAGKRYPFPTTTGNAVASGMMDAVCGSIMMHGRLEKNGAGKPVVDVIIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNMI AEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

a311.seq	1	ATGTTTCAGTT	TTGGCTGGGT	GTTTGACCGG	CCGCAGTATG	AGTTGGGTTC
	51	GCTGTCGCCT	GTTGCGGCAG	TGGCGTGCCG	GCGCGCCTTG	TCGCGTTTGG
	101	GTTTGAAAC	GCAAATCAAG	TGGCCAAACG	ATTTGGTCGT	CGGACGCGAC
	151	AAATTGGGCG	GCATTCTGAT	TGAAACGGTC	AGGACGGGCG	GCAAAACGGT
	201	TGCCGTGGTC	GGTATCGGCA	TCAATTTCGT	GCTGCCAAG	GAAGTGAAA
	251	ACGCCGCTTC	CGTGCAATCG	CTGTTTCAGA	CGGCATCGCG	GCGGGGAAAT
	301	GCCGATGCCG	CCGTGTTGCT	GGAAACGCTG	TTGGCGGAAC	TTGATGCGGT
	351	GTTGTTGCAA	TATGCGCGGG	ACGGATTGTC	GCCTTTGTG	GCGGAATATC
	401	AGGCTGCCAA	CCGCGACCAC	GGCAAGCGG	TATTGCTGTT	GCGCGACGGC
	451	GAAACCGTGT	TCGAAGGCAC	GGTTAAAGGC	GTGGACGGAC	AAGGCGTTCT
	501	GCACTTGGA	ACGGCAGAGG	GCAAACAGAC	GGTCGTCAGC	GGCGAAATCA
	551	GCCTGCGGTC	CGACGACAGG	CCGTTTCCG	TGCCGAAGCG	GCGGGATTTCG
	601	GAACGTTTTC	TGCTGTTGGA	CGGCGGCAAC	AGCCGGCTCA	AGTGGGCGTG
	651	GGTGGAAAAC	GGCAGTTTCG	CAACCGTCGG	TAGCGCGCCG	TACCGCGATT
	701	TGTCGCCTTT	GGGCGCGGAG	TGGGCGGAAA	AGGTGGATGG	AAATGTCCGC
	751	ATCGTCGGTT	GCGCCGTGTG	CGGAGAATTC	AAAAAGGCAC	AAGTGCAGGA
	801	ACAGCTCGCC	CGAAAAATCG	AGTGGCTGCC	GTCTCCGCA	CAGGCTTTGG
	851	GCATACGCAA	CCACTACCGC	CACCCGAAG	AACACGGTTC	CGACCGCTGG
	901	TTCAACGCCT	TGGGCAGCCG	CCGCTTCAGC	CGCAACGCCT	GCGTCGTCGT
	951	CAGTTGCGGC	ACGGCGGTAA	CGGTTGACGC	GCTCACCAGT	GACGGACATT
	1001	ATCTCGGGG	AACCATCATG	CCCGTTTCC	ACCTGATGAA	AGAATCGCTC
	1051	GCCGTCCGAA	CCGCCAACCT	CAACCGGCAC	GCCGGTAAGC	GTTATCCTTT
	1101	CCCGACCACA	ACGGGCAATG	CCGTCGCCAG	CGGCATGATG	GATGCGGTTT
	1151	GCGGCTCGGT	TATGATGATG	CACGGCGGTT	TGAAAGAAAA	AACCGGGGCG
	1201	GGCAAGCCTG	TCGATGTCAT	CATTACCGGC	GGCGCGCGCG	CAAAAGTTGC
	1251	CGAAGCCCTG	CCGCCTGCAT	TTTTGGCGGA	AAATACCGTG	CGCGTGGCGG
	1301	ACAACCTCGT	CATTACGGG	CTGCTGAACC	TGATTGCCGC	CGAAGGCGGG
	1351	GAATCGGAAC	ATACTTAA			

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

a311.pep	1	MFSFGWVFDR	PQYELGSLSP	VAAVACRRAL	SRLGLKTQIK	WPNDLVVGRD
	51	KLGGILIEIV	RTGGKTVAVV	GIGINFLPK	EVENAASVQS	LFQTASRRGN
	101	ADA AVL ETL	LAELDAVLLQ	YARDGFAPFV	AEYQAANRDH	GKAVLLLRDG
	151	ETVFEGTVKG	VDGQGVHLLE	TAEGKQTVVS	GEISLRSDDR	PVSVPKRRDS
	201	ERFLLLDGGN	SRLKWAVVEN	GTFTVGSAP	YRDLSPLGAE	WAEKVDGNVR
	251	IVGCAVCGEF	KKAQVQEQLA	RKIEWLPSSA	QALGIRNHYR	HPEEHGSDRW
	301	FNALGSRRFS	RNACVVVSCG	TAVTVDALTD	DGHHYLGGTIM	PGFHLMKESL
	351	AVRTANLNRH	AGKRYPFPTT	TGNAVASGMM	DAVCGSVMMH	HGRLEKKTGA
	401	GKPVVDVIIITG	GGAAKVAEAL	PPAFLAENTV	RVADNLVIHG	LLNLIAAEGG
	451	ESEHT*				

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPEXEVENAASVQSLFQTASRRGNADA AVLLXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFVLPEXEVENAASVQSLFQTASRRGNADA AVLLLETLLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV DQGVLHLETAEGKQTVVS					
	130	140	150	160	170	180
m311.pep	-EISLRSDXRPVS VXKR RDSERFLLLDGGNSRLKWA WVENGT FATVGSAPYRDL SPLGAE					
a311	GEISLRSDDRPVSV PKR RDSERFLLLDGGNSRLKWA WVENGT FATVGSAPYRDL SPLGAE					
	190	200	210	220	230	240
m311.pep	WAEKADGNVRIVGCA VCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR					
a311	WAEKVDGNVRIVGCA VCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTD DGHYLG GTIMP GFHLMKESLAVRTANLNR					
a311	WFNALGSRRFSRNACVVVSCGTAVTVDALTD DGHYLG GTIMP GFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGN AVASGMMDAVCGSVMMMHGRLKEKTGAGKPV DVIITGGGA AKVAEA					
a311	HAGKRYPFPTTTGN AVASGMMDAVCGSVMMMHGRLKEKTGAGKPV DVIITGGGA AKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNMI A AEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLNLIA A EGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCGGTT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCC TATGTTTCAGT TTCGGCTGGG CGTTTGACCG GCCGAGTAT
451 GAGTTGGGTT CGCTGTGCGC TGTTGCGGCA CTGCGTGCC GGC GCGCTTT
501 GGGGTGTTTG GGT TTGAAA CGCAAATCAA GTGGCCAAAC GATTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTCG TGCTGCCCAA
651 GGAAGTGGA AAGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGCA TGGCGATGCC GCCGATTGCG TGGAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTT

```

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801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TGCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTTGA AACGGCAGaa ggCGAACAGa cgtcGtcag
951 cggcGaaaTC AGcctGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGgcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA GCGGCATGAT
1551 GGACGCGGTT TGGCGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAAGTGAAG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGCGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVLPKPSHWR VLAELADGLP QHVSQALAREA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGDRDLG GILLETVRAG
201 GKTVAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVLEHLETAE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KWAWVENGTG ATVGSAPYRD LSPLGAEWAE KADGNVRIV CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHP EHGSDRWFNA LGSRRFRSNA
451 CVVVSCGTAV TVDALTDGDL YLGGTIMPGF HLMKESLAVR TANLNRPAK
501 RYPFPTTTGN AVASGMMDAV CGSIMMHGR LKEKNAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CACACGCGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 CGCGGCGATT GCCTGGACAA GCGCAGACAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCA TTTGGCTGGG TGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTGCGC TGTGCGGCA GTGGCGGTGC GCGCGCCTT
501 GTCGCGTTTA GGTGTTGATG TGCAGATTAA GTGGCCCAAT GATTGTTGTT
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGA
751 CTGGACGCGG TGTGTTTGA ATATGCGCGG GACGGATTTC GCGCTTTTGT
801 GCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCATTGGA AACGGCAGAG GGCAACAGCA CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTTT CTGCTGTTGG ACGCGCGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGAATA CGGCACGTTC GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCTGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGCGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTAVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVG
301 QGVLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAFYRD LSPGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHPE EHGSDFWENA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMGF HLMKESLAVR TANLNRHAGK
501 RYPPFTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQMPAHIRG	LLRQHDGYWR				
	10	20	30	40	50	60
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVDRPQYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
m311-1.pep	DLVVGRDKLGGILLETVRTGGKTAVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRTVAGGKTAVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVG					
g311-1	AVLLETLLAELGAVLEQYAEAGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVVG					
	250	260	270	280	290	300
m311-1.pep	QGVLHLETAEKGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAUVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVSVKRPDSERFLLLEGNSRLKWAUVENGTF					
	310	320	330	340	350	360
m311-1.pep	ATVGSAFYRDLSPGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQALARKIEWLPSAQAL					
g311-1	ATVGSAFYRDLSPGAEWAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSAQAL					
	370	380	390	400	410	420
m311-1.pep	GIRNHYRHPEEHGSDFWENALGSRRFSRNACVVVSCTAVTVDALTDGHHYLGGTIMGF					
g311-1	GIRNHYRHPEEHGSDFWENALGSRRFSRNACVVVSCTAVTVDALTDGHHYLGGTIMGF					
	430	440	450	460	470	480
m311-1.pep	HLMKESLAVRTANLNRHAGKRYPPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYPPFTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

a311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACCG GCCGCAATAT
451 GAGTTGGGTT CGCTGTCTGC GTTTCGCGCA GTGGCGTGCC GGCGCGCCTT
501 GTCGCGTTTG GGTGTTGAAA CGCAAATCAA GTGGCCAAAC GATTGTTGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAACCGG TTGCCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCACCTGGA AACGGCAGAG GGCAAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCGGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCA GCGCAACGCC
1351 TGCGTCTCGT TCGCTGCGG CACGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAAATCGT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TCGCGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGCGCGG
1651 GCAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

a311-1.pep

```

1  MTVLKPSHWR VLAELADGLP QHVSQARMAD MKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQTKLHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILIVRTVG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVGD
301 QGVHLHETAE GKQTVVSGEI SLRSDRPVS VPKRRDSEF LLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQELARKI EWLPSSAQAL GIRNHYRHE EHGSDRWFNA LGSRRFRSNA
451 RYVVSCTAV TVDALTDGHH YLGGTIPGF HLMKESLAVR TANLNRHAGK
501 CVPFPTTGN AVASGMMDAV CGSVMMHGR LKEKTGACKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTVLKPSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTVLKLSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQTKLHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELTERS GFQTKLHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

```


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	130	140	150	160	170	180
a311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVFD	RPQYELGSLSPVA	AAVACRRALSRLGLKTQIKWPN			
m311-1	GRGRQGRKWSHRLGECLMFSFGWVFD	RPQYELGSLSPVA	AAVACRRALSRLGLDQIKWPN			
	130	140	150	160	170	180
a311-1.pep	DLVVGRDKLGGIL	ETVRTGGKTVAVV	GIGINFVLPKEVENAASVQSLFQTASRRGNADA			
m311-1	DLVVGRDKLGGIL	ETVRTGGKTVAVV	GIGINFVLPKEVENAASVQSLFQTASRRGNADA			
	190	200	210	220	230	240
a311-1.pep	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDG					
m311-1	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDG					
	250	260	270	280	290	300
a311-1.pep	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGTF					
m311-1	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGTF					
	310	320	330	340	350	360
a311-1.pep	ATVGSAPYRDLSP	LGAEWA	EKV	DGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL		
m311-1	ATVGSAPYRDLSP	LGAEWA	EKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL			
	370	380	390	400	410	420
a311-1.pep	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTD					
m311-1	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTD					
	430	440	450	460	470	480
a311-1.pep	HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKP					
m311-1	HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKP					
	490	500	510	520	530	540
a311-1.pep	VDVIITGGGA	AKVAEALPPAFLAENTVRVADNLVIHGLNLNIAAEGGESEHTX				
m311-1	VDVIITGGGA	AKVAEALPPAFLAENTVRVADNLVIYGLNLMIAAEGREYEHIX				
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAAATCG GACGCGGTCA
701 GCCTGACCGA GGTCGCGCGA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTTGT CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCCGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRFN DVRITITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGGMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVFEGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACACTG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAACCT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTCGCCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCTCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACCGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAATTGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTWTGCGC
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTGC GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCCTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCGCCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCGCGGCACA CCATTTCCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGgCTA
1251 CGCGCCTGTG ATGCCGTGTA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGCGT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRITITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGSQDAV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCETHGTTA
301 ALALINDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

```

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
	: : : :					
g312	MSIQSGEILETVKMVADRNFVDVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPPIVNQRISVTPIAQIAAATHADSYSVSAQTLDKAAKAIGVSFIGGFSALV					
	: :					
g312	AKHLSAKYGVPPIVNQRISVTPIAQIAAATKADSYSVSAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIRSIPEAMKTDDIVCXSNIGSTRAGINMDAVKLAGE TVKR TAEITPEG					
	: :					
g312	QKGMSPSDEVLIRSVPEAMKTDDIVCSSINIGSTRAGINMDAVKLAGE TI KR TAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKI VVFCNAVEDNPF XAGAFHGSG--DAVINVGVS GPGVVKA ALENSDAT TLTEVAE					
	:					
g312	FGCAKI VVFCNAVEDNPF MAGAFHGSGEADAVINVGVS GPGVVKA ALENSDAV SLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPT PAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLND AVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLND AVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMI AVPGDT PAHTISGI IADEAAIGMINSKTTAVRI IPVTGKT VGDTV EFGGLLG					
	:					
g312	CSVGLDMI AVPGDT PAHTISGI IADEAAIGMINSKTTAVRI IPVTGKT VGDSVE FGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGG RIPAPVQSMKNX					
	:					
g312	YAPVM PAKEGSCEVFVNRGG RIPAPVQSMKNX					
	430	440	450			

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAATATTATC	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCATC	GCTGATTCTT	TCTGCAGCGT	CGCGCAAAC

719

```

301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGCCCG GGTGTCGTAA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGCGCGG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTGCGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 GTTCGTCAA CCGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FCGAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GPVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKKGMMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          |||
a312       MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90      100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
          |||
a312       AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
          70      80      90      100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEVLIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG
          |||
a312       QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FCGAKIVVFCNAVEDNPF XAGAFHGS--DAVINVGVS GPGVVKAALENSDATTLTEVAE
          |||
a312       FCGAKIVVFCNAVEDNPF MAGAFHGSGEADAVINVGVS GPGVVKAALENSDATTLTEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH
          |||
a312       VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH

```

720

	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTTAALALLNDVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMIAPVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

```

g313.seq
1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttggcgatg
101 ccgccaaagg tttggttgcc gttttgcttg cacgcgtgct tcaagaaccg
151 ctccggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggcgggtgt ttttcggatt taaggcgccg aaaggcggtg
251 caacggcatt gggcgtgctt ctggcactct ctctgcaac tgccttggtc
301 tgccggttga tttggcttgt gatggcattc ggcttcaaag tatcctccct
351 tgccgcgctg gtcgccacaa ccgccgccc ccttgccgca ctgtttttta
401 tgccgcatac ttcttggtat ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

```

g313.pep
1  MDDPRTYGSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIALIV
151 LLRHKSNILN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

```

m313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCGCAAC TGCCTTGCTC
301 TGCCGCTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTCCGCCGA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

```

m313.pep
1  MDDPRTYGSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

721

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

```

      10      20      30      40      50      60
m313.pep  MDDPRTYGSNGPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA
          |||
g313      MDDPRTYGSNGPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA
          10      20      30      40      50      60

      70      80      90      100     110     120
m313.pep  VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL
          |||
g313      VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL
          70      80      90      100     110     120

      130     140     150     160     170
m313.pep  TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIKLLLEGRESKIGGSRX
          :|| |||: || |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
g313      VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIKLNLIKESKIGEKRX
          130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

```

a313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCACAAC TGCCTTGGTC
301 TGCGCGTTGA TTTGGCTTGT GATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CTTGCGCGCA CTGTTTTTTA
401 TGCCGCATAC TTCTTGGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

```

a313.pep
1  MDDPRTYGSNGPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPTTALV
101 CALIWLVMFAGFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNIILN LIKGESKIG EKR*

```

m313/a313 90.8% identity in 173 aa overlap

```

      10      20      30      40      50      60
m313.pep  MDDPRTYGSNGPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA
          |||
a313      MDDPRTYGSNGPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA
          10      20      30      40      50      60

      70      80      90      100     110     120
m313.pep  VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL
          |||
a313      VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL
          70      80      90      100     110     120

      130     140     150     160     170
m313.pep  TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIKLLLEGRESKIGGSRX
          |||
a313      TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKESKIGEKRX
          130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgatttgtgtt
 51  cacgctgctt gtagtcagtg tgggtctgtt gattgaagtt gtgcccttgg
101  cctttaccaa ggccggaaca cagccggcgc cgggctgtaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagegttacg
251  gtcattactc tgttgccgga gtagtcggtt acgaccatcc gttccaatgg
301  gggtccaaac gtaccgggcc tgatttgcca cgtgtgggag gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGACG CGATATTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401

      10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
g401      MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10      20      30      40      50      60

      70      80      90     100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQW GSKRTGPDLARVGGRYSEDE
```

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```

      |||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
g401  HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDAVVAYLQGLGLALKNVRX
      |||
g401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCGGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCG TCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTTGCCGGA GAGTCGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTC CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEEK IGVLVFTLL VSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VPESNMPAF PLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

      10      20      30      40      50      60
m401.pep MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
      |||
a401  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      |||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
a401  HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDAVVAYLQGLGLALKNVRX
      |||
a401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGgtat cgccgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCACTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTCT GCTGctgtcc
551 cTTTGTtTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG GCCGTCCGA TAGGTTGATT GAAAAACAAAC
701 ACGGCATTTG TCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCC
1201 CATgctTTTg CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTccct AATAAAGAAC
1301 TGCTCaagca aCGCCTTcc cgGTTGATTT GGCCGAAAG CGGCAGgcac
1351 gtATTGAGCA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGtctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFIL
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAa AQKVVSRMLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCnTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsa sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTTTCG CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTTCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCyTAC TGCCGGATTC

```

m402.ppt

Computer analysis of this amino acid sequence gave the following results:

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSAFAQSVPPQAFSFTLACFLTGIAVG					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSAFAQSVPPQAFSFLILACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGSFVHHAGIFITLSAVVX					
	:					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGSFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNNVFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
	:					
g402	GLIFPLVHHVGTGDNKSGRQVSNNVFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVVGANVYDGAYNNTDVFNVSNGIERAYLLPSLKSIGIRRIFFVVGSLTGSWARVLS					

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```

g402      |||||:|||||
          HRDGDKVYGANVYDGA YNTDIFNSVNGIERAYLLPSLKS GIRRIFVVG LSTG SWARVLS
          250      260      270      280      290      300

          310      320      330      340      350      360
m402.pep  AIP EMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          |||||
g402      AIP EMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          310      320      330      340      350      360

          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          |:|||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSS TVDAAAQKVSRMLIQMTEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSS TVDAAAQKVSRMLIRMTPEPSAGAE
          430      440      450      460      470      480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTGTGTT ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTC CAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGATTGTT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 CGCAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTPKNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

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```

51 ACFLTGI AVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKV VYG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVVL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLR RH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPN TSLIYMXSFLSGLSLGIEVLWVRMF SFAAQSV PQA FSTLACFLTGI AVG					
a402	MDIVNTKPN TSLIYMLSFLSGLSLGIEVLWVRMF SFAAQSV PQA FSTLACFLTGI AVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRS RFVDIPFIGQ CFLWAGIADFL ILGAAWLLTG FSGFVHHAG IFITLSAVVX					
a402	AYFGKRICRS RFVDIPFIGQ CFLWAGIADFL ILGAAWLLTG FSGFVHHAG IFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVAGS ALGPVLIG FVILDFLSTQ QIYLLICXIS					
a402	GLIFPLVHHV GTDGNKSGRQ VSNVYFANVAGS ALGPVLIG FVILDFLSTQ QIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLF QKSLRLNAVS VAVSLMFGIL MFLLPDSVFQ NIADRPDR LIENKHGIVAVY					
a402	AAVPLFCTLF QKSLRLNAVS VAVSLMFGIL MFLLPDSVFQ NIADRPDR LIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKV VYGANVYDGAYNT DVFNSVNGIERAYLLPSLKS GIRRIFFVVL STGSWARVLS					
a402	HRDGDKV VYGANVYDGAYNT DVFNSVNGIERAYLLPSLKS GIRRIFFVVL STGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLR RH PDEKFDLILM					
a402	AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLR RH PDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP HAFATAVHSI PYAYRYGHMV					
a402	NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP HAFATAVHSI PYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFP NKELLKQRLS RLIWPESGRHV FDSSTVDAAA QKVSRMLI QMTEPSAGAE					
a402	VGSATPVVFP NKELLKQRLS RLIWPESGRHV FDSSTVDAAA QKVSRMLI QMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVE YKYGRGIX					
a402	VITDDNMIVE YKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGLTGT LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```

```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVD FS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETT AETTSGLTG					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETT AETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMPYKVSIGIKPTEGLMVD FS DIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMPYKVSIGIKPTEGLMVD FS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

a406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRSETT AETTSGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFFS DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGPX *

```

m406/a406 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFSIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFSDIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

g501.seq

```

1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

```

101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcgttcg agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgaggc cgtttttgcg gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagaccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgtgcccgc
501  cgaccagggt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atcgccgga
651  taatttccgc tttcagttcg tcgtcttgtt tgtcaaattc caacaaggct
701  ttcgggtgga tgcgatttg gcggtgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agtcgggat
801  tgcgacggt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901  atcgcttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaataccag ttcgcgcgcg
1001 atgatggcgg cgtggcagggt gcgtccgcgg cggttggta cgaaggcgga
1051 agcacgttcc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatt cggagcatt tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttggga tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtggtccaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcgggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 ccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTADT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFVGFVFGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVFKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAFFLG FDGFGAGLQD VEFVAVAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFRVDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atgggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101  tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggg
151  cagttgggtc atgtcgttcg agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgaggc cgtttttgcg gcgttccaag ccgttttctt tcagggtctt
301  gacaacggt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggg caaccctatt tcattcggga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgcgcg
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttccgc ttttaattcg tcgtcttgtt tgtcaaattc caacaargct

```


732

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttgcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact ttacaggtg ctttaggcatt attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgccttcg gcacaggata cggtaacttc ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgcgg cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatt tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcagggtg cggttgccct
1251 cttcttgagg ttttacgggt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagt
1351 tttttcgatg gtcagtgcgt aatgcgcaa ctcagtaatt tcttcgtcgg
1401 taatggagaa gcggttgcgg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatgggt ttacgcagga tggcgggcgt gcccgysitt agcgtgggtt
1551 tgaacacatr aaattcgtcc gggttgaccg caccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHFDG RVAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQRHVFFM RFVYVAADQV GVFGFGEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AADNNGRNAQ FTRDDGGVAG TAAAVGNDR
351 STFHHGFPIR IGHVGNEYVA GFDGIHLGSI FNQAHALTD FLTDGAFAF
401 YGFVAVDGEA AQVAVALFLG FYGFTGLQD VEFVAVAVAS PFDIHRAAV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDID VYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFVRVDRTRY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

```

m501/g501
      10      20      30      40      50      60
m501.pep  MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG
      ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTDADTDFVLLAAGGDGKVQHFDGRVAFVKRFGHQAAVSVEAEGQLGHVVRADG
      10      20      30      40      50      60

      70      80      90      100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
      70      80      90      100     110     120

      130     140     150     160     170     180
m501.pep  QPHFIADAFQGFQAVFFQGETVFEVVDITRRTTEAQRHVFFMRVYVAADQVGVFGFGEVGH
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGFQAVFFQGETVFEALGNITRRTTEAQRHVFFMRVYAAADQVGVFGFGEVGH
      130     140     150     160     170     180

      190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

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g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAAADNFRFQFVVLVFKFQQGFRVDADL
	190 200 210 220 230 240
	250 260 270 280 290 300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDYRCFRHIVXGDIGNLYVQQTGIDKAG
	: : : :
g501	AVDDKFHTRQADAFAGQIGAECEFGIADVHHDYRCFRHIVXGDIGNLYVQQTGIDKAG
	250 260 270 280 290 300
	310 320 330 340 350 360
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
	: : : :
g501	IAFGTGYGNFLTTFVQEFGRIAAADNNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
	310 320 330 340 350 360
	370 380 390 400 410 420
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAHALTDFLT DGA AFAXYGFVAVDGEAAQVAVALFLG
	: : : :
g501	IGHVGNQYVAGFDGIHLGSI FNQAHALTDFLT DGT TFAQDGF FAVDGVAAQVAAAFLLG
	370 380 390 400 410 420
	430 440 450 460 470 480
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDQGQVLRQLSNFFVGNGEAVAVFLGDDID
	: : : :
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQGRVVCQLGDFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
	490 500 510 520 530 540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGGGLARFERGFEXXKFVRVDRTLVDVFAQTVRGG
	: : : :
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXXKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
	550
m501.pep	NKDDLIVXGFGVEGEHHT
	:
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

```

1  ATGGTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51  GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101 TCGTCAAACG ATTCGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151 CAGTTGGGTC ATGTCGTTCG AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201 GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251 AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301 GACAACGGCT TCGGCTTCGC CCAAAGTGGC GACGAACGGA ATCATGATTT
351 CAACGTTGGT CAACCCCATC TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
401 TCCAAGGCGA AACAGTCTTT GAAGTTGTCT GCGACATAAC GCGCCGACCC
451 ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTCTGAT ACGTTGCCGC
501 CGACCAGGTT GGCGTATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551 GTTTTACGCG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTCCGGCGAT
601 TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651 TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701 TTGGGGTGGA TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751 GCCGATGCCT TCGCTGGGCA GGTGGCGGAA GCTGAATGCG AGTTCGGGAT
801 TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCCAAA
851 GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901 ATCGCCTTCG GCACAGGATA CGGTAACCTC TTGACCGTTT TTCAGCAATT
951 CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

```

```

1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCGGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTGCGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCGT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTTC
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACC GGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1  MVGRALTADA DIFVLLAAGG DGKVQHHFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRR
151 TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFVVDLTL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFAVDRKA AQVAAFFFLG FDGFGTGLQD VEFVAVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVGNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

m501.pep	10	20	30	40	50	60
	MVGXALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRLALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
m501.pep	70	80	90	100	110	120
	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
m501.pep	130	140	150	160	170	180
	QPHFIADAFQGFQGETVFEVVDITRRTEAQHRVFFMRVYVAADQVGVFGFVGVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTEAQHRVFFMRVYVAADQVGVFGFVGVGH					
	130	140	150	160	170	180
m501.pep	190	200	210	220	230	240
	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFVVDLTL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFVVDLTL					
	190	200	210	220	230	240
m501.pep	250	260	270	280	290	300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVQSNIGNLYVQQAGVDEAG					
	250	260	270	280	290	300
m501.pep	310	320	330	340	350	360
	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHDDGGSAPVGHHRFPIW					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLTDGAA FAXYGFVAVDGEAAQVAVALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLTDGAAFAQDGF FAVDRKAAQVAAFFLG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFVHRAAVVFFDGCVMRQLGDFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
	490	500	510	520	530	540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEXHKKFVRVDRTLVDVFAQTVRGG					
a501	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGX					
	490	500	510	520	530	540
	550	559				
m501.pep	NKDDLIVXGFGVEGEHHTX					
a501	DKDDLIVTGFGEIEGHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51  cgtcgccgtc gttccgcac aggcgggccc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcgcca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccggttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgccggc agccccgccg ccatacctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgg
451 ctaccaatac atccgcatcg gttcaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQRRR
151 LPIHPHRLQR RQPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51  cgtcgccgtc gttccgcac aggcgggccc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcgcca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgtcg
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgccg ccatacctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta
451 ccaatacatc cgcacggct tcaaaggcgg caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRR
151 PIHPHRLQRR QPRRHAA

```

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPIYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCTG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCGC	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGGTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKKTQTAHG	TFKILRPGLF	KWEYTSFYKQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSFYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGatGAAAc  cgcaCaacct  gttccaaTtC  CTCGCGGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCCTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCT
251 GCGACGGTCA  AACCCTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCAGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTQVQ
51  SKKKTQTAHG  TFKILRPGLF  KWEYTLPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIIG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC  CGCACAACTT  GTTCCAATTC  CTCGCGGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCCTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCCTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGCGGCG  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCAGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTQVQ
51  SKKKTQTAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIIG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	KQFNNDADGISGSFTQTQVQSKKKTQTAHG				
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	KQFNNDADGISGSFTQTQVQSKKKTQTAHG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYD	VDLAQVTKSSQDQAIGGSPAAILSNKT				
g502-1	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYD	VDLAQVTKSSQDQAIGGSPAAILSNKT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIG	FKGGNLAAMQLKDSFGNQTSISF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIG	FKGGNLAAMQLKDSFGNQTSISF				
	130	140	150	160	170	180

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```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACCTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPLGF KWEYTSYKQ TIVGDGQTVW LYDVLQAVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                |||||
m502-1        MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPLGFKWEYTSYKQTIVGDGQTVWLYDVLQAVTKSSQDQAIGGSPAAILSNKT
                |||||
m502-1        TFKILRPLGFKWEYTKPYRQTIIVGDGQTVWLYDVLQAVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKEDGSSNGIDYV LATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                |||||
m502-1        ALESSYTLKEDGSSNGIDYV LATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

739

```

m503.seq
  1  atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
 51  ttcggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
101  tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151  gccagtgcgg cggaaatgcg ttcgctcaga ccgttggtgt cgaggaatgc
201  gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTS NF
 51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503

          10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRA SSATSSTS NFASAAEMRSLR
          |||| ||: ||||||||||||||||||||||||||||| ||||| |||||:|
g503       MSAPSASVIILFHAASISASSCSGKGVSKIHWRI SLPTRASSETSSTSNFAAAEMRSFR
          10      20      30      40      50      60

          69
m503.pep  PLCARNAR
          |||||||
g503       PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
  1  ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
 51  TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101  TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151  GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
201  GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTS NF
 51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

          10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRA SSATSSTS NFASAAEMRSLR
          ||||||||||||||||||||||||||||||||||| ||||| |||||
a503       MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLPTRA SSATSSTS NFASAAEMRSLR
          10      20      30      40      50      60

          69
m503.pep  PLCARNARX
          |||||||
a503       PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
  1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
 51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101  ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151  GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTTGTTC ATGCCGCTTC
201  GATTTCCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAA ATCCATTGGC
251  GGATTCTCTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301  TTTGCCAGAG CGGCGGAAAT GCGTTCGTT AGACCGTTGT GTGCGAGAAA
351  TGC GCGGTAG

```


This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRIAFLLS KPLIFRKVSC WPANDASGRS SAVAERTAT
51  EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN
101 FAAAAEMRSF RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51  AACGTATCC AAGCCGTGA TGTCAAGAA GGTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTGTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGCGCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIALSLTS KPLMFKKVSC CPANDASGRS SAVAERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFLLSKPLIFRKVSCWPANDASGRSSAVAERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALSLTSKPLMFKKVSCCPANDASGRSSAVAERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFASAAEMRSFRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51  AACGTTTTCC AAGCCGTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCGCCGGC ATCGGCAACC ATTTGTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGCGCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALSLTSKPLMFKKVSCCPANDASGRSSAVAERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1   atgtttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccatcgtgta ccgcacccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataaccg ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgccgaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcttc aggtttgcag
1051 atgaccggtt cgccgggtgc gcttttggtc tatctcggct cggatttgtt
1101 ggttttgggt acagtattta tgttttatgt gccccaaaaa cgggcgtggg
1151 tattgttttc aaacdgc aaa atccgttttg ctatgtcttc ggccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cagtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1   MLVQDLPEFV KLKKFHIDFY NTGMPDRFAS DIEVTDKATG EKLETRIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLRL DASREPVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgtga tttcgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgggt gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgggttt gcaggaaacg gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataaccg ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgccgaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttctt
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcttc gggtttgcag

```

742

```

1051 atgacccggt ccccggtgc gcttttggtc tatctcggtc cgggtgctgtt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacgc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

```

1 ILVQDLPPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	:					
g504	MLVQDLPPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGSDLTFAKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	YQASFADGGSDLTFAKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLDGEGRKRLVADATKGAPAEI					
	:					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					

743

g504 YLGSVLLVLGTVFMFYVPKKRAWVLFNSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||

g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq

1	ATATTGGTTC	AGGACTTGCC	TTTGAAGTC	AAACTGAAAA	AATTCCATAT
51	CGATTTTTAC	AATACGGGTA	TGCCGCGCGA	TTTTGCCAGT	GATATTGAAG
101	TAACGGATAA	GGCAACCGGT	GAGAACTCG	AGCGCACCAT	CCGCGTGAAC
151	CATCCTTTGA	CCTTGACCGG	CATCACGATT	TATCAGGCGA	GTTTTGCCGA
201	CGGCGGTTCC	GATTTGACAT	TCAAGGCGTG	GAATTTGGGT	GATGCTTCGC
251	GCGAGCCTGT	CGTGTGAAG	GCAACATCCA	TACACCAGTT	TCCGTTGGAA
301	ATTGGCAAAC	ACAAATATCG	TCTTGAGTTC	GATCAGTTTA	CTTCTATGAA
351	TGTGGAGGAC	ATGAGCGAGG	GCGCGGAACG	GGAAAAAAGC	CTGAAATCCA
401	CGCTGAACGA	TGTCCGCGCC	GTTACTCAGG	AAGGTAAAAA	ATACACCAAT
451	ATCGGCCCTT	CCATTGTTTA	CCGTATCCGT	GATGCGGCAG	GGCAGGCGGT
501	CGAATATAAA	AACTATATGC	TGCCGGTTTT	GCAGGAACAG	GATTATTTTT
551	GGATTACCGG	CACGCGCAGC	GGCTTGCAGC	AGCAATACCG	CTGGCTGCGT
601	ATCCCCCTGG	ACAAGCAGTT	GAAAGCGGAC	ACCTTTATGG	CATTGCTGTA
651	GTTTTTGAAA	GATGGGGAAG	GGCGCAAACG	TCTGGTTGCC	GACGCAACCA
701	AAGGCGCACC	TGCCGAAATC	CGCGAACAAT	TCATGCTGGC	TGCGGAAAAC
751	ACGCTGAACA	TCTTTGCACA	AAAAGGCTAT	TTGGGATTGG	ACGAATTTAT
801	TACGTCCAAT	ATCCCGAAAG	AGCAGCAGGA	TAAGATGCAG	GGCTATTCTT
851	ACGAAATGCT	TTACGGCGTG	ATGAACGCTG	CTTTGGATGA	AACCATACGC
901	CGGTACGGCT	TGCCCGAATG	GCAGCAGGAT	GAAGCGCGGA	ATCGTTTCCT
951	GCTGCACAGT	ATGGATGCGT	ACACGGGTTT	GACCGAATAT	CCCGCGCCTA
1001	TGCTGCTGCA	ACTTGATGGG	TTTTCCGAGG	TGCGTTCGTC	GGGTTTGCAG
1051	ATGACCCGTT	CCCCGGGTGC	GCTTTTGGTC	TATCTCGGCT	CGGTGCTGTT
1101	GGTATTGGGT	ACGGTATTGA	TGTTTTATGT	GCGCGAAAAA	CGGGCGTGGG
1151	TATTGTTTTT	AGACGGCAAA	ATCCGTTTTG	CCATGTCTTC	GGCCCCGAGC
1201	GAACGGGATT	TGCAGAAGGA	ATTTCCAAAA	CACGTCGAGA	GTCTGCAACG
1251	GCTCGGCAAG	GACTTGAATC	ATGACTGA		

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep

1	ILVQDLPF	EVKLKKFH	IDFYNTGM	PRDFASD	IEVTDKATG	EKLERTIRVN
51	HPLTLHG	ITIQASFAD	GGSDLTFK	AWNLDAS	REPVLKATS	SIHQFPLE
101	IGKHKYR	LEFDQFTS	MNVEDM	SEGAEREKS	LKSTLNDV	RAVTQEGK
151	IGPSIVY	RIRDAAGQ	AVEYKN	YMLPVLQ	EQDYFWIT	GTRSLQQQY
201	IPLDKQL	KADTFMAL	REFLKD	GEGRKRL	VA DATKG	APAEIREQ
251	TLNIFAQ	KGYLGLD	EFITSN	IPKEQQD	KMGYFYEM	LYGMNAAL
301	RYGLPEW	QQDEARNR	FLLHSM	DAYTGLT	EYPAPMLL	QLDGFSEVR
351	MTRSPGAL	LVYLGSV	LLVLGTV	LMFYVRE	KRAWVLF	SDGKIRFAM
401	ERDLQKE	FPKHVES	LQRLGK	DLNHD*		

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPF	EVKLKKFH	IDFYNTGM	PRDFASD	IEVTDKATG	EKLERTIRVN
a504	ILVQDLPF	EVKLKKFH	IDFYNTGM	PRDFASD	IEVTDKATG	EKLERTIRVN
	10	20	30	40	50	60
m504.pep	YQASFAD	GGSDLTFK	AWNLDAS	REPVLKATS	SIHQFPLE	IGKHKYR
a504	YQASFAD	GGSDLTFK	AWNLDAS	REPVLKATS	SIHQFPLE	IGKHKYR
	70	80	90	100	110	120
m504.pep	LEFDQFTS	MNVEDM	SEGAEREKS	LKSTLNDV	RAVTQEGK	KYTNIGPSI
a504	LEFDQFTS	MNVEDM	SEGAEREKS	LKSTLNDV	RAVTQEGK	KYTNIGPSI
	130	140	150	160	170	180
m504.pep	YRIRDAAG	QAVEYKN	YMLPVLQ	EQDYFWIT	GTRSLQQQ	YRIRDAAG
a504	YRIRDAAG	QAVEYKN	YMLPVLQ	EQDYFWIT	GTRSLQQQ	YRIRDAAG

a504	MSEGAEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ	130	140	150	160	170	180
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI	190	200	210	220	230	240
a504	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI	190	200	210	220	230	240
m504.pep	REQFMLAAENTLNIFAQKGYLGDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR	250	260	270	280	290	300
a504	REQFMLAAENTLNIFAQKGYLGDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR	250	260	270	280	290	300
m504.pep	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV	310	320	330	340	350	360
a504	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV	310	320	330	340	350	360
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK	370	380	390	400	410	420
a504	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK	370	380	390	400	410	420
m504.pep	DLNHDX						
a504	DLNHDX						

q505.seq

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

q505.pep

1	MFR LQFRLFF	PLRTAMHILL	TALLKCLSL	SLSC LHTLGN	RLGHLAFYLL
51	KEDRARIVAN	MRQAGLNPD	QTVKAVFAET	AKCGLELAPA	FFKKPEDIET
101	MFKAVHGEH	VQQALDKGEG	LLFITPHIGS	YDLGGYISQ	QLPFHILTAMY
151	KPPKIKAIDK	IMQAGRVRG	GKTAPTGIQG	VKQIIKALRA	GEATIILPDH
201	VPSQIEGGGV	WADFFGKPAY	TMTLAKLAH	VKGVKTLFFC	CERLPDQGQF
251	VLHIRPVOGE	LNGNKAHDA	VFNRNTEYWI	RRFETOYLFM	YNNRYKTP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

```

m505.seq (partial)
  1 GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCTTTGC GAACCGCCAT
 51 GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCAGAA ACGGCAAAAG
251 GCGGTTTGGG ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTTCGCGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCAGAC
601 ACGTCCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAG
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

```

m505.pep (partial)
  1 MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCLHTLGN RLGLHAFYLL
 51 KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHD AAVFNRAEYW IRRFPHTI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPFAFFRKPEDIETMFKAVHGEHVQALDKHEG					
	:					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPFAFFKRPEDIETMFKAVHGEHVQALDKGEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGVRGKGKTAPTSIGG					
g505	LLFITPHIGSYDLGGYISQQLPFHILTAMYPKPPKIKAIKIMQAGVRGKGKTAPTGIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGVKTLLFF					
	:					
g505	VKQIIKALRAGEATIIILPDHVPSPQEGG-GVWADFFGKPAYMTLAAXLAHVKGVKTLLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					
g505	CCERLPGGQGFVLHIRPVQGEELNGNKAHDAAVFNRTTEYWIRRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CCGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAGGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1   MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCSLHTLGN RLGHLAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCSLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCSLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYMTLAAKLAHVKGVTLEFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYMTLAAKLAHVKGVTLEFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCACCCCC AAAACGGTCA AAGCCGTTTT TCGGGAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CCGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTTCCC CTCAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGA AAC CCTGTTTT TCCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTG ACATCCGCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VWVDFFGKPA YTM TLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFN RNAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPD PKTVKAVFAETAKGGLELAPAF FRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPD QTVKAVFAETAKGGLELAPAF FRKPEDIETMFKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPQEGG VVWDFFGKPAYTMTLAAKLAHVKG VGTKLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPQEGG VVWDFFGKPAYTMTLAAKLAHVKG VGTKLFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGF DLHIRPVQGE LNNGDKAHDA AVFN RNAEYW IRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGF DLHIRPVQGE LNNGDKAHDA AVFN RNAEYW IRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	299
m505-1.pep	CCERLPGGQGF DLHIRPVQGE LNNGDKAHDA AVFN RNAEYW IRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGF DLHIRPVQGE LNNGDKAHDA AVFN RNAEYW IRRFPTQYLFMYNRYKMPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70 80 90 100 110 120					

748

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
              |||||:|||||
a505         MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKD KIMQAGRVRGKGKTAPTTSIQG
              |||||
a505         LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKD KIMQAGRVRGKGKTAPTTSIQG
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHVPSPQEGEGVWVDFFGKPAYMTLAAKLAHVKGVKTLFF
              |||||
a505         VKQIIKALRSGEATIVLPDHVPSPQEGEGVWVDFFGKPAYMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              |||||
a505         CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT TGTATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAGTCG GGTGTGTTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGGAAGTT CACACCAAG CGGTAACGTT
351 GCGCGTCGCG GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGAATTTC AAAAAAACG
751 TTCGCCCCGT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGGG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACC GCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGCG GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGGCGCGC CGTTGTTCAT
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTTCCT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHQV EQGARLAEVV VIVLAVVPVC
51  RVAVDFFRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEEVFGLIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLDVH

```

745

m505.seq (partial)

```

1 GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTC GAACCGCCAT
51 GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCAGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCGGAA ACGGCAAAAG
251 GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTGCGGCG AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGCGGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCTTC CCCTCAAGAA GCGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAG
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1 MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSLHTLGN RLGHLAFYLL
51 KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MPKAVHGWEG VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSLHTLGNRLGHLAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLSLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWEGHVQALDKHEG					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPAFFKKPEDIETMFKAVHGWEGHVQALDKGEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWEGHVQALDKHEG					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPAFFKKPEDIETMFKAVHGWEGHVQALDKGEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTHI					
g505	CCERLPGGQGFVLHIRPVQGEELNGDKAHDAAVFNNTTEYWIRRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAAC T GCCCCCCGCG TTTTTCAGAA AACC GGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGTTG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGCAAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1   MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGH LAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKG GLELAPA FFRK PED IET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGRYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTS IQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VWVDFFGKPA YTM TLA AKLA HVKG VKTLFF CCERLP GGQ G
251 FDLHIRPVQ G ELNGDKAHDA AVFN RNAEYW IRREPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKG GLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKG GLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGRYISQQLPFP L TAMYKPPKIKAI DKIMQAGRVRGKGKTAPTS IQG					
a505	LLFITPHIGSYDLGGRYISQQLPFP L TAMYKPPKIKAI DKIMQAGRVRGKGKTAPTS IQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKG VKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLA AKLAHVKG VKTLFF					
	190	200	210	220	230	240
	250	260	270	280		
m505.pep	CCERLPGGQGFDLHIRPVQGE L NGDKAHDA AVFN RNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGE L NGDKAHDA AVFN RNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CCGGTTTGAA
201 CCCCCACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CCGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAGAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGWHE VQALDKHEG LLFITPHIGS YDLGGYISQ LPPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YTMTLAAKLA HVKGVKTLEF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	70	80	90	100	110	120
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWHEVQALDKHEG					
	70	80	90	100	110	120
g505	MRQAGLNPDQTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWHEVQALDKHEG					
	130	140	150	160	170	180
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSIQG					
	130	140	150	160	170	180
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSIQG					
	190	200	210	220	230	240
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLEF					
	190	200	210	220	230	240
g505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLEF					
	250	260	270	280	290	299
m505-1.pep	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX					
	240	250	260	270	280	290
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKTPX					

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	70	80	90	100	110	120

748

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG
              |||||:|||||
a505         MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIQAGRVRGKGKTAPTSTIQG
              |||||
a505         LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIQAGRVRGKGKTAPTSTIQG
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              |||||
a505         VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              |||||
a505         CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGC GCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGCAAGTCG GGTTGTTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GGCCTTGTCG GTGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GGCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGCG GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT
651 GATGGCTTTT GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTC AAAAAAACG
751 TTCGCCCCTT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGACGAGG CTTGCGGCGAG CAGCGTCCAG AAGTCCCAGT TGTTTGTTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACC CGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTTACGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGCG GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGGCGCGC CGTTGTTTCAT
1351 GGTTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCTTT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHQQ EQGARLAEEV VIVLAVVPVC
51  RVAVDFFORRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLVDH

```

201 RPFRELAALD GFVQVALMAF AVVGDDFCSF FVGQVFNPLL AAEMEFHPKT
251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVCG
301 GTHIGARIAF DGFVQVGefa RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGOAVL IVGNGRAVVH
451 QQMGYGAFFG SHRSCSFSQV QMGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFAKTM DAILIROFERY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCATTGCG	GCGCGGTGT
51	TGCCGAACAA	TGCCTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGTTGGC	TGAAATAGTC	GTCATCGTCT	TGGCGGTAGT	CCCAGTGTGC
151	CGCGTCGCCG	TTGATTTTCA	AAGGCGGTTT	GGCGAAcCg	GGTTGTTGCT
201	GCCATTGGCC	GAAGCTGTyG	GGTTCTAGT	GCCGCAGGCT	GCCGyAGTTG
251	CCGTCCGGCG	GGCCTTGCC	GTyGCGsTgr	TTgCTGTgAA	CaSGGCAACG
301	CGGACGATTG	ACGGGAATTT	GGCGGAAGTT	TACGCCCCAA	CGGTAGCGTT
351	GTCGCTCGGC	GTAATTGAAC	AAACGCGCTT	GCAGCATTTT	ATCTsGGCTG
401	GCGCCGACAC	CGGGAACGAG	ATTGCTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTTCG	GATTGCGGTT	CTCAAACGGA	TGATAAGSTA
501	CTTTTTCCGC	GTCTGCTTCA	GGCATGACTT	GGATGTACAT	CGTCCATTTT
551	GGAAACTCGC	CGCGTTCGAT	GGCTTCsTAT	AAGTCGCGCT	GATGGCTTTT
601	GCGGTCGTCG	GCGATGATTT	TGGCGGCTTC	TTCGTTGGTC	AGGTTTTTTAA
651	TGCCTTGTTG	GGTGCGGAAA	TGGAATTTCA	CCCCAAAACG	CTCGCCTGCT
701	TCGTTCCAGA	AGCTGTAGGT	ATGCGAACCG	AAGCCGTGCA	TATGGCGGTA
751	GCCGGCGGGG	ATGCCGCGGT	CGCTCATCAC	GATGGTAACT	TGGTGCAGTG
801	CTTCGGGCAG	CAGCGTCCAG	AGCTCCCAGT	TGTTTGTGGC	AGAGCGCATA
851	TTGGTGCGCG	GGTCGCGTTT	GACGGCTTTG	TTTAGTTCGG	GGAACTTACG
901	CGGGTCGCGC	AGGAAGAACA	CGGGCGTGTT	GTTGCCGACC	ACATCCAGT
951	TGCCTTCTTC	GGTATAAAAT	TTCAAGGCAA	AACCGCGGAT	GTCGCGTTCT
1001	GCATCGGCTG	CGCCGCGTTC	GCCTGCCACG	GTGGTGAAAC	GGGCGAACAT
1051	CTCGGTTTTT	TTGCCGACTT	CGCTGAAGAT	TCCTTTGGCG	TGCATACGGC
1101	GTTCCGGGAT	GACTTCGCGC	ACGAAGTCGG	CGAGTTTTTC	AGTCATCGCT
1151	CTTGTTCCCT	TTCTCAGGTT	GGTCAAATGG	GGGTAACGG	CTTACAGTAC
1201	GATTTGGCGG	AAAGCGTATT	CGTAACCGGT	TTCTTGATTG	CAATAAATTT
1251	CTTGAATCGA	CATTTTATTT	CCCTTTTGTA	AAAACATAGG	ATGCGACTAT
1301	ACGCCAAGAT	TTTCGCTATT	AA		

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1	MAVFDEVGRV	AHCGGGVAEQ	CLFLRVVHVQ	<u>EQGARLAEIV</u>	<u>VIVLAVVPVC</u>
51	<u>RVAVDFQRRF</u>	<u>GESGLLLPLA</u>	<u>EAVGFVVRQA</u>	<u>AXVAVGAALP</u>	<u>VAXXAVNXAT</u>
101	RTIDGNLAEV	YAQTVALCVG	VIEQTRLQHF	IXAGADTGNE	VARCEGGLFH
151	IGEEVFGIAV	QLEFAHFNQR	IVFFRPNFGQ	VKRMIRYFFR	VCFRHDLDVH
201	<u>RPFRKLAAFD</u>	<u>GFXXVALMAF</u>	<u>AVVGDDFGGF</u>	<u>FVGQVFNALL</u>	<u>GAEMEFHPKT</u>
251	LACFVPEAVG	MRTEAVHMAV	AGGDAAVAHH	DGNLVQCFCQ	QRPEVPVVCG
301	RAHIGARVAF	DGFVQVGELT	RVAQEEHGRV	VADHIPVAFF	GIKFQGKTAD
351	VAFCIGCAAF	ACHGGETGEH	LGFFADFAED	FGAGVFGDVV	RYGKRTERAR
401	TFGVHTAFGD	DFAHEVGEFF	IQPQILRQQR	AARTGGQAVL	IVGNRRRAVVH
451	QQMGYARAFG	SHRCSFSQSV	QQMGGKRLTV	RFGGKRIRNR	FLDCNKFLFS
501	TFYFPFVKTM	DATIRODFRY	*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

```

      10      20      30      40      50      60
m506.pep  MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF
          |||||:|  ||:|  |||||  |||||  |||||:|  |||||  |||||
g506      MAVFDEVGRIAHCGGVVKQSLFLRVVHQVEQGARLAEVVVIVLAVVPVCRVAVDFQRRF
          10      20      30      40      50      60

```

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAADVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAAPDGFXXVALMAFAVVGDDFGGFFVGVFNALL					
g506	VKRMIRHFFGIGFRHDLDVHRPFRRELAALDGFVQVALMAFAVVGDDFCSFFVGVFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQGFQQRPEVPVVCG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVQVGEFARVAQEEHGRVVADHIPVAFFGKIFQGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVQVGEFARVAQEEHGRVVADHIPVAFFGIEFQRTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVGMGGKRLTV					
g506	IQPQILRQQAARAGGQAVLIVGNRAVVHGMGYGAFGGSHRSCSFQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCCATTTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCCTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGGTTGGC	TGAAATAGTC	GTCATCGTCT	TGGCGGTAGT	CCAGTGC
151	CGCGTCGCGC	TTGATTTTCA	AAGGCGGTTC	GGCGAAGTCG	GGCTGCTGCT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGGCAGGCT	GCCGTAGTTG
251	CCGTCGGCGC	GTCCTTGTCC	GTCGCGCTGG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGGTTG	ACAGGGATTT	GGCGGAAGTT	CACGCCCAAG	CGGTAGCGTT
351	GCGCGTCGGC	GTAATTGAAC	AAACGCGCCT	GCAACATTTT	ATCTGGGCTG
401	GCGCCGACAC	CGGGAACGAG	GTTGCTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTTCGG	GATTGCGGTT	CAACTCGAAT	TCGCCCACTT
501	CAATCAGCGG	ATAGTCTTTT	TTCGGCCAAA	CTTTGGTCAA	GTCAAACGGA
551	TGATACGGCA	CTTTTTCGCG	ATCGGCTTCA	GGCATGACTT	GGATGTACAT
601	CGTCCATTTT	GGAACTCGC	CGCGCTCGAT	GGCTTCGTAC	AGGTGCGGCT

751

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTTG GGTGCGGAAA TGGAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTCCGGGAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGCTTTT TGGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGCGGTC A GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTGTTTCAT
1351 GGTGAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTTCCTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGCGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVCG
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVG RYGRKTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
m506.pep	70	80	90	100	110	120
	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRRATRTVDRDLAEVHAQAVALRVG					
	70	80	90	100	110	120
m506.pep	130	140	150	160	170	180
	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	190	200	210	220	230	240
	VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLDVHRPFRKLAAALDGFVQVALMAFTTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
m506.pep	250	260	270	280	290	300
	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVCG					
a506	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHH DGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGKFKQKTADVAFCIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGKFKQKTADVAFCIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRAARTGGQAVLIVGNRRRAVVGQMGYRAFGGSHRSCSFSQVGMGGKRLTV					
a506	IQPQILRQQRAARTGGQAVLIVGNRRRAVVGQMGYRAFGGXHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTTTCTTG CTTCAGACGG
101 CCTTTGCGCT CTTCGTGCTT GGCAACGGTT TGTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGAATTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCCGC AACCTGCATC GCCATTCCG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTT CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC CGGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGAATTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTTTCTTG TTTCAGACGA
101 CCTTTGCGCT CTTCGTGCTT GGCAATCGTT TGTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCCGC AACCTGCATC GCCATTCCG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTT TCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTA ACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLQQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

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51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng)
 from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVXGLVFLFQTTFFALFVLGNRLFGMGKLLLLLQRQFAAD					
	: : : :					
g507	MLLPALQQGGGFLSGGGFGLVGVQGLVFLQLTAFALFVLGNLFGMGKLLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLLVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRLRCLLVAFDALVQVLLMADLFFQTNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTTCGCTTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTTCTCTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTTCCGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GCGTTTGGA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTCGGGC
251	AGACGCTCTT	CGTGTTCGGC	AACCTGCATC	GCCCATTCCG	CCAATTCGGT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTT	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCCTGCGC	CGCCTGCTTG
401	TCGCGTTCGA	TGCGTTGGTG	CAGGTTTTGC	TGATGGCGGA	TTTGTCTTCT
451	CAAACGGGCA	ATCTGTTCGC	GCAACACGCC	GCGTTTGTG	CCCAATTCGT
501	GCACCGCCTG	CTGCTGCGAC	TGTTCCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQGGG	SFLRGGGFGF	VRQIQGLVFL	FQTTFFALFVL	GNLFGMGKL
51	LLLQRQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LMDALHLRLR	RLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVXGLVFLFQTTFFALFVLGNRLFGMGKLLLLLQRQFAAD					
	:					
a507	MLLLALQGGGSFLRGGGFGFVRQIQGLVFLFQTTFFALFVLGNLFGMGKLLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m507.pep      AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
|||||
a507          AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m507.pep      LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
||:|
a507          LMDALHLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
              130     140     150     160     170     180

m507.pep      VYFVVX
|||||
a507          VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1   ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCGATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1   MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLREFFL
51  HGDVFFVQRV YFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVLF LVEFVDGDFG KPVLA VGFQQ GKLR LFTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1   ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAAAGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GGCGATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1   MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLREFLL
51  HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVLF LVEFVDGDFG KPVLA VGFQQ GKLR LFTAL LLLAAVRGGL
151 LLVFEFGGGF LQNDVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

	10	20	30	40	50	60
m508.pep	MVAFGVDQ	QGFLLQ	QGGLGG	LKLRQL	GLQGLH	FSVLLP
	ALFLNL	REFFLH	NNIFFV	QGL		
g508	MVAFGVDQ	GLLLLQ	QGGLGG	LKLRQL	GLQGLY	AGVLLP
	ALFLNL	REFFLH	GDVFFV	QRV		
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFF	KLDVLL	VVLEL	GLFIGE	GKLLLA	FLPV
	EGLL	FKLGD	LLPV	VLLF	LLVE	FDGDFG
g508	YGFQQL	VELDV	LLVV	LELGL	FIEGK	LLPA
	FLPV	QGGL	LFEP	GDLL	PVVL	FLRVE
	FDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAV	GFQQ	GKLRL	FQTALL	LLAA	VRGGL
	LLLV	FEFGG	GLQND	VV		
g508	KPVLAV	GFQQ	GKLRL	FQTALL	LLAA	VRGGL
	LLLV	FEFGG	GLQSS	DV		
	130	140	150	160		

```

a508.seq
1  ATGGTAGCGT  TTGGCGTTGA  TCAGGGCTTC  CTGCTGCTGC  AACAGGGCGG
51  TTTGGGTGGC  GGCCTGAAGC  TCGCGCAGCT  TGGTTTGCAG  GGTTTGTACG
101 CGGGCGTATT  GTTCCCTACC  CTGCTCCTGA  ATCTGCGCGA  GTTTCTCCTG
151 TACGACAATA  TATTCTTCGT  CCAAACCTCG  TACGGCTTCG  CTCAACTCTT
201 CGAGCTTGAT  GTGCTGCTCG  TCGTTTTGGA  ACTCGGTTTC  ATAGGCAGAG
251 GCAAGCTCTT  GCTGGCGTTC  CTGCCAATCG  AAGGTTTGTT  GTTCAACATG
301 GGCAATTTGC  TGTGCGTAGT  TTTGTTTTTG  CTGGTTGAGC  TTGTGGACGG
351 CGACTTCGCG  AAGCCCGTAT  TGGCGGTTGG  CTTCCAACAG  GGCAAGCTGC
401 GCCTGTTTCA  GACGACCTTG  CTGCTCTTGG  CGGCTGTGCG  CGGCGGTTTG
451 CTGCTGGTGT  TCGAGTTCGG  CGGCGGCTTC  CTGCAAATG  GCATGTGCGT
501 CTGA

```

```
a508.pep
  1  MVAFGVDQGF  LLLQQGGLGG  GLKLRQLGLQ  GLYAGVLFPT  LLLNLRFLFL
51  YDNIFFVQTL  YGFAQLFDGF  VLLVVLGLGF  IGEKLLLAFL  LPIEGLLFLK
101  GNLLLVVLF  LVELVDGDF  KPVLA VG FQ  GKLRLFQTTL  LLLA A VRGGL
151  LLVFEFGGGL  LQNGDVV*
```

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLQGGGLGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLLELGFIFEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
		:				
a508	YGFAQLFELDVLLVVLLELGFIFEGKLLLAFLPIEGLLFKLGNNLLVVLVLLVLDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGKLRRLFQTALLLLAAVRGGLLLVFEFGGGFLQGNDDVXX					
a508	KPVLAVGFQQGKLRRLFQTLLLLAAVRGGLLLVFEFGGGFLQNGDDVXX					
	130	140	150	160		

g509.seq

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```

1   atggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggg aagggtcttc ggtgcgggag atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac ttgacgcgg cggtgggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggg cgcgcggcat ccagccgcgg attttaagg
651 tattcggaac gcggacatcg ggataggcgg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggacg ggcttcaaaa aagctcatcg ggaagatgga
751 cacgcggttg ttgatttcgt cgttgacgct gatttctgtg cggcgcgttt
801 cgctggtctg ccacaagccc agaagcacgg tgtcgatttc gcggcgcagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcgttgc acttcggctc
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgtcgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggcggcg atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggtctctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcggcc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcatcgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagttga acgcgcggcg acggcggcgt
1501 tacaatcgcc cgcaactggt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgcccct gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1   MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NORRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNPV QMPHPCQTVH TLTHVVKCR LKLNAARRRR
501 YNRPLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEFRRAY
551 FGRRLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1   ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTTGCT CTTCTGTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTTC
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTCTG TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAAATC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GCGCGGGGCG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CCGATGGAGA
501 GCGGCAGTTC CCGGTAGAGT TTGTGAGTTC CGCCGCGATA GAAGCGGAAC

```

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```

551  ACGGCATCGG  CGTGGCGGCG  GAAGGCAAAG  CGCAGGGTTT  CGGCAGAAAC
601  AAACGGATTG  CCGTCGCGGT  CGCCGCCGAT  CCAGCCGCCG  ATTTTGAGGA
651  TGTCCGAAC  GCGGACGCCG  GGATAGGCCG  TCTGAAAGTC  GTGTTCCATC
701  TTGCGGTAGA  GCTTGGGCAG  GGCTTCGAAA  AAGCTCATCG  GGAAGATGGA
751  CACGCCGTTG  TTGATTTCGT  CGTTGACGCT  GAGTTTGTGG  CGGCGCGTTT
801  CGCTGGTCTG  CCACAAGCCC  AGCAGGATAG  TGTCGATTtC  GCgGCGCAGC
851  CGTGCCAGCG  CGTCGGCATT  GGTGCAGCGT  TCgCGTTGCG  GCAACAGTGC
901  GCGGATGCGG  CGGTTGAAGC  TTAAGACGGT  TTGGCGTTGC  ACTTCGGTCG
951  GGTGCGCGGT  CAAAACGGCG  GTAACGGACG  TATTGTCCAA  CTGCCGCTGC
1001 ACCGATTTCG  CGTCGGCTTT  CCCCCTTTG  AGCCTGCGGA  CGGTTTCCGT
1051 CAGGCTGCCT  TCCGCGCCGC  CGCGTCCGGC  TTCTTCGTGG  ATTTGGCGGC
1101 GCGGTTTCGT  GTGCACGTCT  TCGGCGATGT  TCAAAATCTG  GGCGAACAGG
1151 CCGCAGGCCA  AGGTAAATC  GTGGGTTTGT  TGTTTCGTCCA  ATTGCGGCAA
1201 TACTTTTCA  ATCAATGCCG  CGCTGTCGTC  GGAAGTGGAC  AAGAGTTTGA
1251 CTGTTTCGAC  AACCAACGGC  GAGGCTTCTT  CGTGCAGGAG  GTTGAACAGG
1301 GATTGTTTCA  GAAATTCGCG  GTCCGCCGCC  AAAGCCGCGT  CCTTTGGATT
1351 GTTCAGAATA  TGCAGTTGCA  TGATTTTCT  CTCTCGTCTG  CCGTAAATAT
1401 GTTAAATGTA  CCCCAAATGC  CGCATCCGTG  CCAAACCGTT  CACACTTTAA
1451 CCGCCCGTGT  CCCGAAATGC  CGTCTGAAGT  TGAACGCCGC  CCGACGGCAG
1501 CGTTACAATC  GCCCGCAACT  GTTTTtTTCC  GAACATCATC  ATGACCACGA
1551 CCGAACACGA  CAACGACGAT  GCATTCTGCG  TCGCGTACAG  CCGCCACATC
1601 CTCTTGACG  AAATCGGCAT  CGAAGGGCAG  CAGAAACTTT  CCGCCGCGCA
1651 TATTTTGGTC  GTCGGCTGCG  GCGGTTTGGG  TGCCGCCGCA  CT.GCCCTAC
1701 CTTGCCGCTT  CGGGTGTCGG  CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.pep

```

1  MVAVCDKRAV  QRTLMAQFAQ  QGGLFLLFVQ  AVVVVFQACVL  EKLGNHIGVF
51  ACVLAQVERH  HVKAEHGYGT  DEVCQTAFGK  QTAAVVDKGT  LQFFQIIQKL
101  LCRSIRLEKA  EFAAHTQTER  ARFAHSARHN  VGDGAAVGFF  GAGDFFVGRF
151  VGQRRYIAVD  FDAADGERQF  AVEFVEFAAI  EAEHGIGVAA  EGKAQGFGRN
201  KRIAVAVAAD  PAADFEDVRN  ADAGIGRLKV  VFHLAVELGQ  GFKAHREDG
251  HAVVDFVVD  EFVAARFAGL  PQAQQDSVDF  AAQPCQRVGI  GAAAFALRQQC
301  ADAAVEAXDG  LALHFGRVRG  QNGGNRIVQ  LPLHRFAVGF  PRFEPADGFR
351  QAAFRAAASG  FFVDLAAAFV  VHVFGDVQNL  GEQAAGQGXI  VGLLFVQLRQ
401  YFFNQCRVV  GSGQEFDCFD  NQRRGFFVQE  VEQGLFQKFR  VRRQSRVLWI
451  VQNMLHDFS  LSSAVNIVNV  PQMPHPCQTV  HTLTARVPKC  RLKLNAARRQ
501  RYNRPQLFFS  EHHHDHDRTR  QRRCPAAVQ  PPHPLGRNRH  RRAAETFERR
551  YFGRRLRRFG  CRRTXPTLPL  RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

```

              10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQGGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      MVAVCDERAVQRTLVAQFAQGGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
              10      20      30      40      50      60

              70      80      90      100     110     120
m509.pep  HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTLQFFQII EKFLGRSIRLEKAEFAAHTQTER
              70      80      90      100     110     120

              130     140     150     160     170     180
m509.pep  ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      ARFAHSARHNVGNAAVRFFGAGDFFVRRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV
              130     140     150     160     170     180

```

758

	190	200	210	220	230	240
m509 . pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
g509	KTEHGIGVAAEGKAQGFARNKRIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509 . pep	GFEEKAHREDGHAVVDFVVD AEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
g509	GFKKAHREDGHAVVDFVVD AEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509 . pep	ADA AVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRFEPADGFRQAAAFRAAASG					
g509	ADA AVEIQNGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRFEPADGFRQAAAFCCVVGAG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509 . pep	FFVDLAAAFVHVFGDVQN LGEQAAGQGXI VGLLFVQLRQYFFNQCRVAVGSGQEFDCFD					
g509	IFVDLAAAFVHVFGDIQN LGEQPAKQRQIVGLPFVQLRQYFFNQCRVAVGSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509 . pep	NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV					
g509	NQRRGFFVQEVEQGLFQKFRVRRQSRVLRIQDMQLHDFPLI - AVNTVNVNVPQMPHPCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509 . pep	HTLTARVPKCRLKLNAARRQRYNRPLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH					
g509	HTLTTHVPKCRLKLNAARRRRYNRPLFFSEHHHDHRTQRRTTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509 . pep	RRAAETFRRAYFGRRLLRRFGCRRTCPTLPLRV SAR					
g509	RRAAEAFRRAYFGRRLLRIGRRRPCPISPPRG SAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

a509 . seq	
1	ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51	ATTCGCGCAA CAGGGCGGCT TGTTTTTGCT CTTCGTTGAG GCTGTTGTAG
101	TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTTT
151	GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201	ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGCAAG CAGGCGGCTG
251	CCGTTGTCGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301	TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351	AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401	GCGCGACGGT AGGGTTCTTC GGCGCGGGCG GTTTCTTCGT CGGGCGATTT
451	GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501	GCGGCAGTTC GCGGTAGAGT TTGTGAGTTC CGCCACGGTA AAAACGGAAC
551	ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601	GAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651	TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTCCATC
701	TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751	CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801	CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGGCGCAGC
851	CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

a509.pwp

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	70	80	90	100	110	120
a509	HVKAEHGYGTDEVCGTAFGKQTAADVDDKGTLLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
	70	80	90	100	110	120
m509.pep	130	140	150	160	170	180
a509	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
	130	140	150	160	170	180
m509.pep	190	200	210	220	230	240
a509	EAEHGIGVAAEGKAQGFGGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
m509.pep	250	260	270	280	290	300
a509	GFEKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
	250	260	270	280	290	300
m509.pep	310	320	330	340	350	360
a509	GFKKAHRKDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					

760

```

m509.pep      ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
              |||||  ||||||||||||||||||||||||||||||||||||||||||||
a509           ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
              310      320      330      340      350      360

              370      380      390      400      410      420
m509.pep      FFVDLAAAFVVHVFGDVQNLGEQAAGQGIXIVGLLFVQLRQYFFNQCRAVVSGQEFDCFD
              |||||  ||||||||||||||||||||||||||||||||||||||||||||
a509           FFVDLAAAFVVHVFGDVQNLGEQAAGQGIXIVGLLFVQLRQYFFNQCRAVVSGQEFDRFD
              370      380      390      400      410      420

              430      440      450      460      470      480
m509.pep      NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNPQMHPHCQTV
              |||||  ||||||||||||||||||||||||||||||||||||||||||||
a509           NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLI-AVNTVNVVQMHPHCQTV
              430      440      450      460      470

              490      500      510      520      530      540
m509.pep      HTLTARVPKCRKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH
              |||||  ||||||||||||||||||||||||||||||||||||||||||||
a509           HTLTARVPKCRKLNAARRQRYNRPQLFXSEHHHDHRTQRRCIPAAVQPPHPLGRNWH
              480      490      500      510      520      530

              550      560      570
m509.pep      RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
              |||||  |||||  |||  :|||
a509           RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
              540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggattattcct gccccaagcg
51 ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggagggttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg atttttcgc tgtccgcgac
201 gcggccgcct tcgcggatgg cttecgcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttgctc gatgttcac ctttaatect
351 tattgctgcg tttcctgccg ttgggggagg cgcgtgccca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVDLF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCGCGGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTACGCCG
301 GCGGTGCAwG ACTTCsAtGT GGACTTGTTG GATGTTGATC CTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG CGCGTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	:					
g510	MPSRTPQGKRGYSCPKRDSA FWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTATTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCGCGGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTCAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTT GATGTTATC CTTAATCCT
351 TATTGCTGCG TTTCTGCGG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA FWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtggt gccggcgat cctccgtgtg

```


763

250

260

270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
  1 ATGAAAGTGC TTGTTT TAGG TGCTGGTGTG GCCGGCGTAT CTTCCGCGTG
 51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCACT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TCGCTGGCA CGCGTTACCG
551 CCAAATTGCG CGGCGGCCTG CACCTGCCCG CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATG TGTACAGAAA AGGCGGTACG
651 GTTTCATTTT AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
  1 MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
 51 YTPWAAPGI PTKALKWLFK SHPLLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMF RFEAQTMNF EGRKKGTLQI FRQKEVEAA
151 KQDIAVLERY GVPYRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVPYRLKPEECAEFEPALARVTAK
                                |||
a512      TGMNFEGRKKGTLQIFRQKEVEAAKQDIAVLERYGVPYRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

              40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGRLRIKTVETKQGGLK
              |||
a512      IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQNISRIDHNGRLRIKTVETKQGGLK
              190      200      210      220      230      240

              100      110      120
m512.pep      QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
              |||
a512      QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
              250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
  1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTGCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTT GGC GCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG
451 CTCTGCCcat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

764

501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKGK DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKGK DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYG DLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYG DLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFM FAFSTVIGNY AYAESNVQFI KSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFM FAFSTVIGNY AYAESNVQFI KSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIM AWINLVAILL LSPLAFMxLRD YTA KLKMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIM AWINLVAILL LSPLAFMxLRD YTA KLKMGKDPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTTGTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTACTCGGCG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCGG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTTGCCCT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCGTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG FVQFRLEGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGFVFEA VQNTNIADTV KAAGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIEMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMIMQLG VFVDTIIVCS CTAFIILIYQ QPYGDLGAA LTQAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMIMQLGVFVD
|||||

a513
260 270 280 290 300 310
DAAAGLLGGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMIMQLGVFVD

40 50 60 70 80 90
m513.pep
TIIIVCSCTAFIILIYQQPYGDLGAA LTQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY
|||||

a513
320 330 340 350 360 370
TIIIVCSCTAFIILIYQQPYGDLGAA LTQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL
|||||

a513
380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL

160 170 180 190
m513.pep
LSPLAFMLLDYAKL KMGKDPEFKL SEHPGLKRRI KSDVW
|||||

```

766

a513 LSPALFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgccgcc ggcgttgccc gtggtctgca
51 ttccgagttt gcgcgcgctg taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgtcgatcag gaaactgctt
251 tggcggtaga gcgcgccgcc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcaaagtgc ggcggcgccg ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
451 gtagtcgcgc tgcattccgt ttctgcgcgc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgacc ggcgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttgcattgt tttgccaagc
651 cgacggcgcc tccgtatcc aaatccatt cgtggtaaag gtcggggtcg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
751 ttccgcggtg tggcgggcga tgtcggcgcc ggcgcggacg gtgtcgcgca
801 gggcttgctt ggagaagtcg gcggtgccgg cgcggccttt gcgtttgccg
851 acgtaaaccg taatgtccag cgatttgcct tgctggaact cgatttgttc
901 gatttcgccc aagcgacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagtgc ggaagcgggt tggttgaaca gcataacaat
1051 ctttcttggg ggagcgttgt ggcattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
51 IAAAEERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDAAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVA*F

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCCGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACCG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGC CGGGCGGCGG TTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG GTTGCCGTA AACGTATTGG
401 TAATGGCCCG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGCTCATC
451 CTCGTTCAAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTk
501 CCGTATCCAA ATCCATTTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCCTG CTGGAACCTG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTG GCTGAAATCG GCTTCGGCGG
801 CCGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGCGGCG GCAGAGGTCTG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFDG VLQGFGEVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

m515.pep				10	20	30
				GKSGGCAFFA	QVEEIGQDFS	ADAVDQETALA
				::		
g515	AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDV	RFFA	QVEEIGQDFF	ADAVDQETALA		
	30	40	50	60	70	80
m515.pep		40	50	60	70	80
		VERAAGECADEVSDKTARN	GGIEEDGVAA	CRDAAAESA	QSAAGGGLTD	GFGAVHIRMAA
g515		VERAAGECADEVSDQPAR	NGGIEEDGVA	ACRDAESA	QSAAGGGLTD	GFGAVHIRMAA
	90	100	110	120	130	140
m515.pep		100	110	120	130	140
		GGIVPVVALHAVFVGGNDA	AGNAVVRALP	VCGKTVGVAV	NVLVMAGLHRR	AFGVFDALIL
g515		GGIVPVVALHSVFVGGDDA	AGNAVVRALP	VCGKTVGVAV	NVLVLSGLHRR	AFGVFDAAVR
	150	160	170	180	190	200
m515.pep		160	170	180	190	200
		VQGGFLFALFCQADGGXRIQ	IPFVVKVGVA	DVFCHQTGIG	KSGATVFGGV	VAGDVGDFDG
g515		VQRCLFALFCQADGGFRIQ	IPFVVKVGVA	DVLRHQLGV	GKSGATVFGGV	VAGDVGFGGADGV
	210	220	230	240	250	260
m515.pep		220	230	240	250	260
		LQGFGEVVGSTGAFAFAD	VNGNVQRLVL	LELDLXDXAQ	PHADALSQXF	AEIGFGGGCAR
g515		AQGLFGEVVGAGAAFAFAD	VNGNVQRFVL	LELDLDFDFA	QAHADALSER	FAEVFGGGRAR
	270	280	290	300	310	320
m515.pep		280	290	300		
		RFCQVERAAAEVEEFGSGV	VEQHRNLSXX	CFAAF		
g515		CFCQVERAAAEVEEFGSGV	VEQHNNLSW	SVVAF		
	330	340	350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTGA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGC GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGC

```


551	TAAACGTATT	GGTAATGGCC	GGTTTGCACC	GCCGCGCCTT	CGGAGTTTTC
601	GATGCGCTCA	TCCTCGTTCA	GGGCGGCTTG	TTTCGATTGT	TTTGCCAAGC
651	CGACGCGGCG	TTCCGTATCC	AAATCCCATT	CGTGGTAAAG	GTCTGGGGTCG
701	CCGATGTGTT	GCGCCATCAA	CTCGGGGTCG	GCAAGTCCGG	CGCAACCGTC
751	TTCTGGCGGTG	TGGCGGGCGA	TGTCNNNNGC	GGCGCGGACG	GTGTCGCGCA
801	GGGCTTGTTCT	GGAGAAATCG	GCGGTGCCGG	CGCGGCCTTT	GCGTTTGCCG
851	ACGTAAACGG	TAATGTCCAG	CGACTTGTC	TGCTGAAACT	CGATTTGTTCT
901	GATTTCTGCC	AGCCGCACGC	TGACGCTTTG	TCCCAATGAT	TCGCTGAAAT
951	CGGCTTCGCG	GCGCGTTGCG	CCCGTCGCTT	TTGCCAAGTC	GAGCGTGCGG
1001	CGGCAGAGGT	CGAGGAGTTC	GGAAGCGGTG	TGGTTGAACA	GCATAGAAAT
1051	CTTCTCTGAT	GATGCTTTGC	GGCATTTTAA		

a515.pcp

m515/a515 92.1% identity in 304 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGC GGCGCGGC GGT TTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAGTGTCG GGT TTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGTGCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGC GCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAGTCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGATAACGC TAATGTCCAG CGATTGTGCC TGCTGGAACG CGATTGTGTC
901 GATTTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCCTGAAGT
951 CGGCTTCGGC GCGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGC GG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNVNLNHEA RRGNTFRIK
51  IAAAEERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGTTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGC GGCGCGGC GGT TTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAAATGGC GGT TTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGTGCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GCGTTTGACG GTGCTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCG TGCTGGAACG CGATTGTGTC
901 GATTTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNVNLNHEA RCGGNAFRIK
51  IAAAEERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSAFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVVK VGVADVFC HQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGF GEVGSTGAFF AFADVNGNVQ RLVLLLELDF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

	10	20	30	40	50	60
g515-1.pep	MVQIQVVRAAGVARGLHSEFARAVTAEIEAFDNVNLNHEARRRGNTFRIKIAAAERAGDV					
	: : : : :					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLFHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFLVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGDFGVLQGGFGEVGGSTGAFAFADVNGNVQRLVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GGCCTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACGTCTGA GGAATAGCC TCCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCCT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGCGCGC GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGATGCG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCCC
551 TAAACGTATT GGTAATGGCC GGTGTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TCGGCGGCTT TGGCGGGCGA TGTCGGCGGC GGCAGCGGAC GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTGTGCC TGCTGAAACT CGATTTGTTC
901 GATTTGCCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVAVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNNGGIED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					
	70	80	90	100	110	120

m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
	70 80 90 100 110 120
a515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
	130 140 150 160 170 180
a515-1.pep	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGADVLRHQ
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGADVLRHQ
	190 200 210 220 230 240
a515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
m515-1	TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
	250 260 270 280 290 300
a515-1.pep	DFAQPHADALSQX
m515-1	DFAQPHADALSQX
	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1  atgttggtcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgcccc attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgcgc tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg ccgcccacca agccctgccc gtcaaattcg aagcgcccg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaa
451 ctcgacaatc ggaccattta cacgcgctgc gtatccgcca aaggcaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagt
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgcg gtgctggtct tgccatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1  MLFRKTTAAV LAATLILNGC TMMLRGMNP VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIIY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1  ATGTTGTTCC GTAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCTT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAATCTG AATCGCCTGG
351 CAGCCAGAAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

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501	CTACGCCACA	CCGCAAAAAC	TGAACGCCGA	TTACCATTTT	GAGCAAAGTG
551	TGCCTGCCGA	TATTTATTAC	ACGGTTACTG	AAGAACATAC	CGACAAATCC
601	AAGCTGTTTG	CAAAATATCTT	ATATACGCCC	CCCTTTTGTG	TACTGGATGC
651	GGCGGGGCCG	GTACTGGCCT	TGCCTGCGGC	GGCTCTGGGT	GCGGTCGTGG
701	ATGCCGCCCG	CAAATGA			

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep						
1	MLFRKTTAAV	LAATLMLNGC	TLMLWGMNNP	VSETITRKHV	DKDQIRAFGV	
51	VAEDNAQLEK	GSLVMMGGKY	WFVVNPEDSA	KLTGILKAGL	DKPFQIVEDT	
101	PSYARHQALP	VKLESPGSGN	FSTEGLCRLY	DTDKPADIAK	LKQLGFEAVK	
151	LDNRTIYTRC	VSAGKGYAT	PQKLNADYHF	EQSVPADIIY	TVTEEHTDKS	
201	KLFANILYTP	PFLILDAAGA	VLALPAAALG	AVVDAARK*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKQIRAFGVVAEDNAQLEK					
	: : :					
g516	MLFRKTTAAVLAATLILNGCTMMLRGMNPNVSQTITRKHVDKQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
	: : :					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m516.pep	FSTEGLCIRYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	: :					
g516	FSTGGLCIRYDTGRPDDIAKLKQLEFAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	130	140	150	160	170	180
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
	: : :					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLILDAAAVLVLPMALIAAANSSDK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

```
a516.seq
  1  ATGTTGTGCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
51  GAACGGCTGT  ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
101 CGACCGCCCG  CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
151 GTTGCCGAAG  ACAATGCCCA ATTGGAAGAA GGCAGCCTGG TGATGATGGG
201 CGGGAATAAC  TGGTTCGTGC TCAATCCTGA AGATTCCGGC AAGCTGACGG
251 GCATTTTGAA  GGCCGGGTG  GACAAGCAGT TTCAATGGT  TAGCCCAAG
301 CCGCGCTTTG  CCTACCAAGC CCTGCCGGTC AAACCTGAAT CGCCCGCCAG
351 CCAGAATTTT  AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
401 CTGCCGACAT  CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTCGAACTC
451 GACAATCGGA  CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
501 CGCCACACCG  CAAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
551 CTGCCGATAT  TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
601 TTGTTTGAAA  ATATTGCATA TACGCCACC  ACGTTGATAC TGGATGCGGT
651 GGGCGCGGTG  CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
701 CCTCAGACAA  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1 MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKQFQMVPEP
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVPADIIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

          10      20      30      40      50      60
m516.pep  MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDKQIRAFGVVAEDNAQLEK
          10      20      30      40      50      60
a516      MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDKDKQIRAFGVVAEDNAQLEK
          70      80      90      100     110     120
m516.pep  GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
          70      80      90      100     110
a516      GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALPVKLESPASQN
          130     140     150     160     170     180
m516.pep  FSTEGLCLRYDTPDKPADIACLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
          120     130     140     150     160     170
a516      FSTEGLCLRYDTPDKPADIACLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
          190     200     210     220     230     239
m516.pep  EQSVPADIIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
          180     190     200     210     220     230
a516      EQSVPADIIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1 atgcatcggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgatt tgatgttttt gggcaggtcg atttggtctg
201 tgtcgccggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagaggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1 MHRVSDGIGV SVVFCRFVGF DDFLHQRPMD NVFAGEGMEI QSCHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACCTTGTGCA GTTCTCTACG
151 CGCATCTTTT AATCCCAGATT TGATGTTTTT GGGCAGGTCTG ATTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCTGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GCGAGCGGG GCGATTTCAA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGSVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCCGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF					

775

	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttgtgtct
51  ttccgcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac cattttttca gcataaatat tctgaccgga
151 agagcggcat ctccacgggc aaccgtgttc agactgcatac aggcgggtacg
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcgggcaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKKSDFPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCA GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCCTGTTC AGACGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRRERR RAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
                |||||
g518           MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
                10         20         30         40         50         60

m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
                ||| || : ||:| ||||| ||| |||||
g518           RLHQAVRFHKMPKTISKMRNRYAVRITPPPRATLHYNRLPL-----
                70         80         90         100        110

m518.pep      120         130
                GRKKSDFPAFVAESEI
                |||||
g518           --KKSDFPAFVAESEI
                110

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCCG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCAGGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCRTINKRRRNYAVRITPSSXAATRHYNRLPSAAGLVRERRRRCVILSNG					
a518	RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatatt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actggtgacg
251 gcatcatcta tttccaagta accgatccca aactcgctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcgcctcc tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

777

101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEGRKIEQINLAS
 201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAN
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)
 1 ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CCGCTTTGGA CGAGGCGGCC GGGgCTTgGG
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAACGCGC
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCa
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
 401 TCCGTCAAAT TGCCGCCGCC CTCAAACCC AAGGCGGTGC GGATGCGGTC
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC
 551 TGATTCTGCG CCGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASQREAE				
	150	160	170	180	190	200
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV				
	210	220	230	240	250	260
m519.pep		160	170	180	190	200
		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL- ISAGMKIIDSSKTAK				
g519		NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
	270	280	290	300	310	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT

```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAGATT CCGGAACAAT ACGTCGCCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKSFV VIPQGEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||:|||||
a519 YFQVTPDKLSYGS SNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRS MQAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||:|||||
a519 GAWGVKVLRYEIKDLVPPQEILRS MQAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
|||||:|||||
a519 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
|||||:|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCGGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA

```

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTAGACGT
 201 ACCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTCG GCTTGGACG AGGCGGCCGG GGCTTGGGT
 451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 CTTTCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCCG AGAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTGTGC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996; *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1   atgcctgcmc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcm
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccc ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcaacagt tcgaacgat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaa gcggcgggaa atttcctctg cgttgccccg caacacggca
501 gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1   MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1   ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCTG TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520
      10      20      30      40      50      60
m520.pep MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW
          |||||::||| ||||| ||||| ||||| ||||| ||||| |||||
g520      MPALLSIRANALPFSRISERMKLLVPLIMPAMDILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90     100     110     120
m520.pep TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520      TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          70      80      90     100     110     120

      130     140     150     160     170     180
m520.pep SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR
          ||||: ||:: : ||||: ||||| ||||| ||||| ||||| |||||
g520      SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
g520      CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51 CATTTCCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACGCCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCAGT TCGAACGGAT CTTTGACAAA GGCTG.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGT GGGCTTTTTC
351 TCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```


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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLRAT	SSNGSLTKAADG	QIWRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSRAT	SSNGSLTKAADG	QVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTAA	APPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	VPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGCG CAGCGGGAAG
151 ATTTCGTTCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGCG GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGCGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSRAT	SSNGSLTKAADG	QVCRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSRAT	SSNGSLTKAADG	QVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTAA	VPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	VPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

```

1  ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG
51  CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

```

151	CCCCCAATCG	GCAACTACAG	CAGCGAACGC	TATATCCTGC	CCCAAACTCC
201	CGAACCGGCA	CCATCACCGT	CAAACGGCGG	ACAGGCTGTC	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AATCCAATAC	GCCGCTCAA
301	CAAGCACCTG	TAAATAACAG	CAGACGCTCC	ATTCTcgaag	caGaatttaag
351	cAatgaacgc	aaagccctGa	ctGaAGCCCA	AAAAATGTTA	TCACAagcac
401	gtctGGCACA	AGGCgGcaAC	AtcaaCCatc	aaaAaatcaa	cgcattgtaa
451	AGCAATGTTt	tggaAGACA	GCAAAATaTC	Caagcactgc	aaaGAgAATt
501	GGGACGTATG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

g521n.pep

```

1  MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTDL
51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

m521.seq

1	ATGAAATCAA	AACTCCTCTT	AATCCTAATC	AACTTTTCCC	TGATTTC AAG
51	CCCATTGGGT	GCGAATGCGG	CCAAAATCTA	sACCTGCACA	ATCAACGGAG
101	AAACCGTTTA	CACCAsCAAG	CCGTCCAAAA	GCTGCCACTC	AACCGATT TG
151	CCCCCAATCG	GCAACTACAG	CAGCGAACGC	TATATCCC GC	CCAAACGCC
201	CGAACCGGTA	TCATCACCGT	CAAACGGCGG	ACwGGTTGTC	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AATCCArTAC	GCCGCCGCCG
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAAGCAT	TGGTTGAAGC	CCAAAAAATG	TTATCACAAG
401	CACGTCTGGC	AAAGGGCGGC	AACATCAACC	ATCAAGAAAT	AAATGCATTA
451	CAAAGCAATG	TATTGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAGGGA
501	ACTGGGGCGT	ATGTAA			

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pep

```

1  MKSKLLLLIL NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL
51 PPIGNYSSER YIPPQTPEPV SSPSNGGXVV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521.pep	MKSKLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
		:		:		
g521	MKSKLPLILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
		:	:		:	
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTTP-QQAPVMNSRRSILEAEELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	:	:				
g521	RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDROQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTC AAG

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```

51  CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTK PSKSCLSTD
51  PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQQN IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTKPSKSCHSTDLPPIGNYSSER					
a521	MKSCLPLILINFSLISSPLGANAAKIYTCTINGETVYTKPSKSCLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRRSILETELSNE					
	: :					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttggcggt gtcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgcgtga aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcgggcg aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcgat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWWILALLAS TALLSQCAM
51  KPQAKQKIVE SCMKNIPIFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCAATG CCGCATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

m522.pwp

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAM
51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
101 LDRLSEKQIR SFGKLGAEQEQ LDLLGGANAF EARDKOCVAD LKSE*

Homology with a predicted ORF from *N. gonorrhoeae*

m522/g522

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1	ATGACTGAGC	CGAAACACGA	AATGCCGACG	GAAGAGCAGG	TTGCCGCGCG
51	CAAAAAAGCA	AAAGCCAAAA	TCCGCACCAT	CCGCATTGG	GCATGGGTCA
101	TTTTGGCGTT	GCTCGCTTCA	ACCGCCCTGC	TCTCCCAATG	CGCGATGTCC
151	AAACCGCAGG	CAAAACAGAA	AATTGTCGAG	TCTTGGGTGA	AGAATATTCC
201	GTTTGGCCGAA	AAATGGCAAA	ACGATTTCGG	GGCCCGCGGT	TTAGATTCAA
251	ACAATACCCG	CCTTACCGTC	GACTACTGCA	AATGTATGTG	GGAGCAGCCT
301	TTGGACAGAT	TGAGCGAGAA	ACAGATTAGT	TCCTTCGGCA	AACTCGGCGC
351	ACAAGAACAG	CTTGACTGTC	TCCGGCGCGC	AAATGCCTTT	GAAACGCGAG
401	ACAAGCAGTG	TGTTGCCGAT	TTGAAATCAG	AATAA	

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAM
51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNRLTV DYCKMWEQP
101 LDRLSEKQIS SFGKLGAEQ LDLLGGANAF ETRDKOCVAD LKSF*

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAUVILALLALTALLSQCAMSKPQAKQKIVE					
a522	MTEPKHEMPTEEQVAARKKAKAKIRTIRIWAUVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIIPFAEKWQNDLRARGLDSSNNTRLAVDYCKMWEQPLDRLSEKQIRSFGKLGAEQ					
a522	SCVKNIIPFAEKWQNDLRARGLDSSNNTRLTVDYCKMWEQPLDRLSEKQISSFGKLGAEQ					
	70	80	90	100	110	120

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```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51 gacgggaacg gtttatcttt tggttgtag cgcggtttg gcgggttcgg
101 gcattgccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcaactgctt ccgcgtggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcatcgccc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVSAAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYEILRYT GGNRYEVFVR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGT CCGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVSAAL LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLT AGQYVEILRH TGGNRYEVFY RGTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng)

from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLTDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|||||

```

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g523 LIVRKEGNLLIIANPX
 130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
  1  ATGACTGTAT GGTTCGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
 51  GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101  GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151  GCTCTGCTTT CCGCGCTGGG TATTGTTTC GTACACGCCA AAACCGCCGT
201  GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251  CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301  GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351  AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401  AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
  1  MTVWFVAAVA VLIIELLTGT VYLLVSAAL AGSGIAYGLT GSTPAAVLTA
 51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101  GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	: : : : : : : :				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
	:				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
  1  atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
 51  agcggcggct gccgaaatgg ttcaaatacg aggcggcagc taccgcccgc
101  tttatctgaa aaaagatacc ggctgatta aagtcaaacc gttcaaactg
151  gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201  ccccaaatgg caaaaaggca ggatcggttc caaacaggca gaaccgcgtt
251  acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301  ggcaattga aacagccggt taccaatatt tcctggtttg ccgccaacgc
351  ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401  ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccg
451  ctacaaccgc actattctcg attggatgac cgacggcgga cggaaaggcc
501  tgacgatgt cggcaaagca ccgccgaac tactggggtg tttatgat
551  gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
  1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101  GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTR
151  LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

```

m525.seq
  1 ATGAAGTATG TCCGGTTATT TTWCTCGGC GCGGCACTCG cCrCACTCA
 51 ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGc TACCGCCCrC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAAC TG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAaCGC
351 CTAtTGC GCCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

```

m525.pep
  1 MKYVRLFXLG AALAXTQXAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQXRLKRTR
151 LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

```

m525/g525

      10      20      30      40      50      60
m525.pep  MKYVRLFXLG AALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
          |||||  ||: || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
g525       MKYVRLFFLG TALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90     100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVTNVSXAAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g525       AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVTNISWFAANAYCA
          70      80      90     100     110     120

     130     140     150     160     170     180
m525.pep  AQGKRLPTID EWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g525       AQGKRLPTID EWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCQSTARTTGV
          130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
g525       FMICTGX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

```

a525.seq
  1 ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
 51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAAC TG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTCG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      ||::||: | |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
      70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCQXVARTTGA
      130     140     150     160     170     180

m525.pep FMICTGX
      |||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGGCGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAAC TG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCTT
501 GCACGATGTC GGCAGAGACC GCCCGAATA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTGGGGGC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCACAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGRRGLHDV GKDRPNYWG VYDMHGLIEW TEDFNSSLLS
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGGCGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAAC TG
```


792

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGRKGLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
g525-1	MKYVRLFFLGTALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTVSWFAANAYCA					
g525-1	AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTNISWFAANAYCA					
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV					
g525-1	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKDRPNYWGV					
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
g525-1	YDMHGLIEWETEDFNSSLSSGNANAQMFCSGASVGSDDSSNYAAFLRYGIRTSLSQSKYV					
	250					
m525-1.pep	LHNLGFRCTSRX					
g525-1	LHNLGFRCASRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1 ATGAAGTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCC GATGGCGACC GGAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```


794

```

201 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGty GrTwATaTCG
251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGT TT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep

```

1  MVLPV SFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR XRVL F
51  IQKPRXGCRA ALVVQTFNXD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPV SFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR XRVL F IQKPRXGCRA					
g527	MVLPV SFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCR FRV FFIQKPR LGCRA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNXD FIGKXNXASV XXIADVYGFT VFDLRAVYLN PTQFDVLLRK GTGLEKTCRP					
g527	ALVVQTFNLD FMGK GIERQVDNIADVYGFT VFDLRAVYLN PTQFDMLLRK GTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR IVLVFHTILF EIIEFVSSLA					
g527	KPFVQPHGGR IVLVFHTILF EIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq

```

1  ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTCCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGT TT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep

```

1  MVLPV SFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR FRVL F
51  IQKPR LGCRA ALVVQTFNLD FIGK GIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPV SFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR XRVL F IQKPRXGCRA					
a527	MVLPV SFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR FRVL F IQKPR LGCRA					
	10	20	30	40	50	60

795

	70	80	90	100	110	120
m527.pep	ALVVQTFN	XDFIGKXNXASVXXIADVY	GFTVFDLR	AVYLNPTQ	FDVLLRK	GTGLEKTCRP
			:			
a527	ALVVQTFN	LDFIGKGI	ERQVDNIADVY	GFTVFDLR	AVYLNPTQ	FDVLLRK
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHG	GRIVLVFHTILFEIIEFV	SSLAX			
a527	KPFVQPHG	GRIVLVFHTILFEIIEFV	SSLAX			
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcgggtg gtatgagtgt ttgtccttgt
101 ccggttggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggccgagaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

m528/g528

	10	20	30	40	50	60
m528.pep	MEIRAIKYT	AMAALLAFTVAG	CRLAGWYECSS	LTGWCKPRKP	AAIDFWDIG	GESPPSLGD
g528	MEIRVIKYT	ATAALFAFTVAG	CRLAGWYEC	LSLSGWCKPR	KPAAIDFWD	IGGESPLSLED
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGN	SSVRANEYESA	QKSYFYRKIG	KFEXCGLDWR	TRDGKPLIET	FKQGGFDCLE
g528	YEIPLSDGN	RSVRANEYESA	QKSYFYRKIG	KFEACGLDWR	TRDGKPLVER	FKQEGFDCLE
	70	80	90	100	110	120

796

```

m528.pep      K
              |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

```

              10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              |||||||
a528           MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED
              10      20      30      40      50      60

              70      80      90      100     110     120
m528.pep      YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
              |||||||
a528           YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK
              70      80      90      100     110     120

m528.pep      K
              |
a528          KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1  ATGGAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCTTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

797

```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GCGCGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          ||||:||||| |||:||||| |||||:||||| |||||:||||| |||||:||||| |||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGCGCGAGA GTCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

g529.seq (partial)

```

1  atgacccata tcaaaccgct cattgccgag ctgcactca tcgggcttgc
51  cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggtcgcaccg cctgatcaaa ctggaagtc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc ggttcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgctgt tgacggcaaa tccccgcgcg aaatctccgc
351 cgctttctg.

```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

g529.pep (partial)

```

1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51  DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

m529.seq

```

1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTG CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGC ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCCAAGTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCGC
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGTCAA AACACCGAAC GCCACGCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAATTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATCCGAAC TCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

m529.pep

```

1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAENVLKS KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
151 PQDSLRLRLFD KVLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDITV WQSPSPDNL EAAFLTRFMQ YLGVDDGQAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPLFKRL LGKGAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

              10          20          30          40          50          60
g529.pep      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

```

```

m529      |||||
           MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
              10         20         30         40         50         60

           70         80         90        100        110        120
g529.pep   GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRPLRAATAANAWLVVDGKSPAEISAAFX
           |||||||:|||||
m529       GSGAVRASDLEKRRTPAVQQPADAENVLKSVMGVRLER-DGSQRWLVDVGKSPAEIWPLLK
              70         80         90        100        110

m529       AFWQENGFDIKSEEP AIGMETEWAENRAKIPQDSLRLFLDKVGLGGIYSTGERDKFIVR
           120        130        140        150        160        170

```

a529.seq

1	ATGACCCATA	TCAAACCCGT	CATTGCCGCG	CTCGCACTCA	TCGGGCTTGC
51	CGCCTGCTCC	GGCAGCAAAA	CGGAACAGCC	CAAGCTCGAC	TACCAAAGCC
101	GGTCGCACCG	CCTGATCAAA	CTCGAAGTCC	CACCTGATTT	GAACAACCCC
151	GACCAAGGCA	ACCTCTACCG	CCTGCCTGCC	GGTTCGGGCG	CCGTCCGCGC
201	CAGCGATTTG	GAAAAACGCC	GCACACCCGC	CGTCCAACAG	CCTGCCGATG
251	CCGAAGTATT	GAAAAAGCTC	AAAGGTGTCC	GCCTCGAGCG	CGACGGCGAGC
301	CAACGCTGGC	TCGTTGTCTA	CGGCAAGTCT	CATGCCGAAA	TCTGGCCGCT
351	CCTGAAAGCC	TTTTCGGCAG	AAAACGGCTT	CGACATCAAA	TCCGAAGAAC
401	CCGCCATCGG	ACAAATGGAA	ACCGAGTGGG	CGGAAAAACC	TGCCAAAATC
451	CCCCAAGACA	GCTTGCGCGC	CCTATTTCAG	ACAGTCGGTT	TGGGCGGCAT
501	CTACTCCACC	GGCGAGCGCG	ACAAATTTCAT	CGTCCGTATC	GACAGGGCA
551	AAAACGGCGT	TTCCGACATC	TTCTTCGCCC	ACAAAGCCAT	GAAAGAAGTG
601	TACGGCGGCA	AAGACAAAGA	CACGACCGTA	TGGCAGCCCT	CCCCGTCCGA
651	TCCCAACCTC	GAAGCCGCTT	TCCTGACGCG	CTTTATGCAA	TATTTGGGCG
701	TTGACGGACA	GCAGGCGGAA	AACGACATCG	CAAAAAAAC	TACCCTTCCC
751	CGCGCCAACG	AAATGGCGCG	TATCGAAGCG	AAAAGCTGA	TTGCTTTTGG
801	CGACTTACGC	AGAAACTGGC	GGCGCACCGC	GCTCGCCCTC	GACGCATATC
851	GGCTGACCGT	CGTCGGTCAA	AACACCGAAC	GCCACGCTTT	CCTGGTTCAA
901	AAAGCCCCGA	ACGAAAGCAA	TGCAGTTACC	GAACAAAAAC	CCGGCCTGTT
951	CAAACGCCTG	CTGGGCAAAG	GCAAAGCCGA	GAAACTGCC	GAACAGCCGG
1001	AACTGATTAG	CTATGCCGAG	CTGTGCGCA	ACGGCTCGCG	CATCGTCTCT
1051	CTCAACAATG	ACGGCAGCGC	ACATGCGCCG	AAAGACGCAT	CCGCATTATT
1101	GGGCAAACTC	CATTCCGAAC	TGCGTTAA		

a529.pep

1	<u>MTHIKPVIAA</u>	<u>LALIGLAACS</u>	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNNP
51	DQGNLYRLPA	GSGAVRASDL	EKRRTPAVQQ	PADAEVLKSV	KGVRLERDGS
101	QRWLVDGKS	HAEIWPLLKA	FWQENGEDIK	SEEPaIGQME	TEWAENRAKI
151	PQDSLRLRLFD	TVGLGGIYST	GERDKFIVRI	EQGKNGVSDI	FFAHKAMKEV
201	YGGKDKDQTTV	WQPSPSDPNL	EAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
251	AAENMARIEG	KSLIVFGDYG	RNRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
301	KAPNESNAVY	EQKPGLFKRL	LGKGKAELPA	EQPELIVYAE	PVANGSRIVL
351	LNKDGSAVAG	KDASALIGKL	HSEL*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSPAEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep    FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDKVGlgGGIYSTGERDKFIVRI
|||||
a529        FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDTVGLGGIYSTGERDKFIVRI
              130      140      150      160      170      180

              190      200      210      220      230      240
m529.pep    EQGKNGVSDIFFaHKAMKEVYGGKDKDttVWQPSpSDPNLEaAFtRFMQYlGVdGQQAe
|||||
a529        EQGKNGVSDIFFaHKAMKEVYGGKDKDttVWQPSpSDPNLEaAFtRFMQYlGVdGQQAe
              190      200      210      220      230      240

              250      260      270      280      290      300
m529.pep    NASAKKPTlPAaNEMaRIEGKSlVFGDyGRNWRRTVlALDRIGlTVVGQntERHaFlVQ
|||||
a529        NASAKKPTlPAaNEMaRIEGKSlVFGDyGRNWRRTAlALDRIGlTVVGQntERHaFlVQ
              250      260      270      280      290      300

              310      320      330      340      350      360
m529.pep    KAPNESNAVTEQKpGLfKRllGKGKaEKPaEQPeLiVYAEPVANGSRIVlLNKdGSAYAG
|||||
a529        KAPNESNAVTEQKpGLfKRllGKGKaEKPaEQPeLiVYAEPVANGSRIVlLNKdGSAYAG
              310      320      330      340      350      360

              370
m529.pep    KDASALLGKLHSELRX
|||||
a529        KDASALLGKLHSELRX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga gcgcggaat gacgggttg atatgggtca tcgtgtcatc
51  ctgtgtgatg gatattaaag tgttgtcat gttatgccgt ccgaacgggt
101 cagacggcat ggctatat tt aaagttgtcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgccc aa ggcggatacc gcccatctcg gtgcggcggg
251 actgggttcg cagaacatgg tgctgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVm DIKVFVmlCR PNGSDGMAIF KVVLRlSGRR
51  GLLPVRLPSa ERAAGARaVR IRPRlPPIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  wTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTcATC
51  sTGtGTGATG GATATTAAAG TGtYTGtTGC GwTATGCCGT CCGAACGgTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGAckTTGC wTGTCGGTTT yCCGTcAGCG GAACGAGCGG CAGGCGGACG
201 TGCGGTTCGc ATCTGCCCAG GCGGATaCC GCCCATtTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTtGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVm DIKvXvAXCR PNGSDGMXIF KVVLRlSGRR
51  GLLXVRFPsa ERAAGGRAVR ICPGRlPPIS VRRGWVRRTW CRKSESvGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep    XSASAAMTGLIWVIVSSCVmDIKvXvAXCRPNGSDGMXIFKVVLRlSGRRGLLXVRFPsa  60
|||||

```

g530	MSASAAMTGLIIVIVSSCVMIDIKVFVMLCRPNNGSDGMAIFKVVLRSLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVIRICPGRIPPISVRRGWVRRTWCRKSESVGR	99
	: :	
g530	ERAAGARAVRIRPRRIPPISVRRDWVRRTWCRKSESAGR	99

```
a530.seq
1  ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCA TC
51  CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCCGCCCT TCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TCGGGTTCGC ATCTGCCCCAG GCGCGATACC GCCACTTTCG GTGCGGCGGG
251 GCTGGGTTTC GAGAACATGG TGTCGTAAAT CGGAATCAGC CGGTCGTTGA
```

```
a530.ppe
1  MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVVLRSLGRR
51 GLLPVRLPSA ERAAGGRAVR TCPGRIPPIS VRRGWVRRTW CRKSESAGR*
```

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM	DIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA				
a530	MSASAAMTGLIWVIVSSCVM	DIKVFVALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA				
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRI	CPGRIPPISVRRGWVRR	TWCRKSES	SVGRX		
a530	ERAAGGRAVRI	CPGRIPPISVRRGWVRR	TWCRKSES	SAGR		
	70	80	90	100		

```
g531.seq
  1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151  ATCTTGTTGA CGGTCTGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
201  TATGGCAGGC ATGTTGGGGG TAAATACAC TGGGCAGGC AAACTCGCCG
251  TCCGAGGTGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301  GGACTAATAC TCGGCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
351  TCGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
401  GGCTTGTCGT CGGCACGGCG TTCAAATCG GCTGCGCCGT ATCCATCTTG
451  TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMag</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>LF</u>			

m531.seq		GTTTGGGAGG		GTTTGGGAGG	
1	ATGACCGTAC	TGACCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGTCGGCAC
51	GGCGGGCATC	GTTTaCCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACATGGCT	GCTTGCCCTAT	GCCGGCGGCT	ACCAATCTA	CGGCGCGGGC
151	GTTTTGTGGA	CGGTCGGACT	CATCAGCCTT	GCCGGCATAc	TGGCGGACTA
201	TGTGGCAGGc	ATATGGGGAG	CAAAATATAc	CGGAGCGGGc	AAGCTCGCCG
251	TTCGCGCGCG	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAc	TCGGTCCCTT	TATCGGCCGC	GCGGcGAGCG	AACTGATCGA

351 ACGGCGCAAT ATGCTTCAGG CAGGTAAGC GGGCTTGGGT ACGTGTGTGG
401 GGCTTGTCTG CGGCACGGCG TTCAAATCG GCTGCGCnGT ATCCATCTTG
451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTTAA

This corresponds to the amino acid sequence <SEQ ID 1534; ORF 531>:

m531.pcp

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTTYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPPFIGA AAGELIERRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 531 shows 94.4% identity over a 162 aa overlap with a predicted ORF (ORF 531.ng) from *N. gonorrhoeae*:

m531/g531

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
	: :					
g531	MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERNR					
	: : : : :					
g531	GGILADYMAGMLGVKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIDRRN					
	70	80	90	100	110	120
	130	140	150	160		
m531.pep	MLQAGKAGLGTLTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLF					
g531	MLQAGKAGLGTLTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLF					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1535>:

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCCG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTGGCT	GCTCGCCTAC	TCCGGCGGCT	ACCAAACTCA	CGGCGCGGGC
151	GTTTTGTGGA	CGGTCGGACT	CATCAGCCTT	GCCGCATAC	TGGCGGACTA
201	TGTGGCAGGC	ATATGGGGGA	CAAAATATAC	CGGAGCGGGC	AAGCTCGCCG
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA
351	ACGGCGCAAT	ATGCTTCAGG	CAGGTAAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGCGC	TTCAAAATCG	GCTCGCCCGT	ATCCATCTTG
451	TTTATCCTGT	TGGTGAATAA	CATCGCCTAC	CTGTTTTAA	

This corresponds to the amino acid sequence <SEO ID 1536; ORF 531.a>:

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTTYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERRN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLTVLILALIALI	AVGTAGIVYPALPGL	LALMFAGTWLLAYAGGYQIY	GAGVLWTVGLISL		
a531	MTALLVILALALIAA	GTAGIVYPALPGL	LALMFAGTWLLAYSSGGYQIY	GAGVLWTVGLISL		
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTYT	GAGKLAVRGALAGSIIGIFFSLPGL	LILPGFIGAAAGELIERN			

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```

      |||
a531  AGILADYVAGIWGTYKTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
      70      80      90      100      110      120

      130      140      150      160
m531.p  MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
      |||
a531    MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cggccgcgct gattgtgggc
151 ggcgcgctgg aattgccggg ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTCGACGC TCTTGGGCGT ATCGTTTGTC GCGCGGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CCGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CCGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTGCTGTA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTACGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTGCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTG CGTTTGAGCC
1251 GGAAGTGTG AAAAACCTGC CCGTCTTGT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

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201 VLVFNCKMKNP LLRMSGIAVG LIAGYIVALE LGKVDFSALQ NLPLVTLVPV
 251 FKYGFAPDWH AFIVAGAIPL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
 301 RGGLADGLV SVIATLGLS PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	:	:				
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLS IQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGVPVSGSGMLS IQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCT GCACCTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT CTCGTTTCGTT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCT GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAACAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCACGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGCTTT TGACTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTC ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG TGTGGCGGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGACAA AAACAACGGC GTGATTGAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCT CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCTT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

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101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
 151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
 201 VLVFNCKMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
 251 FKYGFAFDWH AFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
 301 RGGVLADGLV SVIATLGS LPLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532	MSGQLGKGADAPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
	10 20 30 40 50 60
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
	70 80 90 100 110 120
m532.pep	ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
a532	ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
	130 140 150 160 170 180
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCKMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ
a532	ADGTFGSMENLGLASLVLLIVLVFNCKMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ
	190 200 210 220 230 240
m532.pep	NLPLVTLVPVPFKYGFADFWDHAFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
a532	NLPLVTLVPVPFKYGFADFWDHAFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
	250 260 270 280 290 300
m532.pep	RGGVLADGLVSVIATLGS LPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG
a532	RGGVLADGLVSVIATLGS LPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG
	310 320 330 340 350 360
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRRREAVIAATSVGLGLGVAFEPEVF
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRRREAVIAATSVGLGLGVAFEPEVF
	370 380 390 400 410 420
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
	430 440 450 460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

1 atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
 51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
 101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
 151 gcctgcattt caaatattaca tcgcttccaa tttcgcaaac ttggtatcca
 201 gttctttcac gccctgtttg ccgaagttag tggtcagtcg ggcggattcg
 251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
 301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

806

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351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tcgaggccgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcgttgaa ttccaagcct ttggcggcgt ggacggtcac cagttggacg
701 gctttttcgc ctgcccctgc ttgggttttcg ccggaattcga gggcggcgtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFVGYEYPT
51 ACISNLHRFQ FRKLGQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 atGCCCTTtC CCGTTTTCAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACCTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTCGCCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGGCGGAC
301 GTTTTGTCGG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGT GCGGTAAC
401 TCGTAGGCAG GCTTTTTCAG GGACAGGTAG TGCAATACTT CCGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTTCGAGG CCGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCCGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDTETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

	10	20	30	40	50	59
m535.pep	MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ					
	: : : :					
g535	MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ					
	10	20	30	40	50	60
	60	70	80	90	100	110
m535.pep	FRKLGVLQFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVLGLFVVVDD					
	: : : :					
g535	FRKLGQFFHALFAEVDGQSGGFAFVCGIDNHAGAEFGVTDVLSDAEACVGLRLFVIDD					
	70	80	90	100	110	120

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	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKQFAFGGVDGHELDGLFACAC						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHQLDGFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENEGGGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq	(partial)
1	TTTACACGGC CTTTTGCCTT GTCCTTGCTA CAGTTTTTTTG CCATAGGTCG
51	GATTCTCGAA TCCGACATTT CCAACAGCGG TTTTTCGGAA ACGATAGACG
101	CGTCAAATAT TTTTGTGCGA TACGAGTATC CAGCCTGCAT TTCAAATTTA
151	CATCGCTTCC AATTTGCGAA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201	TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCCTTTATC TGCGGCATCG
251	ATAATCACGC CCGTGCCGAA TTTGCGTGG CGGACGTTTT GTCCGATACG
301	GAACCTGCG TAGGTTTGGG GCTGTTTGTG GTCGTCGATG ATTTTGTCTT
351	TGGGCGCGGC GGTGTGCGC GTGTTGCCAT AGCGGTCGTA GCGGGTGGT
401	TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTCTT CGACGAAGCG
451	GGAGACGATG CCGAATTGGG TTTGTCCGTG CAGCATGCGT TGTGCGCCA
501	TGGTGATGTA GAGGCGTTTG CGGGCGCGG TGATGGCGAC GTACATCAGG
551	CGGCGTTCTT CTTCGAGGCC GCCGCGTTCG GCAAGGCTCA TTTCGCTGGG
601	GAAGCGGCCT TCTTCCATGC CCGTGAGGAA TACGGCGTTA AATTCCAAGC
651	CTTTGGCGGC GTGCACGGTC ATGAGTTGTA CGGCTTTTTT GCCCGCGCCT
701	GCTTGGTTTT CGCCGATTTC GAGAGCAGCA TGGCTTAGGA AAGCGAGGAT
751	GGGAAGGCG GGGTCGCTG A

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep	(partial)
1	FRRPFALSL QFFAIGRILE SDISNSGFSE TIDASNIFVG YEYPACISNL
51	HRFQFRKLGV QLFHALFAEI DGQSGGFAFI CGIDNHAGAE FGVADVLSDT
101	ETCVGLGLFV VVDDFVFGRG GLARVAIAVV GGFFDGQVVQ YFGRDFFDEA
151	GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEA AAFGKAHFAG
201	EAAFFHAGEE YGVKFQAFGG VHGHELYGFF ARACLVFAGF ESSIA*ESED
251	GEGGVV*

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRRPFALSLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF					
	: :					
a535	FRRPFALSLQFFAIGRILESDISNSGFSETIDASNIFVGVEYPTYISNLHLRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : :					
a535	VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

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                190      200      210      220      230      240
m535.pep      AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL
                |||||:||||||||||||||||||||||| ||||| ||| :|| |||
a535           AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL
                180      190      200      210      220      230

                250      260
m535.pep      VFTGFEGGIAXEGENEGGVVX
                ||:||||:|||||:|||||
a535           VFAGFESSIAXESEDGEGGVVX
                240      250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

```
g537.seq
.1  atgaaatccc  tttttatttg  gctgcttcta  ttgggctcgg  cggcaggcgt
51  tttctaccat  acccaaaacc  aatccctgcc  cgcgggcgaa  cttgtctatc
101 cgtccgcacc  gcaaatcagg  gacggcgggc  atgcgctgca  ctacctcaac
151 cgcattccga  cacaaatcgg  ttgacacgcy  ctggcacacg  cgccggtttt
201 ggaaaattcc  gccgcaggc  acgcacgcta  tctcacgctc  aatcccgaag
251 acggcacagg  cgaacaccat  ccgcacaatc  cgcactacac  cgcacaaaag
301 ctgaccgaac  gcacacgcct  tgccgggtat  ctctacaacg  gcgtgcatga
351 aaacatcagc  acggaagagg  aagccgccga  atcgtccgac  agcgacatcc
401 gcacgcagca  acgccaagtg  gacgctttga  tgagcgcaat  ctaccaccgc
451 ctttcgctgc  ttgaccgcca  taccgacgaa  gcaggtgcgg  catttgtgcy
501 cgaaaacggc  aaaaccgtcc  tcgtattcaa  tcagggcaac  ggcagcttcg
551 agcgcgcctg  tgcaaaagga  aggcggcagc  cggaagcagg  acgaaaatat
601 taccgcaacg  cttgccacaa  cggtgcgggc  gtttatgctg  acgaagccat
651 gcccgtaacg  gaattcgctt  ataccgccta  tccggttggc  ggcggcgcgc
701 tgccttattt  taatcgggaa  cgtcccgacc  ccgtgcggga  atatgaattc
751 acaggcaatc  ctgccagcat  tgatttttcc  gaggcgcgag  gcaaaattgc
801 gatgaaaagt  ttcaagctgt  atcagggtaa  aaacgaaatc  cgccccgtca
851 gggtttttaac  cgccggcaac  gaccctaacg  gcaggctgac  cgcgcaccaa
901 ttcgcctttt  tcccgctcaa  acctttggaa  tacggcacgc  tttatacggc
951 ggtattcgac  tatgtccgca  acggacggca  cgcgcaggcg  aaatggcagt
1001 ttagaaccgg  aaaaccgat  tacccttatt  ttgaggtaaa  cggcgggcag
1051 acacttgcg  ttagaaaagg  cgaaaaatat  ttcattccact  ggcgcgagcg
1101 ctggtgtctg  gaagcgtgta  cccgttatat  ctaccggcgg  cagttcggca
1151 acagcgtgtc  catactccgg  cacgaagcgg  gcgcgattgt  cttcagcgtc
1201 agcggaatgg  cgggaagcgg  catcaggctt  actccggaag  acagcccgga
1251 acgcggtgta  accctttatt  tgcaggattg  a
```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

```

g537.pep
1  MKSLFIWLLL  LGSAAGVFYH  TQNQSLPAGE  LVYPSAPQIR  DGGDALHYLN
51  RIRTQIGLHA  LAHAPVLENS  ARRHARYLTL  NPEDGHGHEH  PDNPHYTAQK
101 LTERTRLAGY  LYNGVHENIS  TEEEAESSD   SDIRTQQRQV  DALMSAIYHR
151 LSLDRHTDE  AGAAFVRENG  KTVLVFNQGN  GSFERACAKG  RRQPEAGRKY
201 YRNACHNGAA  VYADEAMPVT  ELLYTAYPVG  GGALPYFYGE  RPDVPVEYEI
251 TGNPASIDFS  EAAGKIAMKS  FKLYQGKNEI  RPVRVLTAGN  DPNGRLTAHQ
301 FALFPLKPLE  YGTLYTAVFD  YVRNGRHAQA  KWQFRTRKPD  YPYFEVNGGE
351 TLAVRKGEKY  FIHWRGWCL  EACTRYTYRR  QFGNSLSILR  HEAGGIVFSV
401 SGMAGSRIRL  TPEDSPERGV  TLYLQD  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1551>:

m537.seq	(partial)	1	2	3	4	5
1	ATGAAATCCC	TTTTTATTCG	GCTGCTCCTG	TTGGGTTCGG	CGGCAGGCGT	
51	TTTCTACCAT	ACCCAAAmCc	AATCCCTGCC	CGCGGGCGAA	CTTGTCATATC	
101	CGTCCGCACC	GCAAATCAGG	GACGGCGGCG	ATGCCTGCA	CTACCTCAAC	
151	CGCATCCGAG	CCCCAATCGG	TTTGACAAGT	CTGGCACACG	CGCCGGTTT	
201	GGAAAACATCC	GCCCGCAgC	ACGCAAGCTA	CCTCACGCTC	AATCCCCAAG	
251	ACGGACACGG	CGAACACCAT	CCCCGACAATC	CGCTACTAC	CGCACA AAAAG	

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

```

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

```

m537.pep (partial)
  1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE SGAA...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

```

m537/g537
      10      20      30      40      50      60
m537.pep MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g537      MKSLFIWLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRITQIGLHA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      70      80      90     100     110     120
m537.pep LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g537      LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      70      80      90     100     110     120
      130     140     150     160
m537.pep TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g537      TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      130     140     150     160     170     180
g537      GSFERACAKGRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

```

a537.seq
  1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAAATTCC GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTTGTGCG
501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
701 TGCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
851 GGGTTTTAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
1001 TTAGAACCAG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
1051 AACTTTGCGG TTAGAAAAGG CGAAAATAT TTCATCCACT GCGCGGACG
1101 CTGGTGTGTT GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

```

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```

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT
1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

```

a537.pep
  1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE AGAAVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI
251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPSRLSIGR HKAGGIVFSV
401 DGMAGSRITL APEGETERGV TLYLQD*

```

m537/a537 98.2% identity in 164 aa overlap

```

              10      20      30      40      50      60
m537.pep      MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK
              |||||||
a537           MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK
              10      20      30      40      50      60

              70      80      90     100     110     120
m537.pep      LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              |||||||
a537           LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              70      80      90     100     110     120

              130     140     150     160
m537.pep      TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
              |||||||
a537           TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
              130     140     150     160     170     180

a537           GRFERHCAQGRNQPEAGRKYRYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE
              190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

```

g538.seq
  1  atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51  cgtcatgctg gtgggcgtaa tggtggataa agatgatacg ggcagcaatg
101  ccgcccgtct gaacggtttt cagacggcat tggcgggaagc cgtcagagctg
151  gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga
201  ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
251  cggaagcagt tgccgcagac ggcattgatt tggtcgtatt caaccacgaa
301  cttactccca cgcaggaacg caatttgga aaaatcctcc aatgcccgct
351  attggacaga gtggggctga ttctggcgat ttctgcccgc cgcgcccgcg
401  cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
451  ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
501  cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
551  ccgcccacat gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
601  cagcgcgccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaaacggt
651  tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
701  tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
751  acgacggcgc ggcggctgta catcagtccc gcatgcagca ttatcctgac
801  cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttccgcct
851  tttccgcac cttggaagaa accgtgcaag ccgatgtgct gctgcagctc
901  gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa
951  cgtactgcaa gaaatccatg ccacgatata tccgtgcatc aaggtgtaca
1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaatac

```

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

q538 . pep

1	MSGRTGRNSA	TQAQPERVML	VGVM LDKDDT	GSNAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVG TGKA	AELSEAVAAD	GIDL VVFNHE
101	LTPTQERNLE	<u>KILQCRVLDR</u>	<u>VGLILAI</u> FAR	RARTQEGRLQ	VELAQLSHLA
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLTAHRINA	LKKQLANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDQLFATLD
251	TTARRLYISQ	ACSIILTDTV	GFVSDLPHKL	ISAFSATLEE	TVQADVLLHV
301	VDAAARNSSG	QIEDVENVLQ	EIHAIHDIPCI	KVYNKTDLLP	SEEQNTGIWR
351	DAAGKIAAVR	ISVAENTGID	ALREATAEYC	AAAPNTDETE	MP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

1	ATGACAGGCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGTAGTG
101	CCGCCCGTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCAAAGCGG	CGGGCGGCGA	TTCGTGCGC	GTGGAGACTG	CCAAACGCGA
201	CCGTCCGCAC	ACCGCGCTGT	TGTTCGGCAC	GGGCAAGCGC	GCGGAGCTGT
251	CAGAAGCAGT	TGCCCGAGAC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTCACGCCCA	CGCAGGAACG	CAACCTTGAA	AAAGAACTsA	AATGCCCGCT
351	ATTGGACAGG	GTAGGGCTGA	TTCTGGCGAT	TTTCGCTCGC	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CGCAATTGAG	CCATTTGGCG
451	GGACGCTTGA	TGACGCGTTA	CGGCCATCTG	CAGAGCCAGC	CGGGCGGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAACT	GGAACCCGAC	CGCCGATTGA
551	TCGCCCATCG	GATCAATGCC	TTGATAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCC	TGCGCCGCAA	GTCnCGCGAA	TCGGGCACAA	TCAAAACGTT
651	TGCGCTGGTC	GGCTATACAA	ATGTCGGAAA	ATCCAGCCTG	TTCAACCGGC
701	TGACAAAGTC	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCCTGA	CCGATACCGT	CGGATTCTGn	AGCGATCTGC	CGCACAAACT
801	GATTTCCGCC	TTTTCgCC .A	CGCTGGAAGA	AACCGCGCAA	GCCGATGTGC
851	TGCTGCACGT	CGTCGATGCC	GCCGCTCCGA	ACAGCGGACA	GCAGATTGAA
901	GACGTGGAAA	ACGTA CTGCA	AGAAATCCAT	GCCGGCGATA	TTCCGTGCAT
951	cAAGGTGTAC	AACAAGAACCG	ACCTGCTCGC	GTCTGAAGAA	CAAAACACGG
1001	GCATATGGCG	CGACGCTGCG	GGAAAAATTG	CCGCGCTCCG	CATTTCGGTT
1051	GCTGAAAATA	CCGGTATAGA	CGCACTGCGC	GAA GCATTG	CCGAGTCTTG
1101	TGCCGCCGCA	CCAAACACAG	ACGAAACCGA	AATGCCATGA	

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pcp

1	MTGRTGGNGS	<u>TQAQPERVML</u>	<u>VGVM LDKDGT</u>	<u>GSSAARLNGF</u>	<u>QTALAEAVEL</u>
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEA AAD	GIDL VVFNHE
101	LTP TQERNLE	<u>KELKCRVLDR</u>	<u>VGLILAIFAR</u>	RARTQEGRLQ	VELAQLSHLA
151	GRLLRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLIAHRINA	LIKQLANLKK
201	QRALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPECS
251	IILTDTVGVF	SDLPHKLISA	FSXTLEETAQ	ADVLLHV VDA	AAPNSGQQIE
301	DVENVLQEIH	AGDIPCIKVY	NKTDLLPSEE	QNTGIWRDAA	GKIAAVRISV
351	AENTGIDALR	EIAEASCAA	ENTDET EMP*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/q538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	: : :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLDR					
	:					
g538	VETAKRDRPHTALFVGTKAAELSEAVAADGIDL VVFNHELTPTQERNLEKI LCRVLDR					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI	FARRARTQ	EGRQLQ	VELAQL	SHLAGRL	IRGYGHL
g538	VGLILAI	FARRARTQ	EGRQLQ	VELAQL	SHLAGRL	IRGYGHL
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHR	INALIKQ	LANLKK	QORALRR	KSRRESG	TIKTFAL
g538	RRLTahr	INALIKQ	LANLKK	QORALRR	KSRRESG	RIKTFAL
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL	-----	SPECSI	IILTD	TVGFV	SDLP
g538	AKDQL	FATLDT	TARRLY	ISPACSI	IILTD	TVGFV
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAP	NSGQ	QIEDV	ENVLQ	EIHAGD	IPCIKV
g538	VDAAAR	NSGQ	QIEDV	ENVLQ	EIHAGD	IPCIKV
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAEN	TGIDAL	REIAIE	SCAAAP	NTDE	TEMPX
g538	ISVAEN	TGIDAL	REIAIE	YCAAAP	NTDE	TEMPX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

a538.seq					
1	ATGACAGGCA	GAACAGGCCG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGCAGTG
101	CCACCCGTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCAAAGCGG	CGGGCGGCCA	TTCCGTGCGC	GTGGAGACTG	CCAAACGCGA
201	CCGTCCGCAC	ACCGCGCTGT	TTGTCGGCAC	GGGCAAGGCG	GCGGAGCTGT
251	CGGAAGCAGT	TGCCCGCAGC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTTACGCCCA	CGCAGGAACG	CAATTGGGAA	AAAATCCTCC	AATGCCGCGT
351	ATTGGACAGA	GTGGGGCTGA	TTCTGGCGAT	TTTCGCCCCG	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CACAATGAG	CCATTTGGCG
451	GGACGCTTGA	TACGCGGTTA	CGGCCATCTG	CAGAGCCAGC	GCGGCGGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAAC	GGAAACCGAC	CGCCGATTGA
551	TGCCCCATCG	GATCAATGCC	TTGAAAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCC	TGCGCCGCAA	GTCCCGCGAA	TCGGGCACAA	TCAAAACGTT
651	TGCGCTGGTC	GGCTATACCA	ATGTCGGCAA	ATCCAGTCTG	TTCAACCGGC
701	TGACCAAGTC	GGGCATATAT	GCGAAAGACC	AGCTTTTCGC	CACACTCGAC
751	ACGACGGCGC	GGCGGCTGTA	CATCAGTCCC	GAATGCAGCA	TTATCCTGAC
801	CGATACCGTC	GGATTCTGCA	GCGATCTGCC	GCACAACTG	ATTTCCGCCT
851	TTTCCGCCAC	GCTGGAAGAA	ACCGCGCAAG	CCGATGTGCT	GCTGCACGTC
901	GTCGATGCCG	CCGCTCCGAA	CAGCGGACAG	CAGATTGAAG	ACGTGGAATA
951	CGTACTGCAA	GAAATCCATG	CCGGCGATAT	TCCGTGCATC	AAGGTGTACA
1001	ACAAAACCGA	CCTGCTGCCG	TCTGAAGAAC	AAAACACGGG	CATATGGCGC
1051	GACGCTGCGG	GAAAAATTGC	CGCCGTCCGC	ATTTCCGTG	CTGAAAATAC
1101	CGGTATAGAC	GCACTGCGCG	AAGCCATTGC	CGAGTATTGT	GCCGCCGCAC
1151	CAAACACAGA	CGAAACCGAA	ATGCCATGA		

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

a538.pep					
1	MTGRTGRNGS	TQAQPERVML	VGVMLEKDG	T	SSATRLNGF
51	VKAAGGDSVR	VETAKRDRPH	TALFVG	TGKA	AELSEAVAAD
101	LTPTQERNLE	KILQCRVLDR	VGLILAI	FAR	RARTQEGRLQ
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLIAHRINA	LKKQLANLKK

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILDTV GFVSDLPKLI ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM	LDKDG	TGSSAARLNGFQTALAEAVELVKAAGGDSVR			
a538	MTGRTGRNGSTQAQPERVMLVGVM	LDKDG	TGSSATRLNGFQTALAEAVELVKAAGGDSVR			
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL	VFNHELTPTQERNLEKELKCRVLD				
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL	VFNHELTPTQERNLEKILQCRVLD				
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRL	LIRGYGHLQSQRGGIGMKGPGETKLETD				
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRL	LIRGYGHLQSQRGGIGMKGPGETKLETD				
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQRALRRKSRES	GTIKTFALVGYTNVGKSSLENRLTKSGIY				
a538	RRLIAHRINALIKQLANLKKQRALRRKSRES	GTIKTFALVGYTNVGKSSLENRLTKSGIY				
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILDTVGFVSDLPKLI	ISAFSXTLEETAQADVLLHV				
a538	AKDQLFATLDTTARRLYISPECSIILDTVGFVSDLPKLI	ISAFSATLEETAQADVLLHV				
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLP	SEEQNTGIWRDAAGKIAAVR				
a538	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLP	SEEQNTGIWRDAAGKIAAVR				
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagatcc ggcaacggca
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcgcgtca taggggtcgg cggtgtagcc tgtctgccgg attttcaaca
201 gaatgtcggg gagggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggattgg
401 acttcgggca ggtcgtacag gcggatttgg tgcaggattt cttggggcgg
451 cagttcgggt tttttcgcgt cggcgggtgc tgcgttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggg cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtggg aacaggtttt tttcatggca tttcggtttc

```

814

```

651 gtctgtgtttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccgggctg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacgggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgtcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccgggtga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFVF VADGQMQVFG
201 NVQPAVETGF FHGISVSSVF GAAQAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPFLRA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVTSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GG GTGAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCGT TACGCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CCGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaCAgG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACA GTCAGGTGGA GGTGTTTCGGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTATGGCA TTTCTGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
751 CCCGACGCGT CGCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGTTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTcAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLVGGA LfVITAQARV NNALCDRLTA GAQGFVAVVF VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVTSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||:|||||
g539      MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

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	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFVAVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDPFQQNVGEADFVAVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	130	140	150	160	170	180
m539.pep	LARAAGVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGVGFHKVGLDFGQVVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMQVFGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFSTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSTFSTSSICCPFLRA					
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRVAKS					
	350	360				
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTCTG TACGCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCGTACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CGGCGGTGCG TTGTTTGTA TAAC TGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACG GTCAGATGCA GGTTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGT TTGTTCTT CAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHRRLHHPQP GNGEADDVLF AFFLVGGFDF

```


816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAVRAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LEVITAQARV NNALCDCLTT GAAGFAVFVF VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTCSSTS ACAVSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR
351 RAVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

              10      20      30      40      50      60
m539.pep      MEDLQEIIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA
              |||||
a539           MEDLQEIIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA
              10      20      30      40      50      60

              70      80      90      100     110     120
m539.pep      YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
              |||||
a539           YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m539.pep      LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA
              |||||
a539           LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT
              130     140     150     160     170     180

              190     200     210     220     230     240
m539.pep      GAQGFAVFVFVTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS
              || |||||:|:|:|:| |||||
a539           GAAGFAVFVFVTDGQMVFVGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS
              190     200     210     220     230     240

              250     260     270     280     290     300
m539.pep      ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFSTSSICCPLFGA
              |||||
a539           ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFSTSSICCPLFGA
              250     260     270     280     290     300

              310     320     330     340
m539.pep      AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
              |||||
a539           AASTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS
              310     320     330     340     350     360

a539           WSFAYMPDLVSRLNRLDLPTLVX
              370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgccct cccgacgcgg caacgggggtg ttttatcaaa acggcaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101 tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcgggtgt
151 ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgctgc
201 cgtaatacag cagccgaggt ttgacgggga tgcgtccctg cgatttgagg
251 tgggcggttg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301 gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgcgcg
351 ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
401 gcacggtgtc cgcagtcggt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

```

1  MPSSRRNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```

51 L FVHSDGCRF V LCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
101 VEVFADFADFN HTRAAAAFAP VEVPIGHIIV RRGGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

```
m540.seq (partial)
1  ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTATTGTG
51  CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
201 TTTCACGTTT GCTGATTTCA ATCATGCGCG CGTGCCGCCC CCCTTTGCGC
251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
301 TCCGCAGTCG TTGATTTGCG CCATATTTTT CCAGCGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

```
m540.pep      (partial)
      1  ..PNMPMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHA2AEFDG DSAL*FAVGI
     51  GIPQGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
    101  SAVVDLRHIF PA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

```
m540/g540
```

m540.pep PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
| | | | | | | | | | | | | | | | |
g540 GNGVFYQNGKLANAVSACRLPNRQTFFVPVPPNMPSEPSDGIGCLFVHSDGCRFVLCRFV
10 20 30 40 50 60

m540.pep AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHAAAAAFAPVEIPIH
| | | | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
g540 AVIQHAEFDGDSLRFVGVGVIAQQIRAAAVFLLEVFVAFADFHNHTRAAAAFAFPVEVPIG
70 80 90 100 110 120

m540.pep HIIVRRGGA VSAVVDLRHIFPAX
| | | | | : | | | | | | | | | | |
g540 HIIVRRG GTVS AVVDLRHIFPAX
130 140

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq

1	ATGCCGTCCT	CCCACGCGG	CAACGGGGTG	TTTTATCAA	ACGGCAAAC
51	TGCCAATGCG	GTTTCCGATT	GCAGATTGCC	AAACCGGCA	ACCTTTCCCG
101	TGCCGATGCC	GAACCCGATG	CCGTCTGAAC	CTTCAGACGG	CATCGGGTGT
151	TTATTTGTCC	ACCCGGATGG	GTGCAGGTTC	GTATTGTGTC	GATTCGTGCG
201	CGTAATACAG	CACGCCGAGT	TTGATGGGGA	TTCTGCCCTG	TGATTTGCGG
251	TGGGCGATTG	AATCCCTCAG	GGAATAGGCA	CAACCGCAAT	ATTCCTGCTG
301	GTAGAAGTTT	TCACGTTTGC	TGATTTCAAT	CATACGCGCG	CTGCCGCCCG
351	CTTTGCGCCA	GTTGAAATCC	CAATACACCA	CATCATCGTA	AGGCGCGGCG
401	GCGCGGCGGC	CGCAGTCGTT	AATCTGGTTC	ATGTTTTTCC	A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

```
a540.pep (partial)
      1 MPSSRRNGV FYQNGKLANA VSDCLPNRQ TFPVMPNPM PSEPSDGIGC
     51 LfvHPDgCRF vLcRFvAIVQ hAEFDGDSAL *fAVGVGIpQ GIGTTAIFLL
    101 VEFTFADFN HTRAAAAFAP VEIPHHIIV RRGGAAAaVV NLVHVFP
```

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m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVFYQNGKLANAVSDCRLPNRQTFVPMPNPMPSEPSDGIGCLFVHPDGGCRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAAFAPVEIPIH
              |||||
a540      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHTRAAAAFAPVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
              |||||
a540      HIIVRRGGAAAVVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1   atgccgaat  ggtcgcgcat  acggcggttg  agcgctcctt  cgctgatgtt
51  cagcgcggt  gtcagcggt  tgacttggt  tgcgcgcg  tcgaacgcg
101 cattcaggt  gcggctgaag  tcttcagacg  gcatagcg  tgcttcgcc
151 gtttgcccc  ccgcccgtc  gatgccgtc  gaaaccgtg  cccacaaat
201 cgacagcagc  cgcaacacgt  ccgcctcgcg  gcgcaatgt  tcgcccagt
251 gcccctttg  gacggtttg  aggcaggatg  ccgccaagcc  gcgcaggtt
301 gggggcaat  cccatatact  gaccggttcg  cggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1   MPKWSRIRRC  SVLSLMFSAA  VSRLTWCAPP  SNAAFRVLK  SSDGIASASA
51  VCPAAGSMPS  ETVSHKSDSS  RNTSASRRNV  SPKCPFGTVC  RQDAAKPRRF
101 GGKSHILTGS  R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1   ATGCCGAAAT  GGTGCGCGAT  ACGGCGTTGC  AGCGTCCTTT  CACTGATGTT
51  CAGCGCGTCT  GTCAGCCGGT  TGACTTGGTG  TGCGCCGTCG  GCAAACGCGG
101 CATTAGGGT  GCGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTCCGCC
151 GTTTGCCCG  CCGCCGGCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  .CGCAATGTT  TCGCCCAAAT
251 GCCCCTTTGG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTC
301 GGGGGCAAAT  CCCATATCCT  GACCGGTTTC  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1   MPKWSRIRRC  SVLSLMFSAS  VSRLTWCAPS  ANAAFRVLK  SSDGIASASA
51  VCPAAGSMPS  ETVSHKSDSS  RNTSASRAMF  RPNAPLGRNV  SPKCPFGTAF
101 RQDAAKPRRF  GGKSHILTGS  R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVLK SSDGIASASAVCPAAGSMPS
              |||||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPP SNAAFRVLK SSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAF RQDAAKPRRF GGKSHILTGSRX

```

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```

|||||
g542  ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1   ATGCCGAAAT GGTTCGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCGG
101 CATTCAGGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1   MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLRK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GGKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep    MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVLKSSDGIASASAVCPAAGPMPS
              |||||
a542        MPKWSRIRRC SVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep    ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              |||||
a542        ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1   atgggtttgtc ggttatttgc cgccgttttt ggctttcaac tcggcaatca
51  gcccgctcgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggtaacca ggctcgtgcc ttcgatggcg acgttgtagg tacggtattt
151 gccgcccgtt tggtaggtgg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgaggatca gcagggtttg aaattccttg gccaacgctt
351 gtttttgcgc gtcggacgcg gtacgccaa ggttgccgac cgccaatgcg
401 gtcatacggt ggaaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
501 cgttttggcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcccga gtcaggattt gcgcggaac gtcactgtcg
851 aactgatact tgccgtccaa atcaaggcgc accctcgctt gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
951 tgacgggggc attgaccttc aaaccgcca tgcgcgcaa atcggcataa
1001 acggcgtaag ttttgtccga accgccaac gccgcgccg ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcccgcgc gatcaagacg aacagtccga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1   MVCRLFAAVF GFQLGNQPV D AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

m543.seq

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

m543 . pep

1	MVCRLFAAAVF	GFQLGNQSVH	AFRFDNFael	VAVHGnQARA	FDGDVVGTVF
51	TAALVGGEVH	VDGFLPGYAD	FGADDDFFAA	FIDDGIVFDV	DVGVFxFQHR
101	AGIGADQQGL	KFFGQRLFLR	VGRGAPRVAD	RQCgHTLEIE	IGNRIGFGFL
151	ASGVGIAVFX	DAQYLSGVLT	DLAYRVGRGG	KCHADAQNTD	AQCADEGGFF
201	HDXVSXFEYD	GIRLFGGFFR	IAAVGIFLGK	TRHEFADKVF	QNHCRtGYGD
251	GVAGSKVFRV	AALLQPDVLL	AQKRSQDLR	GNVAAELILA	VQIEAHPRLI
301	GFRVKSAD	APDQYACGFD	GGIDLTADV	AEINGNVSF	VRTAERRTAG
351	HAESEKGNRR	RANQDEQSDP	KFOYVLLH*		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNF	AELVAVHGNQARAFDGDVVGTVFTAALV	GGEVH			
g543	MVCRLFAAVFGFQLGNQPVDAFGFDDF	AELVAVHGNQARAFDGDVVGTVFAAALV	GGEVH			
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADF	GADDDFFA	FIDDGIVFDV	DGVXFQHR	RAGIGADQ	QGLKFFGQRLFLR
	: :	:	:	:	:	:
g543	IDGLLTGDADF	GTDDDFL	AALIDDGIVFDV	DGRVFEFQHR	RAGIGADQ	QGLKFFGQRLFLR
	70	80	90	100	110	120
	130	140	150	160	170	180

```

m543 . pep      VGRGAPRVADRQCQGHSTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
|||:||||||||||||||||||| | :|:| | |||:|:| ||||
g543            VGRGTPRVADRQCQGHSTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGVLADLSHCVGRGG
              130          140          150          160          170          180

              190          200          210          220          230          239
m543 . pep      KCHADAQNTDAQCADEGGFFHDXVSXFYDGI-IRLFGGFFRIAAGVIFLGKTRHEFADKV
||||||||||||||||||| | :|:| | |||||||:|:| |||:|:|
g543            KCHADAQNTDAQCADEGGFFHDXV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
              190          200          210          220          230

240            250            260            270            280            290            299
m543 . pep      FQNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAELILAVQIEAHPRL
|||||||||||||||||||:|||||:|:| |||:|:| |||:|:|
g543            FQNHCRGTGYGDGVAGSKVFRVAALLQPDVLFQAKRSQDLRGNVTAEILILAVQIKAHPRL
              240          250          260          270          280          290

300            310            320            330            340            350            359
m543 . pep      IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
|||||||||||||||||||:|||||:|:| |||:|:| |||:|:|
g543            IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEKGNR
              300          310          320          330          340          350

360            370            379
m543 . pep      RRANQDEQSDPKFYVLLHX
|||:|||||||||||:|
g543            RRADQDEQSDPKFYVLFHX
              360          370

```

```
a543.seq
1 ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51 GTCCGTCCAC GCCTTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA TCGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGCGCGCG ACGATGATTT CTTTGCCGCG TTTTATGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTTTAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAATACGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGGGCGGTG TTGGCATCA CCGTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCGGG AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCCGCGC TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGTTTTC CAGAACCATT GCAGAACCTG TTACGGAGAT
751 GGTGTCCCGG GCAGCAAGGT TTTCCGTGTC GCGGCCCTGG TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GATTTGCGC GAAACGTCG
851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCGGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGGACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAAGAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTTCAAT ATGTCTTTTT TCATTAA
```

```
a543.pep
1  MAYGLLAAVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCCHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGK KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGVFR IAAVGIFLGK TRHEFADKVF QNHCRTPGYD
251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTAADV AEIGINGVSF VRTAERRTAG
```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
a543	MAYGLLAAVXSLQLXNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
m543.pep	VDGFLPGYADFAGDDDDFAAFIDDGIVFDVDVGVEFXFQHRAGIGADQQGLKFFGQRLFLR					
a543	VDGFLPGXADFAGDDDDFAAFIDDXIVFDVDVGVEFXFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
m543.pep	VGRGAPRVADRQCCHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCCHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGIFLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGIFLGKTRHEFADKVF					
	190	200	210	220	230	240
m543.pep	QNHCRRTGYGDGVAGSKVFRVAALLQPDVLLAQKRSRQDLRGNVAAELILAVQIEAHPRLI					
a543	QNHCRRTGYGDGVAGSKVFRVAALLQPDVLLAQKRSRQDLRGNVAAELILAVQIEAHPRLI					
	250	260	270	280	290	300
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370	379				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

1	atgaaaaaaa	tactcaccgc	cgccgccgtc	gcactgatcg	gcatcctcct
51	cgccaccgtc	ctcatccccg	acagtaaaac	cgcgcccgcc	ttctccctgc
101	ccgacctgca	cggaaaaaac	gtttccaacg	ccgacctgca	aggcaaagtc
151	accctgatta	atTTTTggtt	tccctcctgt	ccggttgtg	tgagcgaaat
201	gccc aaagtc	acaaaaacgg	caaacgacta	caaaaataaa	gatttccaag
251	tcttcgccgt	tgcccagccc	atcgatccga	tagaaagcgt	ccgccaatac
301	gtcaaagact	acggactgcc	gtttaccgct	atttatgatg	cggacaaagc
351	cgtcggacag	gcattcggca	cacaggttta	tccgacttcc	gtccttatcg
401	gcaaaaaagg	cgaaatcctc	aaaacttatg	tcggcgaacc	cgatttcggc
451	aaactctacc	aagaaatcga	taccgcgctg	gcgcaatag	

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544 . pep

1 MKKILTA~~AAV~~ ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGKV
51 TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLGKKGEIL KTYVGEPDFG

m544.seq

m544 . pep

m544/g544

a544.seq

a544.pcp

1	MKKILTAAVV	ALIGILLAIV	LIPDSKTAPA	FSLSLHGKX	VXNADLQGXV
51	XLIXFWFSC	PGCVSEMXI	IKTANDYKNK	NFQVLAVAQP	IDPIESVRQY
101	VKDYGLPFTV	MYDADKAVGQ	AFGTQVYPTS	VLIGKKGEIL	KTYVGEPDFG

824

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544 . pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
a544	MKKILTAAVVALIGILLAIVLIPDSKTAPAFSLSLXHLGKXVXNADLQGXVXLIXFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVSXXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547 . seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gccttttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggg atatctcggt
151 gatataattta caagatgcgg cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc ccttactcag aaaatatatta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaaccgaa
401 aaaagcgggt tgttttttgt tgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547 . seq

```

1  ATGTTCTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTT CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTTATAA TGTACATAT ATTTACAAAT ATTAAAGTTT TTTwTTGTGT
351 TGCGGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTGTGTTTT TGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXCVCKV ELLTILVKNL SPNGKKRFV CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```

a547.seq
1  ATGTTCTAG  ATAACGATT  TAATAAACG  GTAGCGAGT  TTGCCCCAAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTTTTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T

```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```

a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSEKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRKYL
101  KFIMLHIFTN  IKVFXCVCVK  ELLTILV

```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYPLLRKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```

g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgccgcgcaa  gccgttctt
101 caagtgcata  cgcgccggct  gcggaaaatg  cggcaaagcc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  ttgaaaggc  aaggtcgtga
251 ttctgtcttt  cggtcttacg  cactgtcccg  atgtctgcc  gacagggctt

```

826

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acggggcgcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttatt gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTGCGG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CCGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCa CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAATATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTCTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFLPGVFVLAALAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
g548	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
g548	FVSIDPERDTPEIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRLTLX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRLTLX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TGCCTAAGGA AGACATCGGC GCGATTTC ACGTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AACTATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTCCTCG
601 CTTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVQ QYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
a548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV					
a548	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIVQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIVQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRLTLX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRLTLX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

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```

151  caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201  cggcagccgt agcgacgcga ggcagcaggc gggaaatcgaa cggagtagga
251  atcagggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301  ttcttcgggtt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351  cgcgtttcat ttcttcggtt atggtggttg cgccgacatc caacgcgccc
401  cgggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451  ggagcggccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501  gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551  tcgttcacatc tgttcaacat ttcaggcgtc agcagggttg cgccggagag
601  gcccaagaag atgtctttgc ctttaaccgc atcggaagt acgcgccggc
651  cggtgtcttc aacggcgtag aattttttgg attcgtccat gcggtctttg
701  tcttcgcggg ttgggtaaat cacgcctttg gagttgcaaa cggttacgtt
751  ttcacgtttc aagcccaaata ccagcagttg gttcaggcag gcaatcgcg
801  cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
851  gtataacgca ggcggttcaa tacggcgggc gcggtaatga tggccgtgac
901  gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

```

g550.pep
  1  MITDRFHLFH FPVSFIYQSD NKMPPESSD GILTTNGLQL PFAQLGSVSF
 51  QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFAE FEFLTVSGNH
101  FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVHLVREV
151  GAAGTDNHVR TGFFRQRRQD FRIRVHGHEH DGFFVHRVQH FRRQQVCAGE
201  AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251  FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301  VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

```

m550.seq (partial)
  1  ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
 51  GTTTGGACTC GTCCATACGG TCTTGTCTT CGCGGGTTTG GTAAATCACG
101  CCTTTGGAGT CGCAAACGGT CACGTTTTTCG CGTTTCAAGC CCAAATCCAG
151  CAATTGGwTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201  AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACCGAKGGC GTTCAATACG
251  GCGGCGGCCG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301  GATTTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

```

m550.pep (partial)
  1  ..DGIGKHALAV VFNGVELFGL VHTVVFAGL VNHAFGVANG HVFAFQAQIQ
 51  QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101  DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGVELFGLVHTVVFAGLVN
                                     |||:| ||||| |||:| |||:| |||||
g550      DGFFVHRVQHFRQQVCAGEAQEDVFAFNRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
          190      200      210      220      230      240

          40      50      60      70      80      90
m550.pep      HAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA
          ||||| |||:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g550      HAFGVANGYVFTFQAQIQQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
          250      260      270      280      290      300

          100
m550.pep      VLVVVEYGDFAAFAX
          |||:| |||||
g550      VLVIMKYGDFAAFAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGGCGGC AGGATTTCCG GATTCCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTC AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCAGCGG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTCGC GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCGGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCTGCTGT GAATACGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNO VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGLVEL FGLVHTVEVF AGLVNHAFAV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGLVELFGLVHTVEVFAGL
                                     |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGLVELFGLVHTVEVFAGL
              170      180      190      200      210      220

              40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIIQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGNDG
              |||
a550      VNHAFGVANGHVFAFQAQIIQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYSGGNDG
              230      240      250      260      270      280

              100
m550.pep      RAVLVVVEYGDFAAFAX
              |||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg catttgtgtgc
51  caacgcattt gccgccccgc ccgcgacgc gtcgttgga cgttggtctg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtca gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcgggtatc ttggactgca
```

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
501 acggcgcatc atctgcggcg gtatagtqga ttaa

g552.pcp

```

1  MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51  NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKS MSEIAVSWTA
151 LSGKIARHHL PEFTEELRRI ICGGIVD*

```

m552.seq (partial)

1	..ATTAAACTGA	AAACCTTGTT	ATTGCCCTTC	GCCACGCTGG	CATTGTGCAC
51	CAATGCTTTT	GCCGCCCGC	CCAGCGACGC	GTCGTTGGCG	CGTTGGCTGG
101	ATACGCAGAA	TTTTGACCGG	GATATAGAAA	AAAATATGAT	TGAGGGCTTT
151	AATGCCGGAT	TTAACCCGTA	TGCGGACAAA	GCCCTTGCCG	AAATGCCGGA
201	AGCGAAAAAA	GATCAGCGCG	CAGAAGCCTT	TAAACGTTAT	CGTGAGAATG
251	TTTTGAAAGA	TTTGATTACG	CCCGAAGTGA	AACAGGCTGT	CGCAATACT
301	TTATTGAAGA	ATGCCCGTGA	GATATACACG	CAAGAAGAAA	TTGACGGCAT
351	GATTGCCTTT	TACGGTTCGC	CTGTCGGTCA	GTCGTCGTT	GCCAAAAATC
401	CGCGCTTAAT	CAAGAAATCG	ATGAGTGAAG	TAGCGGTATC	TTGGACTGCA
451	TTGTCAGGGA	AAATCGCGCA	ACATCATCTG	CCCAGTTTTA	CGGAAGAGTT
501	CGGCGCATC	ATCTGCCGCG	GTAAAAATCC	CGATGCGGGC	TGTAAACAAG
551	CCGGACAGGT	TGGGAAAAAG	CTAGAAAAAT	AA	

m552.pep (partial)

```

1  ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51  NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGKKNPDAG CKOAGOVGKR HOK*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : : : : : : :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : : : : : :					
g552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMS EIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	: : : : : : : : :					
g552	YGSPVGQSVVAKNPRLIKKSMS EIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKOAGOVGKRHOKX					

a552.seq

1	ATTAAACTGA	AAACCTTGTT	ATTGCCCTTC	GCCACGCTGG	CATTGTGCAC
51	CAATGCTTTT	GCCGCCCCGC	CCAGCGACGC	GTCGTTGGCG	CGTTGGCTGG
101	ATACGCAGAA	TTTTGACCGG	GATATAGAAA	AAAAATATGAT	TGAGGGCTTT
151	AATGCCGGAT	TTAAACCGTA	TGCGGACAAA	GCCCTTGCCG	AAATGCCGGA

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCTGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGAAGTGA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
a552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMSSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
a552	YGSPVGQSVVAKNPRLIKKSMSSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCC AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CCGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCACTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSPVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

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```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCC AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEAKKDQAAEAFN RYRENVKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEAFN RYRENVKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAKKDQAAEAFN RYRENVKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEAFN RYRENVKDL ITPEVKQAVR NTLLKNAREI YTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGKNPD					
m552-1	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGKNPD					
	130	140	150	160	170	180
a552-1.pep	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGKNPD					
m552-1	AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVG KRHQKX					
m552-1	AGCKQAGQVG KRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctacgggctg
101 tggccggatt ttatggttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcgggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcgc aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtctcgaggc aggggaagaa
451 aagcaggaaa tccgcatcct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggtcttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaagt catgataaat gggcacgaca
701 ttacagctt accgccact tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggg ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

833

```

1 MDYLQNLSLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNH
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FQLLALAAAM EVFAPLQNVF FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECGQ
251 GRTMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAAGTT CTGAATGTGG TTAGCATGTC CTGACATCCA
101 TCTTGTCCCTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCCTGT CATTAAAGGG CGCAATCTT GCAGACATCA TGAGATTTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAAGTT AAACCATTTT
301 GTTGTACTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTCGGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAAGAA
451 ACAAAGAAAA TCAAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGFG HTDLRTLRLQK
51 YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCSISKDS IVIMDPAVGM RKIKMDEVSO KFTGIALELF PNTHFEEKKE
151 TKKIKILSLR RGXSGLKRSI IQMLILAIISL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAECGLACLAAVAGFYGFYTDLRALRSKYCLSLKGENL					
	: : :: :: : : :					
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACLTSLSYGFGHTDLRTLRLQKYTLSLKGANL					
	10	20	30	40	50	60
g553.pep	70	80	90	100	110	120
	ADIVRFADDMGLTGRALRLDLDELGSLRLPCILHWDNLNHFVVLESVSSDGAAMVMDPASGR					
	: : :: : : : : : : :					
m553	ADIMRFGNEMNLTPRALRLELDELSNLQLPCILHWNLNHFVVLCISISKDSIVIMDPAVGM					
	70	80	90	100	110	120
g553.pep	130	140	150	160	170	180
	RKVKTEEISRKFTGIALELWPNTRFEAGEEKQEIRILPMLRGISGLGRTLFLQLLALAAAM					
	: :: : : : : : : : : : : :					
m553	RKIKMDEVSO KFTGIALELFPNTHFEEKKETKKIKILSLLRGXSGLKRSIIQMLILAIISL					
	130	140	150	160	170	180
g553.pep	190	200	210	220	230	240
	EVFAPLQNVSFKIGRGESLALIGRSGCGKSTLLDILSGNLPPESGKVMINGHDIYSLPPP					
	:					
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

a553.pep
1 MPHQLNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
51 Y

m553/a553 62.7% identity in 51 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
  1  atgacagcac  ataaaatcct  gcccgtcctt  cttcccatca  tcttaggcgt
 51  ttctcacgca  acggctgcat  cgcccgcgcc  caacagaccg  acggtacacg
101  cgccccccac  gctccaaaca  cccgaaaccc  tcacggcggc  acacatcggt
151  atcgaccttc  aaagcaggca  gactttatcc  gccaaaaaca  ccaatacccc
201  tgtcgaaccg  gcggcactaa  cccaactgat  gaccgcatat  ttggttttca
251  aaaacatgaa  atcgggaaat  atccaatctg  aagaaaactt  aaaaataccc
301  gaatccgcat  gggcttcaga  aggaagcaga  atgtttgtac  gtcccggcga
351  tacggtcagc  accgacaaac  tcttaaaagg  catgattgcc  ctatgcgcaa
401  acgatgccgc  cctaaccctt  gccgaccggc  tgggcaacgg  ctcgattgaa
451  aattttgttc  aacaaatgaa  caaagaagcc  cgacgcttgg  gcatgaagaa
501  caccgtatgc  aaaaaccgga  caggcttggg  tagagaagga  caggtttcca
551  ccgccaaaga  cctctccctg  ctgtctgaag  cattatgctg  cgactttccg
601  gaatattacc  cgctgttttc  catcaaactg  ttcaagtttg  aaaaataga
651  acaaaacaac  cgcaatatcc  ttttatatag  ggacaacaat  gtaaacggcc
701  tgaaagccgg  gcacacagaa  agcggcggct  acaaccttgc  cgtgtcatac
751  tccggcaacg  gcaggcacat  ccttgtcatc  aactagggtt  cggaatcggc
801  ggaaaccgcg  gcatcggaca  acagcaagct  gctgaaccgg  gcattgcagg
851  ccttcgatac  gcccaaaaata  tatccgaaag  gcaaaaccgt  tgcccaaatc
901  caaatttccg  gaggcagcaa  aaaaaccgtc  cgcgcaggct  tcctcaaaga
951  agcctacatc  actctgccac  ataaagaagc  gaaaatggca  gaacagattt
1001  tggaaacatt  acagccgatt  cccgccccgg  taaaaaaagg  gcagatttta
1051  ggaaaaatca  aaatcaggta  aaacggacat  accattgccg  aaaaagaaat
1101  cgtcgcactg  gaaaacgtag  aaaaaagaag  ccggtggcaa  aggctttgga
1151  cqcqtctgac  aqqqcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

g554.pcp..

1	MTAHKILPVL	LPIILGVSHA	TAASPAPNRP	TVHAAPTQ	PETLTAAHIV
51	IDLQSRQTLS	AKNTNTPVEP	AALTQLMTAY	LVFKNMKSGN	IQSEENLKIP
101	ESAWASEGSR	MFVRPGDTVS	TDKLLKGMIA	LCANDAATL	ADRLNGSIE
151	NFVQOMNKEA	RRLGMKNTVF	KNPTGLGREG	QVSTAKDLSL	LSEALMRDFP
201	EYYPLFSIKS	FKFENIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY
251	SGNGRHILVI	TLGSESAETR	ASDNSKLLNR	ALQAFDTPKI	YPKGKTVAQI
301	QISGSGSKTV	RAGFLKEAYI	TLPHKEARMA	EQILETIQPI	PAPVKKGQIL
351	GKIKIRONGH	TIAEKEIVAL	ENVEKRSRWO	RLWTRLTGO*	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1627>:

```
m554.seq..
      1  ATGACAGCAC  ATAAAATCCT  GCCCGTCCTG  CTTTCCATCA  TCTTAGGCGT
     51  TTCTCACGCA  ACGGCTGCAT  CGCCCGCGCC  CAACAGACCG  ACGGTACACG
    101  CCGCCCCCAC  GTTCCAAACA  CCCGAAACCC  TCACAGCGGC  ACACATCGTT
    151  ATCGACCTTC  AAAGCAAACA  GATTTTATCC  GCCAAAAACA  TCAATACCCC
    201  TGTTTGAACG  GCGGCACATA  CCCAACTGAT  GACCGCATAT  CTGTTTTCAT
    251  AAAACATGAA  ATCGGGCAAT  ATCCAATCTG  AAGAAAACCT  AAAAATACCC
```

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AACCGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IQSEENLKIP
101 ESAWASEGSR MFVRPGDTSV TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQOMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLQSKQILS					
	: :					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPT LQTPETLTAAHIV IDLQSRQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTSV					
	: :					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTSV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLNGSIE NFVQOMNKEARRLGMKNTVFNPTGLSREG					
	: :					
g554	TDKLLKGMIALCANDAALTADRLNGSIE NFVQOMNKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
	: : :					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNRHLIVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	: : :					

836

```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

           370      380      390
m554 . pep TIAEKEIVALENVKKRSRWQRLWACLTGQX
           |||||||||||||:|||||||||:|||||
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTCA
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAAACCT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTA C GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTC AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IRSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAAATL AGRLGNGSIE
151 NFVQQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQTPETLTAAHIVIDLQSKQILS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQTPETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDVS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSGNIRSEENLKIPESAWASEGSRMFVRPGDVS

```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	310	320	330	340	350	360
m554.pep	370	380	390			
a554	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc  tggccgcttg
101 ccattcctgct tgcgcgcgtc atcgctcgccg ccgctgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATTA TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTGTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCGCAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

838

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAAACT	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTTTA	AGCCTCATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT
201	CGACATCGAT	CCCGAAAAAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC
301	CTGTGCGAAA	AATGTTCGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCGACACGT	CAGGAAATCA	ATCAAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKTCLRGLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLAIV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKKRPTR	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

```

a557.seq
  1  ATGAACAAAC  TGTTTCTTAC  TGCCGCAGTG  CTGATGCTGG  GCGCGTGCGG
 51  TTTCCACCTG  AAAGGTGCAG  ACGGCATTTC  TCCGCCGCTG  ACCTACCGGA
101  GCTGGCACAT  CGAAGGCGGA  CAGGCATTGC  AGTTTCCTTT  GGAAACCGCG
151  CTGTATCAGG  CTTCGGGTAG  GGTGGACGAT  GCTGCCGCGG  CGCAGATGAC
201  CCTGCGTATA  GACAGCGTTT  CCCAAAACAA  GGAAACCTAC  ACCGTTACCC
251  GTGCGGCAGT  CATCAACGAA  TATCTTTTGA  TATTGACGGT  TGAAGCGCAG
301  GTATTGAAAC  GCGGCGAGCC  GGTCCGGCAA  CCGATGACCG  TGTCCGTCGG
351  CCGCGTCCTT  GCTTATGCCG  ACAACGAGAT  CTTGGGCAAA  CAGGAAGAGG
401  AAGCGGCATT  GTGGGCGGAA  ATGCGGCAGG  ATGCCGCCGA  ACAGATTGTC
451  CGCCGCCTGA  CCTTTCTGAA  GCGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
  1  MNKLFLTAAV  LMLGACGFHL  KGADGISPPL  TYRSWHIEGG  QALQFPLETA
 51  LYQASGRVDD  AAGAQMTLRI  DSVSQNKETY  TVTRAAVINE  YLLILTVEAQ
101  VLKRGEVPGK  PMTVSVRRVL  AYADNEILGK  QEEEAALWAE  MRQDAAEQIV
151  RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
a557	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALQFPLE
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTL	RIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGEV
a557	AAGAQMTL	RIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGEV
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL	GKQEEEA	ALWAEMRQ	DAAEQIVR	RRLTFLKA	EX
a557	AYADNEIL	GKQEEEA	ALWAEMRQ	DAAEQIVR	RRLTFLKA	EX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
  1  ATGGATGCTT  GTTTTTTCGT  CATTCCCGCA  CAGGCGGGAA  TTCGGAGATT
 51  CGGGATTGTT  TTCAAACGTT  CGGGTCGGAT  TCTTGCCGGT  GCGGGAATGA
101  TGCCCTTATA  TACTTTCTCC  GAGCTTTATA  TGCTTCAACA  GGGGACGGCA
151  CATCAAGCAC  CGCACTGCGT  GTTGCCCGAA  CGAGGCTGCC  CTCCGATTAG
201  ATTCTATCGC  TATAAACAGA  CGGGTTTCAA  CCGAAAAGGA  ATGGGGATAA
251  AGTCCATTTT  CGACACCTCT  CGGGCGATGC  CGTCTGAAAA  CCAATCTCCA
301  CTTTCAGACG  GCATTGTTTA  G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
  1  MDACFFVIPA  QAGIRRFQIV  FKRSGRILAG  AGMMPLYTFS  ELYMLQQGTA
 51  HQAPHCVLPE  RGCPIRFYR  YKQTGFNRKG  MGIKSISDTS  RAMPSENQSP
101  LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
  1  ATGAATGCTT  GTTTTTTCGT  CATTCCACAC  CAGGCGGGAA  TTCGGAGATT
 51  CGGGATTGTT  TTCAAACGTT  CGGGTCGGAT  TCTTGCCGGT  GCAGGAATGA
101  TGCCCTTATA  TACTTTCTCC  GAGCTTTATA  TGTTTCAACA  GGGGACGGCA
151  CATCAAGCAC  CGCACTGCGT  GTTGCCCGAA  CGAGACTACC  CTCCGATTAG
201  ATTCTATCGC  CATAAACAGA  CGGGTTTCAA  CCGAAAAGGA  ATGGGGATAA
251  AGTCCATTTT  CGACATCTsT  CGGGCGATGC  CGTCTGAAAA  CCAATCTCCA
301  CTTTCAGACG  GCATTGTTTA  G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

m558/g558

a558.seq

a558.pap

g560.seq

1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccaqcct

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```

51 gattttcctc tttcccttta tgctgctcgc ctgcgctttc cgggacgggg
101 cgcacaagat ggcgcggggc tgggtcggca tcctcaactg gtcgctcaaa
151 cacatcgctc ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201 ccgccccctc gtcattctgcg ccaaaccacca aagcggtctg gaaacgctcg
251 cgctccaaga gatttttccg ccgcagggtt acgttgccaa gcgcgagttg
301 ttcaaaatcc cttttttcgg ctggggcttg aaactggtca aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttggcgcg caaaaacgaa ggttattgga ttaccatttt ccccgaggcg
451 acgcgccttg cgcccggaaa acgcggcaaa tacaactcgc gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcattcatc gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651 gatggaaaaa tgcaaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1 MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51 HIVGLKYRII GAEHIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1 ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51 GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTGCGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACGTGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGGTGGTG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGCG
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACCTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCCG
701 GCGCAGGCCG GTTGTCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1 MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51 HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g560       MLIIRNLIYWLILCSSLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90     100     110     120
m560.pep  GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g560       GAEHIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1  ATGCTCATCA TCCGCAACCT GATTTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CCTTTTCCG CTGGGGCTTG AAATGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTTGGCGCG CAAAACGAA GGCTATTGGA TTACCATTTT CCGGAAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAAA TACAAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCG
701 GCGCAGGCCG GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMKCEHLIETQQPLISGAGPFAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMGKCEHLIETQQPLISGAGPFAA				
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```
m561.seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCTT
301 TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCGTCCA GTCTTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCGGAAACA TCGAACTGTT TTTGACGGCA
451 TTGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTGCTC TGTACTGATG CTGTTTGGC
551 ACCAGATTG GGTATCCGG CCGCTGACAG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTTCAA TCAAATGGG GGCAGGTTGA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGC GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGG TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTTCCCATTT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGT CATTTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGCGGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAG CCGCCTTTGC
1251 CGAAACAAA CGGGAGGAAG CCGCAGAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAATCA GCAATAAAGA ATTTCCCGAA GCCGTGCCG ACCTATTGCG
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTCTT GCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCTTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTCGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA
```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```
m561.pep
1  MILPARFSDG ISLSLRKL TGLWVGLAAL SVVLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLTLY QTTTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAAENISF IKTGVEQECY DVRELLLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMIFIL
```

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501 QESLSNIRKH ARATHVKFTL SEHGRFTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRL	ENAASVIEEAGNLR	MQAY			
g561	MILPTRFSDGIPLSRLKLLTGLWVGLAALSVVLTLLLSFRL	ENAASVIEEAGNLR	KMQAY			
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
g561	RLAYMAGEGSPRAQIDNQIAEFKSLKRISQSDAIHPLIPSDNPLAYDLIQSMLIIDWQA					
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
g561	NILPPLQAYRRPTQIELYRFAGNIELFLQALENAGEKNTWWLRRFQWVIMLMTLVSSVLM					
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
g561	LFWHQIWVIRPLQALREGAERIGQRHFDIPVPEDVRPNNSRSGGVSTKWRSGX					
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQONQLTLLYQTTTRDLHQSYIPQQA AEHFLNRILPAVGADSGRVCLDG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCCGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCGTC	TGTACTGATG	CTGTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCCGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCATTT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTCG
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGAAGTG ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
  1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
 51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMILIOWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIWWIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEERL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFANR REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFD ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

          10          20          30          40          50          60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY
a561      MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY
          10          20          30          40          50          60

          70          80          90          100         110         120
m561.pep RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMILIOWQA
a561      RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMILIOWQA
          70          80          90          100         110         120

          130         140         150         160         170         180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
a561      HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
          130         140         150         160         170         180

          190         200         210         220         230         240
m561.pep LFHWQIWWIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRLKILYDDL
a561      LFHWQIWWIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRLKILYDDL
          190         200         210         220         230         240

          250         260         270         280         290         300
m561.pep EGQVAEQTRSLEKQNQNLTLLYTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
a561      EGQVAEQTRSLEKQNQNLTLLYTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
          250         260         270         280         290         300

          310         320         330         340         350         360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
a561      GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
          310         320         330         340         350         360

          370         380         390         400         410         420
m561.pep LGRQLGVSLAGAKQEEERLLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFANR
a561      LGRQLGVSLAGAKQEEERLLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFANR

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	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFRTKISNKEFPPEAVADLFARFTQQTGITVETA					
	: : : : :					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFRTKISNKEFPPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENGSLPPEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
	: : : : : : :					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
	: : : : : :					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

1	atggcaagcc	cgtcagagtct	gcctttcaat	tcgggcaaga	ccaaaccgac
51	ggcttttgcc	gcgccggttt	tggtcggaat	catgttttcc	acgccgctgc
101	ggcgcgggcg	caggtccttg	tggcgacagt	cggtaacggt	ttggtcggtg
151	gtcagtgctg	ggatggtggt	cattgcgcct	ttgacgatgc	cgacgctttc
201	gctcaacact	ttggcaaccg	gcgagaggca	gttggtggtg	caggaagcgt
251	tggaaacgac	ggtcatgtcg	gcggtcagga	cgtgtcgtt	cacgccgtac
301	acgacggttg	catcgacatc	gtcgccgccc	ggtgcggaaa	tgaggacttt
351	tttcgcgccg	ctttcgaggt	ggattttg	tttttctttg	ctggtgaacg
401	cgccggtgca	ttccatgacc	aaatcgacac	cgagttcttt	ccacggcagt
451	tcggcagggg	tgcgggtcga	gaagaagggg	attttgtcgc	cgttgacgat
501	gaggttgccg	ccgtcgtggg	atacgtcggc	ttcaaagcgt	ccgtgtacgg
551	tgtcgaattt	ggtcagatgg	gcgttggttt	caaggctgcc	gctggcgttg
601	acggcgacga	tttgaggttg	gtcttga		

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

1	MASPSLPFN	SGKTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAMMVVIAP	LTMPTLSLNT	LATGERQLVV	QEALETTVMS	AVRTLSFTPY
101	TTVASTSSPP	GAEMRTFFAP	LSRWILAFSL	LVNAPVHSM	KSTPSSFHGS
151	SAGLRVEKKG	ILSPLTMLRP	PSWDTSASKR	PCTVSNLVRW	ALVSRLPLAL
201	TATIWSWS*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

1	ATGGCAAGCC	CGTCGAGCCT	GCCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCGGTTT	TGGTCGGAAT	CATGTTTTCC	ACGCCGCTGC
101	GGGCGCGGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	CGCTGTCGTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCAGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTTCGAGGT	GGATTTTGGC	TTTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCEA	GAAGAAGGGG	ATTTTGTGCG	CGTTGACGAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTCAGATGG	CGGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	GTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

1	MASPSLPFN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAMMVVIAP	LTMPTLSLNT	LATGERQLVV	QEALETTVMS	AVRTLSFTPY

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101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
 201 TATSWSWS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
g562	MASPSSLPFNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMP TSLN TLA TGERQLV VQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMP TSLN TLA TGERQLV VQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGS SAGLRVEKKGILSPLTMLRPPSWDTASAKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGS SAGLRVEKKGILSPLTMLRPPSWDTASAKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWSWSX					
g562	PCTVSNLVRWALVSRLPLALTATIWSWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq

1	ATGGCAAGCC	CGTCGAGTTT	GTCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCAGTTT	TGGTCGGAAT	CATGTTTTCC	ACGCCGCTGC
101	GGGCGCGGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	TGCTGTCGTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTCCAGAT	GAAC TTTGGC	TTTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCNA	GAAGAANGGG	ATTTTGTCGC	CGTTGACGAT
501	GAGGTGCGCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTGAGGTGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	TTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep

1	MASPSSLSFN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMVVIAP	LTMP TSLN T	LATGERQLV V	QEALETTVMS	AVRMLSF TPY
101	TTVASTSSPP	GAEMRTFFAP	LSR*TLAFSL	LVNAPVHSMT	KSTPSSFHGS
151	SAGLRVXKXG	ILSPLTMLRP	PSWDTASAKR	PCTVSNLVRW	ALVSRLPLAL
201	TATIWSWS*				

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL VSAWMVVIAP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSTFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRMLSTFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMKSTPSSFHGSAGLRVEKKGILSPLTMRLLPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMKSTPSSFHGSAGLRVXKXGILSPLTMRLLPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRPLALTATSWWSX					
a562.	PCTVSNLVRWALVSRPLALTATIWSX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

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1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GCGGTTGGA TTCAAGGCAA TCCTTGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAACG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCAGCATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 AACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACTTGC AAGCAGGAAA ACGCATTCCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CCGTACGACA GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAA ATCCAAGCCG GGCAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGCGCGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACG CGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101	GGCGGCCAAT	TGCTTGTGCA	AACAGAAAAA	GACGGTTTGC	ATAACGAGCA
2151	AACCTTTGGC	GAGAAGAAAG	TCTTCAGCGA	AAATGGTAAG	TTGCACAAC
2201	ACTGGCGTGC	GCGTCGTAAA	GGACATGATG	AAACAGGGCA	TCGTGAACAA
2251	AATTATACTT	TGCCGGAGGA	AATCACACGC	GACATTTCAC	TGGGTTCATT
2301	TGCCTATGAA	TCGCATAGCA	AAGCATTAAAG	CCGTCATGCG	CCCAGCCAAG
2351	GCACTGAGTT	GCCACAAAGT	AACCGGGATA	ATATCCGTAC	TGCGAAAAGC
2401	AACGGTATTT	CGCTACCCTA	TACGCCCAAT	TCTTTTACCC	CATTACCCGG
2451	CAGCAGCTTA	TACATTATCA	ATCCTGCCAA	TAAAGGCTAT	CTTGTGAAA
2501	CCGATCCACG	CTTTGCCAAC	TACCGTCAAT	GGTTGGGTAG	TGACTATATG
2551	CTGGGCAGCC	TCAAAC TAGA	CCCAAACAAT	TTACATAAAC	GTTTGGGTGA
2601	TGGTTATTAC	GAGCAACGTT	TAATCAATGA	ACAAATCGCA	GAGCTGACAG
2651	GGCATCGTCG	TTTAGACGGT	TATCAAAACG	ACGAAGAACA	ATTTAAAGCC
2701	TTAATGGATA	ATGGCGCGAC	TGCGGCACGT	TCGATGAATC	TCAGCGTTGG
2751	CATTGCATTA	AGTGCCGAGC	AAGCAGCGCA	ACTGACCAGC	GATATTGTTT
2801	GGTTGGTACA	AAAAGAAGTT	AAACTTCCTG	ATGGCGGCAC	ACAAACCGTA
2851	TTGATGCCAC	AGGTTTATGT	ACGCGTAAA	AATGGCGGCA	TAGACGGTAA
2901	AGGTGCATTG	TTGTCAGGCA	GCAATACACA	AATCAATGTT	TCAGGCAGCC
2951	TGAAAACTC	AGGCACGATT	GCAGGGCGCA	ATGCGCTTAT	TATCAATACC
3001	GATACGCTAG	ACAATATCGG	TGGGCGTATT	CATGCGCAAA	AATCAGCGGT
3051	TACGGCCACA	CAAGACATCA	ATAATATTGG	CGGCATTCTT	TCTGCCGAAC
3101	AGACATTATT	GCTCAATGCG	GGTAACAACA	TCAACAACCA	AAGCACGGCC
3151	AAGAGCAGTC	AAAATGCACA	AGGTAGCAGC	ACCTACCTAG	ACCGAATGGC
3201	AGGTATTTAT	ATCACAGGCA	AAGAAAAAGG	TGTTTTAGCA	GCGCAGGCAG
3251	GCAAAGACAT	CAACATCATT	GCCGGTCAAA	TCAGCAATCA	ATCAGATCAA
3301	GGGCAAACCC	GGCTGCAGGC	AGGACGCGAC	ATTAACCTGG	ATACGGTACA
3351	AACCGGCAAA	TATCAAGAAA	TCCATTTTGA	TGCCGATAAC	CATACCATCC
3401	GAGGTTCAAC	GAACGAAGTC	GGCAGCAGCA	TTCAAACAAA	AGGCGATGTT
3451	ACCctatTGT	CAGGGAATAA	TCTCAATGCC	AAAGCTGCCG	AAGTCGCGAG
3501	CGCAAAAGGC	ACACTTGCCG	TGTATGCTAA	AAATGACATT	ACTATCAGCT
3551	CAGGCATCCA	TGCCGGCCAA	GTTGATGATG	CGTCCAAACA	TACAGGCAGA
3601	AGCGGCGGCG	GTAATAAATT	AGTCATTACC	GATAAAGCCC	AAAGTCATCA
3651	CGAAACTGCT	CAAAGCAGCA	CCTTTGAAGG	CAAGCAAGTT	GTATTGCAGG
3701	CAGGAAACGA	TGCCAACATC	CTTGGCAGTA	ATGTTATTTC	CGATAATGGC
3751	ACCCGGATTG	AAGCAGGCAA	TCATGTTTCG	ATTGGTACAA	CCCAAACCTCA
3801	AAGCCAAAGC	GAAACCTATC	ATCAAACCCA	AAAATCAGGA	TTGATGAGTG
3851	CAGGTATCGG	CTTCACTATT	GGCAGCAAGA	CAAACACACA	AGAAAACCAA
3901	TCCCAAAGCA	ACGAACATAC	AGGCAGTACC	GTAGGCAGCC	TGAAAGGCGA
3951	TACCACCATT	GTTGCAAGCA	AACACTACGA	ACAAACCGGC	AGCAACGTTT
4001	CCAGCCCTGA	GGGCAACAAC	CTTATCAGCA	CGCAAAGTAT	GGATATTGGC
4051	GCAGCACA AAA	ACCAATTAAA	CAGCAAAACC	ACCCAAACCT	ACGAACAAAA
4101	AGGCTTAACG	GTGGGCATTTC	AGTTCGCCCG	TTACCGATTTC	GGCACAACAA
4151	GCGATTGCCG	TAGCACACAA	AGCAGCAAAC	AAGTCGGACA	AAGCAAAAAC
4201	GACCGCGTTA	ATGCCATGGC	GGCTGCCAAT	GCAGGTTGGC	AGGCCTATCA
4251	AACAGGCAAA	GGCGCACAAA	ACTTAGCCAA	TGGTACAACC	AATGCCAAAC
4301	AAGTCAGCAT	CTCCATAACC	TACGGCGAAC	AGCAAAACCG	ACAAACCACC
4351	CAAGTTCAAG	CCAATCAAGC	CCAAGCGAGT	CAAATTCAAG	CAGGCGGCAA
4401	AACTACCCTT	TATTGCCGAA	GGTGCGGCGA	ACAATCCAAT	ATCAACATCA
4451	CAGGCTCAGG	TGTTTCAGGC	AGAGCAGGAA	CCGGCCTGAT	TGCCGATAAG
4501	CAAATCCATC	TGCAATCAGC	CGAGCAAAGC	AATACCGAAC	GCAGCCAAAA
4551	CAAATCAGCA	GGCTGGAACG	CAGGTGCTGC	CGTATCATTC	GGACAAGGAG
4601	GCTGGTCAAT	AGGCGTTGCC	GCAGGCGGCA	ATGTCGGCAA	AGGCTACGGC
4651	TATGGCGATA	GCGTAACCCA	CCGCCATAGC	CATATTGGCG	ACAAAGGCAG
4701	CCAAACCTTT	ATCCAAAGTG	GTGGCGATAC	CATCATCAAA	GGCGCGCAAG
4751	TACGCGGCAA	AGGCGTACAA	GTCAATGCCA	AAAACCTAAG	CATTCAAAGT
4801	GTACAAGATA	GAGAACTTTA	TCAAAGCAAA	CAACAAAACG	CCGGTGCACA
4851	AGTTACCGTA	GGTTATGGCT	TCAGTGCCAG	TGGCGATTAC	AGCCAAAGCA
4901	AAATCCGAGC	CGACCATGCT	TCGGTAACCG	AGCAAAGCGG	TATTTATGCC
4951	GGAGAAGACG	GCTATCAAAT	CAAGGTCGGA	AACCATAACG	GCCTCAAAGG
5001	CGGCATCATC	ACCAGCAGCC	AAAGCGCAAA	AGACAAGGGT	AAAAACCGAT
5051	TCAGCAGAGG	CACACTCGCC	GGCAGTGATA	TTCAAAATTA	CAGCCAATAC
5101	GAAGGAAAAA	GTTTGGATT	GGGTGCCAGC	GTTGCCGTAA	GCGGCAAAAC
5151	ACTGGGACAG	GGCGCAAAAA	ATAAACCTCA	AGACAAACAC	CTGACAAGCA

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5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CAAAAACAT
5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
5401 CGACATTTCG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
5451 TGAAGTGGAT TTACAAAgAa CCGTCAGCCA AGATTTTAGT AAAAATGTTC
5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
5651 CAGATAATTG GCAACAAGGC AAAGTCATTC TCAACATGTT AGCCTCAGGT
5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
5751 GCCagaCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
5801 AAAACGCGAA TGGCAAAC TAACGCCAGTC AagaAACCGC TCACGTTCTT
5851 GCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgaggag
6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtA cGgctGCCGG
6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
6101 cggctTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

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1  MNKTLRYVIF NRKRGAVVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
51  SKAFCFSALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNGIP
101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
201 ASRATLTGQ PQYQAGDFSG FKIRQGNAVI AGHGLDARDT DFTRILLYAN
251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
351 SLNNQNGEIA TNQQLIIHDG QSTVVIDNT NGTIQSGRDV AIQAKSLSN
401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
451 IKANNLDNAV QGNIQSGGTT DIGTQHNLN RGLIDGQQTK IQAGQMNNIG
501 TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
551 SGNDMAVGA LDTNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH
601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWFVYNN ESDHLRTPDG
651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNYWRARRK GHDETGHREQ
751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGTELPOS NRDNIRTAKS
801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGSDYM
851 LGSCLKDPNN LHKRLGDGYY EQRLINEQIA ELTGHRRLDG YONDEEQFKA
901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVWLQKEV KLPDGGTQTV
951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
1001 DTLDNIGGRI HAQSAVTAT QDINNIGGIL SAEQTLLLNA GNNINNQSTA
1051 KSSQNAQSS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
1101 GQTRLQAGRD INLDTVQTK YQEIHFADN HTIRGSTNEV GSSIQTKGDV
1151 TLLSGNNLNA KAAEVGSAGK TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
1201 SGGGNKLVIT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
1251 TRIQAGNHVR IGTTQTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
1301 SQSNEHTGST VGSLKGDTTI VASKHYEQTG SNVSSPEGNN LISTQSMDIG
1351 AAQNQLNSKT QTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVGQSKN
1401 DRVNAMAAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQNRQTT
1451 QIQANQAQAS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK
1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGWSLGVVA AGGNVKGGY
1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTIIK GAQVRGKGVQ VNAKNLSIQS
1601 VQDRETYQSK QQNAGAQVTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGTLA GSDIQNYSQY
1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTSIADKNGA SSSVGYGSDS
1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTTDTAE
1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNTEI NQHLDKLKAD
1851 KEAAETAAAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQNANGKL TASQETAHVL
1951 AHAVLGAAVA AAXGNNAPAG ALGAGGSEAA APIIGKWLYG KGDGGSLNAE
2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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1  ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATT A
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAACGGCA TACCGCAAGT CAATATTCAA ACCCCTACTT CGGCAGGGGT
351 TTCTGTTAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAATCCTT GGTGCGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAA T
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATTT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTCTG
801 TGTCGTCGCG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTTCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATTC
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAAGTCAA TATCCGAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTCGGGC AGCCTGAAA AATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC AACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT CACTACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTGCGACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTCATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAATTATC AGTGATGCGG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCTT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTTCAG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATTT TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTTCG ATTAAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
2451 CATCGGACAA TTAACAACC GTGAAAACAG TCTGATTTAC AGCGGTAACG
2501 ATATGGCCGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTTGA
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2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAGTT
2851 ACCCAAACCT CGCCAGCCAA AATCATTTCA GGTAATGATT TAACCATTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
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 3101 TGCCGGAGGA AATCACACGC AACATTTTAC TGGGTTCATT TGCCATGAA
 3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
 3201 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
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 3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA
 3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC
 3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC
 3601 GATATTGTTT GGTGGGTACA AAAAGAAGTT AAGCTTCCTG ATGGCGGCAC
 3651 ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA
 3701 TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT
 3751 TCAGGCAGCC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT
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 3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
 3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA
 3951 AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
 4001 ACCGAATGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA
 4051 GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAA TCAGCAATCA
 4101 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG
 4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
 4201 CATGTTATTC GCGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
 4251 AGCGGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG
 4301 AAGTCAGCAG CGCAAACGGT AACTCGCTG TGTCTGCCAA AAATGACATC
 4351 AACATCAGCG CAGGCATCAA CACGACCAT GTTGATGATG CGTCCAAACA
 4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
 4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAG CAAGCAAGTT
 4501 GTATTGCAGG CAGGAAACGA TGCCAACATC CTTGGCAGCA ATGTTATTTT
 4551 CGATAATGGC ACCCAGATT CAGCAGGCAA TCATGTTTCG ATTGGTACAA
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 4651 TTGATGAGTG CAGGTATCGG CTTCATATT GGCAGCAAGA CAAACACACA
 4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
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 4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
 4851 AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT
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 5001 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
 5051 CCTATCAAAC AGGTAAGAGT GCACAAACT TAGCCAATGG TACAACCAAT
 5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
 5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG
 5201 GTGGTAAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC
 5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
 5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG
 5351 GCCAAACAAA ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTCGGA
 5401 CAAGGAGGCT GGTCAATTAG CGTTACCGCA GGCGGCAATG TCGGCAAAGG
 5451 CTACGGCAAT GCGGACAGCA TCACCCACCG CCATAGCCAT ATCGGCGACA
 5501 AAGGCAGCCA AACCCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
 5551 GCGCAAGTAC GCGGCAAAGG CGTACAAGTC AATGCCAAA ACCTAAGTAT
 5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAAACGCCA
 5651 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC
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 5751 TTATGCCGGA GAAGACGGCT ATCAAATCAA GGTGCGAAAC CATACAGACC
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 5851 AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCACAG
 5901 CCAATAACAA GGCGAAAGTT TTGGATTGGG CGCAAGTGCG TCCATAAGCG
 5951 GCAAAACACT GGGACAGGCG GCACAAAATA AACCTCAAAA CAAACACCTG
 6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
 6051 CGACAGCGAC AGTCAAAGCA GCATCAACAA AAGCGGCATC AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAACCT GGATTTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTAGACA AACTCAAAGC
6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
6601 GGTCAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTCGGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAAATT TATTCCTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
7151 GCAAAGATAT TGCTGTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TAAATACCA
7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAAGAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACCT AGATAATACT GGTCCCGGAT TTAATAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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1  MNKTLRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVPFGTTH
51  APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
151 GNPWLARGEA RVVQNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIDAP VWQDVRVVA GQNDVVATGN AHSPILNNA ANTNNNTANN
301 GTHIPLFAID TGKLGGMYAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSQTAV SQQGTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQGLKSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QQGLNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQQLIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK
851 AQRHINAGAT IEAAGKMRLG VEKLHNTNEH LKTQLVETGR EHVVDYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGSYDM LDSLKLDPNN LHKRLGDGYE EORLINEQIA
1151 ELTGHRRLDG YQNDDEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
1301 SAEQTLNNA GNNINSQSTT ASSQNTQGSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGQDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
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855

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1651 AQQAIAVAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSIISITY GEQQNRQTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYG GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKKG
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPONKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLDKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGKV ILNMLASGLA APTQSGAGIA AATASPAVSY AIGQHFKDLA
2201 GQNANGKLTA SQETAHVLAH AVLGAAVAAGV GDNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAGVN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAIGS VHKDPGSTLE PNISTIATF
2351 QLNLFNPSEF GEGGVGNF RHVLWQATIT REFGKDIQV VGNSHESGK
2401 INYSIRRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563.pep      MNKTLYRVIFNRKRGA VVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
               |||||
m563.pep      MNKTLYRVIFNRKRGA VVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
               10      20      30      40      50      60

              60      70      80      90     100     110
g563.pep      FSALGFSLCLALGTVNIAFADGIITDKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
               || |||||: ||: |||||: |||||
m563.pep      FSLLGFSLCLAVGTANIAFADGIADKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
               70      80      90     100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIOGNPWLTRGEARVVVNQINSSHPSQLNGYIE
               |||||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIOGNPWLARGEARVVVNQINSSHSQMNGYIE
               130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIROGNAVIAGHGL
               |||||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLGFKIROGNVVIAGHGL
               190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
               |||||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPI LNNA AANTSNTANN
               250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
               : |||||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
               310     320     330     340     350     360

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857

g563 . pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSENGKLHNYWRARRK
m563 . pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSENGKLHSYWREKHK
	970 980 990 1000 1010 1020
	750 760 770 780 790 800
g563 . pep	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563 . pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHRKALSHHAPSQGTLPQSN-----
	1030 1040 1050 1060 1070
	810 820 830 840 850 860
g563 . pep	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLPNN
m563 . pep	-GISLPYTSNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDSLKLPNN
	1080 1090 1100 1110 1120 1130
	870 880 890 900 910 920
g563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
	930 940 950 960 970 980
g563 . pep	SAEQAAQLTSDIVWLQKEVKLPDGGTQTVLMPQVYVRVKNGGIDGKGALLSGSNTQINV
m563 . pep	SAEQVAQLTSDIVWLQKEVKLPDGGTQTVLVPQVYVRVKNGDIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
	990 1000 1010 1020 1030 1040
g563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGILSAEQTLNNA
m563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGMLSAEQTLNNA
	1260 1270 1280 1290 1300 1310
	1050 1060 1070 1080 1090 1100
g563 . pep	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAQAQKDINI IAGQISNQSDQ
m563 . pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAQAQKDINI IAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
	1110 1120 1130 1140 1150 1160
g563 . pep	GQTRLQAGRDINLDTVQTKGYQEIHFADNHTIRGSTNEVGSSIQT KGDVTLLSGNNLNA
m563 . pep	GQTRLQAGRDINLDTVQTSKHQATHFDADNHVIRGSTNEVGSSIQT KGDVTLLSGNNLNA
	1380 1390 1400 1410 1420 1430
	1170 1180 1190 1200 1210 1220
g563 . pep	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGKNLVI TDKAQSHHETA
m563 . pep	KAAEVSSANGT LAVSAKNDINISAGINTTHVDDASKHTGRSGGKNLVI TDKAQSHHETA
	1440 1450 1460 1470 1480 1490
	1230 1240 1250 1260 1270 1280
g563 . pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTRIQA GNHVRIGTTQTQSQSETYHQTQKSG
m563 . pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTQIQAGNHVRIGTTQTQSQSETYHQTQKSG
	1500 1510 1520 1530 1540 1550
	1290 1300 1310 1320 1330 1340
g563 . pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS LKGDTTIVASKHYEQTSNVSSPEGN

859

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGN NAPAGALGAGGSEAAAPI IGKWL YGKG DGGS LNAE					
	: : : :					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWL YGKEKGS DLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX					
	: : : : : :					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGS LNAQSAVENNDTVEQVKFALRHPRIAIAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLPNSEFGGEGGVGNAFRHLVWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1  ATGAACCGCA  CCCTGTACAA  AGTTGTATTT  AACAAACATC  GAAACTGCAT
51  GATAGCCGTT  GCTGAAAATG  CCAAACGCGA  GGGCAAAAAC  ACAGCCGACA
101 CCCAAGCTGT  AGGTATTTTG  CCAAATGATA  TTGCGGGCTT  TGCGGGTTTT
151 ATCCATTCTA  TCTCTGTTAT  CTCATTCTCC  CTTTCATTAC  TGCTCGGTTC
201 TGCCCTTATC  CTGACTTCTT  CTTCTGCTAC  TGCCCAAGGT  ATCGTTGCCG
251 ACAAATCCGC  ACCTGCACAG  CAACAGCCTA  CCATCCTGCA  AACAGGTAAC
301 GGCATACCGC  AAGTCAATAT  TCAAACCCCT  ACTTCGGCAG  GGGTTTCTGT
351 TAATCAATAC  GCCCAGTTTG  ATGTGGGTAA  TCGCGGGGCG  ATTTTAAACA
401 ACAGTCGCAG  CAACACCCAA  ACACAGCTAG  GCGGTTGGAT  TCAAGGCAAT
451 CTTTGGTTGG  CAAGGGGCGA  AGCACGTGTG  GTTGTAACC  AAATCAACAG
501 CAGCCATTCT  TCACAACTGA  ATGGCTATAT  TGAAGTGGC  GGACGACGTG
551 CAGAAGTCGT  TATTGCCAAT  CCGGCAGGGA  TTGCAGTCAA  TGGTGGTGGT
601 TTTATCAATG  CTTCCCGTGC  CACTTTGACG  ACAGCCCAAC  CGCAATATCA
651 AGCAGGAGAC  CTTAGCGGCT  TTAAGATAAG  GCAAGGCAAT  GTTGTAAATCG
701 CCGGACACGG  TTTGGATGCA  CGTGATACCG  ATTACACACG  TATTCTCAGT
751 TATCATTCCA  AAATTGATGC  ACCCGTATGG  GGACAAGATG  TTCGTGTCGT
801 CGCGGGACAA  AACGATGTGG  CCGCAACAGG  TGATGCACAT  TCGCCTATTC
851 TCAATAATGC  TGCTGCCAAT  ACGTCAAACA  ATACAGCCAA  CAACGGCACA
901 CATATCCCTT  TATTTGCGAT  TGATACAGGC  AAATTAGGAG  GTATGTATGC
951 CAACAAAATC  ACCTTGATCA  GTACGGTCGA  GCAAGCAGGC  ATTCGTAATC
1001 AAGGGCAATG  GTTTGCCTCA  GCCGGCAATG  TGGCAGTGAA  TGCTGAGGGT
1051 AAATGGTCA  ACACGGGCAT  GATTGCAGCG  ACGGGAGAAA  ATCATGCGGT
1101 TTAATTCAT  GCCCGCAATG  TTCATAATAG  CGGTACGGTT  GCCTCACAGG
1151 ATGATGCCAA  TATTCACAGC  CAGACGCTGG  ACAATTCAGG  TACGGTCTTA
1201 TCCTCAGGTC  GATTGACTGT  TCGTAATTTA  GGCCGTCTGA  AAAACCAAAA
1251 CAACGGTACG  ATCCAGGCTG  CCCGCTTAGA  TATGTCAACA  GGTGGTTTGG
1301 ATAACACAGG  TAATATTACT  CAAACAGGTT  CACAAGCATT  GGATTTGGTA
1351 TCTGCCGGCA  AATTCGATAA  CAGTGGCAAG  ATTGGTGTA  GTGACGTTCC
1401 ACAGACCGGT  TTGAATCCCA  ATCCATCAGT  CATACCACAG  ATTCCGAGTA
1451 CTGCAACAGG  TTCAGGCAGC  AGCACTGTCT  CGGTATCTAA  GCCTGGTTCA
1501 AACAATCCCG  TTTCACCTAC  AGCACCTGCA  AAAAATACG  CCGTAGGACG
1551 CATTCAAACA  ACAGGAGCAT  TTGACAATGC  AGGATCAATT  AATGCGGGTG
1601 GGCAAATTGA  CATTGCCGCC  CAAAACGGTT  TGGGAAATTC  GGGTAGTCTG
1651 AATGCGGCTA  AACTACGAGT  ATCAGGCGAT  TCATTTAACA  ATACGGTAAA
1701 AGGCAAATC  CAGGCACACG  ATCTGGCTGT  TAACACTCAA  ACTGCTAAAA
1751 ACAGCGGTCA  CTTATTAAC  CAAACCGGCA  AGATTGATAA  CCGTGAAC  CTG
1801 CATAATGCCG  GAGAAATTGC  CGCCAACAAT  CTGACACTCA  TTCATTCCGG
1851 CCGCTTGAGC  AATGATAAAA  AAGGCAATAT  TCGAGCTGCA  CATTTACAGC
1901 TTGATACCGC  CGGTTTACAT  AATGCAGGTA  ACATTCTTGC  CGATAGTGGA
1951 ACCGTTACCA  CCAAGAATAA  TCTTCGCAAT  ACAGGAAAAG  TTTCTGTTGC
2001 ACGACTGAAT  ACCGAAGGTC  AGACTCTAGA  TAATACGCGC  GGACGTATAG
2051 AGGTGAAAC  GGTTAACATC  CAAAGTCAGC  AACTGACTAA  CCAAAGCGGC
2101 CATTTACTG  CTACCGAACA  ACTGACTATC  AATAGTCGAA  ATGTAGACAA
2151 CAAAACGGC  AAACCTCTAT  CTGCAAACCA  AGCACAATTA  GCTGTTTCAG
2201 ACGGCCTATA  CAACCAACAT  GGTGAAATTG  CCACCAACCG  GCAGTTGTCT

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2251	ATTCACGATA	AAAATCAAAA	CACTTTGGCG	TTAAACAATG	CGGATGGCAC
2301	GATTCAATCT	GCCGGTAATG	TATCGCTACA	AGCCAAATCA	CTCGCCAACA
2351	ATGGCACATT	AACAGCCGGT	AACAACTGG	ATATTGCTTT	GACGGACGAT
2401	TTCGTCGTAG	AGCGCGACCT	CACTGCAGGC	AAACAATTAA	ATCTAAGCAT
2451	AAAAGGCCGT	CTGAAAAATA	CCCATACCCT	ACAAGCAGGC	CATACGCTCA
2501	AACTCAATGC	CGGCAATATA	GATAACCAAG	TTACAGGCAA	AATTATTGGT
2551	GGAGAACAAA	CGGACATCAC	ATCCGAACAG	CATGTTGACA	ACAGGGGCTT
2601	GATCAACAGC	GACGGTTTGA	CCCACATCGG	TGCAGGTCAA	ACCCTGACCA
2651	ACACCGGGAC	AGGCAAAATC	TATGGCAACC	ATATTGCCCT	GGACGCGCAA
2701	ATACTGCTTA	ACCGGGAAGA	AACGACGGAA	GGCAGTACCA	AAGCGGGGGC
2751	AATAGCTGCA	AGGAAACGTT	TGGATATTGG	AGCGAAAGAG	ATTCATAACC
2801	AGAAGGTGC	CCTACTATCC	AGCGAAGGTA	TTTTTGCCGT	AgGTAATCGA
2851	CTGGATGAAC	AACATCATGC	GGCAGGCATG	GCCGATACCT	TTGTTAATGG
2901	CAGTGCCGGT	TTGGAAGTAC	AAGGTGATGC	ATTGATGTCC	GTTCGGAATA
2951	TGCAGAATAT	CAATAATCAC	TTTAAACAG	AGACATACTT	AGCCAAAGCG
3001	GAAAAGCAAG	TCCGCGACTA	CACCGTACTG	GGGCAAAATA	CCTACTATCA
3051	GGCGGGAAAA	GACGGTTTAT	TCGACAACTC	GCAAGGACAA	AAAGACCAAA
3101	CTACTGCTAC	GTTCCATTTA	AAAAATGGTT	CTCGTATTGA	GGCCAACCAA
3151	TGGCATGTCC	GAGACTACCA	CATCGAGACT	TATAAAGAAC	GCATCATCGA
3201	AAACCGGCCG	GCACACATTA	CTGTGGGCGG	TGATTTGACT	GCCTCAGGTC
3251	AAAATTGGCT	GAACAAAGAC	AGCCGGATTG	TAGTAGGCGG	GCGTATTATC
3301	ACTGATGATT	TAAACCAGAA	AGAAATTACC	AATCAAAGTA	CAACAGGCAA
3351	AGGTCGCACA	GATGCTGTCC	GCACACAGTG	GGATTCAAGT	ACAAAAAAG
3401	GATGGTACAG	CGGTAGAAAA	AGACAACGCC	GTAAGTAAAG	AAACCATACT
3451	CCTTACCATG	ATACCCAACT	ATTTACCCAC	GACTTCGACA	CGCCTGTATC
3501	CGTCATCCAA	CAGAATGCCG	CCTCCCCTTC	CTTTCAACCC	GCCGCATCTG
3551	CAATCAAAC	GATTGACGGA	GTATCCACGG	CAGCCGTCAA	TGGTCAGCGC
3601	ATCCATACCG	GTAATGTGGT	CTCGTTAAAT	AACGCTACTG	TTACTCTGCC
3651	TAACAGCAGC	CTCTATACCA	CCCATCCTGA	CAATAAAGGC	TGGTTGGTTG
3701	AAACCGATCC	TCAATTTGCA	GACTACCGCC	GCTGGTTGGG	CAGCGACTAC
3751	ATGTTGCAAC	AACTGCAATT	GGACACCAAT	CATCTACACA	AACGGCTTGG
3801	CGACGGCTAC	TACGAACAAA	AACTTGTAA	TGAACAAATC	CATCAGTTAA
3851	CAGGCTACCG	CCGACTCGAC	GGCTACAGGA	GTGATGAAGA	ACAATTCAAA
3901	GCTCTGATGG	ACAACGGCCT	TACTGCTGCC	AAAACATTCG	GTCTCACCCC
3951	AGGTATCGCC	TTGAGTGCAG	AGCAAGTTGC	CCGCTTAACT	TCAGATATCG
4001	TTTGGATGGA	AAATCAAACC	GTCACCCTGT	CTGACGGTTC	GACTCAAACC
4051	GTAAGTCTTA	CTAAAGTCTA	TGCCCTGGCG	CGCAAAGGTG	ATCTCAATAC
4101	CTCCGGTGGC	CTGATTAGTG	CCGAACAAGT	CTTACTTAAA	CTGCAAAACG
4151	GCAACCTGAC	TAACAGCGGT	ACCATTGCGG	GGCGACAGGC	CGTACTCATC
4201	CAGGCACGGA	ATATTAACAG	CAACGGTAAC	ATTCAAGCCG	ACCAAATCGG
4251	CTTAAAGCT	GAAAAAAGTA	TCAATATCGA	CGGCGGGCAG	GTACAAGCAG
4301	GCAGACTGCT	GACTGCCCAA	GCGCAAAATA	TCAACCTTAA	CGGTACAACC
4351	CAAACCTCCG	GTAATGAACG	TAACGGCAAT	ACCGCCATCG	ATCGTATGGC
4401	CGGCATTAA	GTGGTCGGAA	GCCATACTGA	ACAAGTAGAT	AACAGAAGTT
4451	CAGACGGCAT	CCTATCCCTG	CATGCCAGCA	ACGATATCAA	CCTCAATGCG
4501	GCCACCGTCT	CTAACCAAGT	TAAAGACGGC	ACTACCCAAA	TTACCGCCGG
4551	CAATAATCTC	AACCTCGGCA	CCATCCGTAC	CGAACATCGC	GAAGCCTATG
4601	GTACATTAGA	TGACGAGAAC	CATCGCCATG	TCCGCCAAAG	TACCGAAGTC
4651	GGCAGCAGTA	TCCGCACGCA	AAACGGCGCA	CTGCTTAGAG	CCGGTAACGA
4701	CTTAAAAATC	CGCCAAGGCG	AACTGGAGGC	CGAAGAAGGC	AAAACCGTCC
4751	TTGCCGACAG	ACGTGATGTC	ACTATCAGCG	AAGGACGCCA	AATAACCGAA
4801	CTGGATACCT	CGGTAAGCGG	AAAAAGCAAA	GGCATCCTTT	CCAGTACCAA
4851	AACACACGAC	CGCTACCGCT	TCAGTCATGA	TGAAGCAGTC	GGCAGCAACA
4901	TCGGCGGCGG	CAAAATGATT	GTTGCAGCCG	GGCAGGATAT	CAATGTACGC
4951	GGCAGCAACC	TTATTTCTGA	TAAGGGCATT	GTTTTAAAAG	CAGGACACGA
5001	CATCGATATT	TCTACTGCCC	ATAATCGCTA	TACCGGCAAT	GAATACCACG
5051	AGAGCAAAAA	ATCAGGCGTC	ATGGGTACTG	GCGGATTGGG	CTTTACTATC
5101	GGTAACCGGA	AACTACCGA	TGACACTGAT	CGTACCAATA	TTGTCCATAC
5151	AGGCAGCATT	ATAGGCAGCC	TGAATGGAGA	CACCGTTACA	GTTGCAGGAA
5201	ACCGCTACCG	ACAAACCGGC	AGTACCGTCT	CCAGCCCCGA	GGGGCGCAAT
5251	ACCGTACAG	CCAAAAGCAT	AGATGTAGAG	TTCCGAAACA	ACCGGTATGC
5301	CACTGACTAC	GCCCATACCC	AGGAACAAAA	AGGCCTTACC	GTCGCCCTCA
5351	ATGTCCCGGT	TGTCCAAGCT	GCACAAAAC	TCATACAAGC	AGCCCCAAAT
5401	GTGGGCAAAA	GTAATAATAA	ACGCGTTAAT	GCCATGGCTG	CAGCCAATGC
5451	TGCATGGCAG	AGTTATCAAG	CAACCCAACA	AATGCAACAA	TTTGCTCCAA
5501	GCAGCAGTGC	GGGACAAGGT	CAAAACAACA	ATCAAAGCCC	CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCTG
6101 GTTACGGATT CAGTGAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATTGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAAG
6351 CTTCGGCATA GGCGGCAGTT TCGACCTGAA CGGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCTG
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCCTGC TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCATTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGATTGG AACAAATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCTCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCATGAA
7551 CGTTGCCGAA GGACTGACGA GCCTTGTCAA CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GGCGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

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m564.pep
1  MNRTLYKVVF NKHRNCMIAV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPOYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPVPIQ IPSTATGSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKL RVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNLRLN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVNDQNG KLLSANQAQL AVSDGLYNQH GEIATNRQSL
751 IHDKNQNTLA LNNADGTIQS AGNVSQAQS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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Homology with \mathbb{F}_2

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ID      FHAB BORPE          STANDARD;          PRT;   3591 AA.
AC      P12255;
DT      01-OCT-1989 (REL. 12, CREATED)
DT      01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT      01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE      FILAMENTOUS HEMAGGLUTININ. . . .

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		10	20	30	40	50	60
m564	.pep	MNRTLYKVVFENKHRNCMI	AAVENAKREGKNTADTQ	AVGILPN	DIAGFAGFIHSISVISFS		
		: :: :: :: :: :: : : : :: ::					
fhaf_borpe		MNTNLYRLVFSHV	RGMLVPVSEHCTV-G-NTFCGRTRG---	QARSGARATSLSV	APNALA		
		10	20	30	40	50	
		70	80	90	100	110	119
m564	.pep	LSLLLG-SALIL	TSSSATAQ	GIVADKS	APAAQQPTIL	QTGNGIPQVNIQT	PTSAGVSVNQ
		: :: : : :: :: : : :: :					
fhaf_borpe		WALMLACTGLPLV	TH---AQGLV----	P-QGQTQVLQGG	NKVPVNIADP	NSGGVSHNK	
		60	70	80	90	100	
		120	130	140	150	160	170
m564	.pep	YAQFDVGNRGAIL	NNSRNTQTQLGG	WIQGNPWLARGE	ARVVVNQINSS	HSSSQLNGYIEV	
		: :: :: :: : : ::: : : : : : : : : : : : :					
fhaf_borpe		FQQFNVANPGVVF	NNGLTDGVS	RIGGALTKNPNL	TR-QASAILAEV	TDTPSRLAGT	LEV
		110	120	130	140	150	160

864

m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVS	LQAKSLANNGTLTAGNK	LDIALTD	DDFVVERDLTAGKQL	NLS	
fhab_borpe		RL-----DGA-HAGGQLRVSSD	GQAALGSLAAK	GELTVS	AARAATVA-EL---	KSLDNIS	
			720	730	740	750	760
m564	.pep	820	830	840	850	860	870
		IKGRLK-NHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINS	DGLT				
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---	VGKV--SAKSGIGLE----	GWGAVGADSL-			
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETTEGSTKAGATAARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG----	AEGGATLGAVEAAGSIDVRGGSTV--				
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQNNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTEVLGQNTYYQAGKDGLFDNSQGQKDQTTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVVQGEHLDLGTLAAVGAVDV----	NGTGdVRVAKLVSDAGADLQAGRS				
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRITDDLNQKE					
fhab_borpe		MTLGIVDTTGDLOARAQQKLELGSVKSDDGLQAAAGGALSALAAEVAGALELS---	GQGV				
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRTDVAGTQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSVGIGALKAGAVEAASPRRARRALR-----	QDFFTPG				
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIAKLIDGVSTAAVNGQRIHTGNVVSLLNNATVTLPNSSLYT					
fhab_borpe		SVVVRQQGNVTVGRGDPHGVLAQGDIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGSYMLQQLQLDNLHLKRLGDDGYEQKLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRIQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFGTLPG-IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI-----TDAVTGEARKDESVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

		1350	1360	1370	1380	1390	1400
m564	.pep	TLSDGSTQTVLVPKVYALARKGDLNTSGGLISAEQVLLKLQNGNLNSGTIAGRQAVLIQ					
fhab_borpe	--ENGASVTVRTT-----GNLVNKGYSAGKQGVLGV--GGALTNEFLVGSDDGTQRIE						
		1260	1270	1280	1290	1300	
		1410	1420	1430	1440	1450	
m564	.pep	ARNINSNGNIQ-----ADQIGLKAESINIDGGQVQAGRLLTAQ---AQNILNLNGTT					
fhab_borpe	AQRIENRGTFQSQAAPAGTAGALVVKAAEAIVDHGVMAATKGEQMIAQKGGGSPPTVTAGAKA						
		1310	1320	1330	1340	1350	1360
		1460	1470	1480	1490	1500	
m564	.pep	QTSGNERNGNTAI-DRMAGINVV-GSHTEQVDNRSTD-GILSLHASNDINLNAAATVSNOV					
fhab_borpe	TTSANKLSVDVASWDNAGSLDIKKGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV						
		1370	1380	1390	1400	1410	1420
		1510	1520	1530	1540	1550	
m564	.pep	--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLDDENHRHRVRQST-----EVGS					
fhab_borpe	TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNTGNLKVREGVTVTAASFNETGA						
		1430	1440	1450	1460	1470	1480
		1560	1570	1580	1590	1600	
m564	.pep	SIRTQNGALLRAGNDLKIRQGELEAEEGKTVLAAGRDV--TISEGRQITELDTS---VSG					
fhab_borpe	EVMKASATLTTSGAARN--AGKMVQKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG						
		1490	1500	1510	1520	1530	
		1610	1620	1630	1640	1650	1660
m564	.pep	K---SKGILSSTKTHDTRYF---SHDEAV-GSNIGGGKMIVAAGQDINVRGSNLISDKGI					
fhab_borpe	KMESNKDIVIKTEQFSNGRVLDKHLDTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG						
		1540	1550	1560	1570	1580	1590
		1670	1680	1690	1700	1710	
m564	.pep	VLKAGHDIDISTAHNRYTG-----NEYHESKKSVMGTGGLGFTIGNRKTTDDTDRTNIV					
fhab_borpe	TMAAGHDATLTKAPHLRNTGQVVAGHDIHIINSAKLENTGRV--DARNDIALDVADFTN--						
		1600	1610	1620	1630	1640	1650
		1720	1730	1740	1750	1760	1770
m564	.pep	HTGSIIGSLNGDVTTVAGNRYRQT----GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
fhab_borpe	-TGSLYAEHDA-TLTLAQGTQRDLVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGSLIA						
		1660	1670	1680	1690	1700	1710
		1780	1790	1800	1810	1820	1830
m564	.pep	HTQEQQGLTVALNVPPVQAAQNFIQAAQNVGKSKNRKVNAAMAAA-WQSYQATQMQQ					
fhab_borpe	EVQE-----NIDNKQA----IVVGKDLTLS-SAHGNVANEANALLWAAGELTVKAQN						
		1720	1730	1740	1750		
		1840	1850	1860	1870	1880	1890
m564	.pep	FAPSSSAGQGQNNNQSPSISVSITYGEQKRNEQKRHYTEAAASQIIGKQTTLAATGSG					
fhab_borpe	ITNKRAALIEAGGNARLTAADVALLNKLGRIRAGEDMHLD---APRI---ENTAKLSGEV						
		1760	1770	1780	1790	1800	1810
		1900	1910	1920	1930	1940	1950
m564	.pep	EQSNINITGSDVIGHAGTALIADNHIRLSAQKQDGSEQSKNKSSGWNAGVAVKIGNGIRF					
fhab_borpe	QRKGQVDVGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAAPWYGDDLTAEQSLIEV						
		1820	1830	1840	1850	1860	

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHVHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
				::		::: ::	:
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHI--DVDNRSV-					
		1870	1880	1890		1900	

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTQSGIYAGE				
		::: :	:::	: : :	: : :	: :
fhab_borpe		VRTVSAMEYFKTPLPVSILTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGKNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
		:::::		: :		::: :	::: :
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990		2000	2010

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGS DSKNSTTRSGVNTNHIHITDEAG				
		: :: :	::: :	: :		::: : : ::: : :
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKFGRNAA					
		::	:	:	:	: : : :::	: :
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRVT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		::	::	::: ::: :	: :	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLNNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYDTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		: ::	:	: : : :	: :	:	:
fhab_borpe		AQNRGRPEGLKIGAHSAHSVSGSFDALRDVGLEKRLDIDDALA AVLNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgccc aacgacaccg gtcgcctgc acttctggct
151 acctgcacgc gtgcgatgct caagtcgagc gcgaaatacg gaatatcctc
201 tttgggcgaa gacgcgtccg accgtctgcc cgccctgcc gaagccgaca
251 atcagcacat gatcagactt gtcacgctt tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCC AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

867

```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGA CTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SR TAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSFA NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

m565.pep      10      20      30      40      50      60
MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
|||||
g565          10      20      30      40      50      60
MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS

m565.pep      70      80      90      100     110     120
AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
|||||
g565          70      80      90      100     110     120
AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51 CGTAACCACC ACCATTTTCG CCCGTC CCGAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGA CTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SR TAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSFA NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

m565.pep      10      20      30      40      50      60
MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
|||||

```

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```

a565      MDSTLSKTCVSCILLSVTTFIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10          20          30          40          50          60

           70          80          90         100         110         120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           |||||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           70          80          90         100         110         120

           130         140         150         160         170         180
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130         140         150         160         170         180

           190         200         210
m565.pep  KAMANTTSAFNTSSSIANSINTCRQPPINAX
           |||||
a565      KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190         200         210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct ttccagacgg cattttgtat ggggggtaac
51  ggttggttcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggtc
151 gccggctttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggaac agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTGAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10          20          30          40          50          60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||

```

868

```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60

           70      80      90      100     110     120
m565.pep  .AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           |||||
a565      .AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120

           130     140     150     160     170     180
m565.pep  .PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||
a565      .PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180

           190     200     210
m565.pep  .KAMANTTSAFNTSSIANSTINCRQPPINAX
           |||||
a565      .KAMANTTSAFNTSSIANSTINCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51  ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggccttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgcgggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHs*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTCAG CCCGAGTAGC TCCTGCATAT CGTACAAACC CGTTTTGCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHs*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||

```

g566	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
	10 20 30 40 50 60
	70 80 90 100 110
m566.pep	AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
g566	AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
	70 80 90 100 110

```
a566.seq
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTACG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACCAG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCCTTG TGGGTGATTT CCACGCGCTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A
```

a566.pep

1	<u>MPSEQYLFRR</u>	<u>HFVWGLTVVQ</u>	<u>PEYVLHIVQT</u>	<u>RFTVPNCGA</u>	<u>DGAGGKGHAA</u>
51	<u>ACLVGDFHAL</u>	<u>AVGGEEGGVV</u>	<u>ADDVARADGG</u>	<u>KADGGRIARA</u>	<u>GVAFAAVNGA</u>
101	<u>LFEVSAERAG</u>	<u>DDFAHA*</u>			

	10	20	30	40	50	60
m566.pep	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL					
a566	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL					
	10	20	30	40	50	60
	70	80	90	100	110	
m566.pep	AVGGEEGGVADDVACADGGKADGRRIRARTGVAFAAVNGALFEVSAERAGDDFAHAX					
a566	AVGGEEGGVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX					
	70	80	90	100	110	

```
g567.seq..
1  atgcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattgggcga  tgcggacgtg  cagtcggcgg  cggtacgcag
101  caaagagggc  ggatacggcg  tgttgggtgc  gaacgcggc  gcttgccggc
151  gcggaatcgc  agctggtgca  ggaaatcgcc  cgggaagtcg  gtttgaaaaa
201  cgcgctcaag  gcagtgcgcg  aagattacga  ctttatcctg  atcgaactgtc
251  gcgcttcgct  gacgctgttg  acgcttaacg  gcttggtggc  ggcgggcggc
301  gtgattgtgc  cgatgttggt  cgaatattac  gcgctggaag  ggatttcgca
351  tttgattgcg  accgtgcgca  aaatccgcca  ggcggtcaat  cccgatttgg
401  acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctgggt
451  gccgaagtca  gcgaacagat  ggcgcagcat  ttcggggatt  tgctttttga
501  aaccgccatc  ccgcgcgaat  tccgccttgc  ggaagcgccg  agccacggta
551  tgccggtgat  ggcttacgac  gcgcagggca  agggtgccaa  ggcgtatcct
601  gccttggcgg  acgaaactggc  ggcgaggggt  tcggggaaat  ag
```

g567.pep

1	MRRRAA	ASTR	RVCSPAFIRS	YWAMRTCSRR	RYAAKRADTA	CWVRTRALAG
51	AEIELV	QVEIA	REVRLKNALK	AVAEDYDFIL	IDCPPSLTLL	TLNGLVAAGG
101	VIVPML	CEYY	ALEGISDLIA	TVRKIRQAVN	PDLDTGIVR	TMYSRSRLV
151	AEVSEQL	LRSH	FGDLLFETAI	PRNIRLAEAP	SHGMPVMAYD	AQAKGAKAYL
201	ALADELA	ARV	SGK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
  1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTGATTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251  CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301  CAGGAAATCG CCCGGGAAGT GCGTTGAAA AACGCGCTCA AGGCAGTGGA
351  AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCTTCG CTGACGCTGT
401  TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451  TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
501  CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCACG GGCATCGTGC
551  GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601  TTGCGCAGCC ATTTGCGGGA TTTGCTTTTT GAAACCGTCA TCCCGCGCAA
651  TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701  ACGCGCAGGC AAAGGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751  GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
  1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101  QEIAREVRLK NALKAVEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151  CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201  LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251  AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

      60      70      80      90     100     110     119
m567.pep  GVIYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEED
              |||||
g567      AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAVEED
              20      30      40      50      60      70

      120     130     140     150     160     170     179
m567.pep  YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
              |||||
g567      YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
              80      90      100     110     120     130

      180     190     200     210     220     230     239
m567.pep  TGIVRTMYDSRSLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
              |||||
g567      TGIVRTMYDSRSLVAEVSEQLRSHFGDLLFETAIPRNIRLAEAPSHGMPVMAYDAQAKG
              140     150     160     170     180     190

      240     250
m567.pep  TKAYLALADELAARVSGKX
              :|||
g567      AKAYLALADELAARVSGKX
              200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
  1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTGATTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```


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```

251 GCGTGTGGG TGC GAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAT AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
  51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
 101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
 151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
 201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
 251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep    MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG
              |||||
a567         MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep    VYQVLLGDADVQSAAVRSKEGGYAVLGNR ALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||||
a567         VYQVLLGDADVKSAAVRSKEGGYVGLGNR ALAGAEIELVQEIAREVRLKNALKAVAEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep    DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              |||||
a567         DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep    GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              |||||
a567         GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep    KAYLALADELAARVSGKX
              |||||
a567         KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
  51 gataccttgc agaactctgcc gattaaagcg ttcgcggctg cccaatattt
 101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
 151 tgtaaaaaca gcccacatcag gaacgaaact tcgtcttcgg ggcgacgcca
 201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
 251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
 301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
 351 aattacggcg atgtgcctcg ggatggcggg gtgttccaaa atggtctgcg

```

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401 tgctgctctt catatctgcc tttcgcgggt cggcggttaa atgccgtctg
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCTTGC AGAATCTGCC GGTTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTAAAAACA GCCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGT CCGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTGGAG
601 GAGTTTTTGG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep.
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRIKRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLNCHQIFFFGSQEFVGFGNVFVGQ					
g568	MCLGMVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFRFAAYDFNQVFAAFLGQHG					
g568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFRFAAYDFNQVFAAFLGQHG					
g568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG .CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVNASASSMPFRIKRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
	250					
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgtatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttggtttggt tatgttggtt
251 tggcattttg gctcgccggt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATT A C T C G C C G C A A C C T T G G T T T C G G C G T G G T
201 TGCTATGCGG GCGGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTC AAC G G C G G T T T G G C A G G T T A T G C C G T C G G C T G G C T T C T G G T C A T G C C
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTCT ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGGCGTGT TCGACCGTAC CGACAGCTG
751 ATTGCCGTGA TCAGCGCTCA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVVYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVVYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

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875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GGCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGATCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVVSVCDDL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

          10      20      30      40      50      60
m569.pep  MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCCKIKTNHYLAA
          |||||||
a569      MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCCKIKTNHYLAA
          10      20      30      40      50      60

          70      80      90      100     110     120
m569.pep  TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLVMPFWF
          |||||||
a569      TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLVMPFWF
          70      80      90      100     110     120

          130     140     150     160     170     180
m569.pep  ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEGAIGGAVC
          |||||||
a569      ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEGAIGGAVC
          130     140     150     160     170     180

          190     200     210     220     230     240
m569.pep  VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVVSVCDDLLESWLKRAAGIKDSSKLLPGH
          |||||||
a569      VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVVSVCDDLLESWLKRAAGIKDSSNLLPGH
          190     200     210     220     230     240

          250     260
m569.pep  GGVFDRTDSLIAVISVYAAMMSVLNX
          |||||||
a569      GGVFDRTDSLIAVISVYAAMMSVLNX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

```

g570.seq..
1  atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51  caccacaggc gcgcagccg acacctcca aaaaatcggc tttatcaaca
101 ccgagcgcct ctacctgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc cgcgcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaa ggcagctcgc cggcgcaaaa cttaggagcg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggg cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgccaa ccgcgtcctc gtcaaaatcg

```

876

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
451 acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgtg
501 a

```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

```

1 MTRLTRFAAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

```

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTGGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCCTG
501 A

```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

```

1 MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAP
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVYVN
151 TQYDVTDSVI KEMNAR*

```

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRFAAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAPFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRIVVKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRIVVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

```

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTGGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCCTG

```

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570    97.6% identity in 166 aa overlap

                10      20      30      40      50      60
m570.pep      MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
                |||||
a570           MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
                10      20      30      40      50      60

                70      80      90      100     110     120
m570.pep      ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
                |||||
a570           ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
                70      80      90      100     110     120

                130     140     150     160
m570.pep      SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
                |||||
a570           SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
                130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tcggcggcgg
 51  tataggttct gccgtccac acgctgcctg cgtcggcaaa caggctcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgccgccgta gctgattttt tcgccgtatt
201  cgtcatacac tttcggggccg agcgtgccgc tttcgtagcc gcgcaccgaa
251  cccagggccgc cgcgctagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgct...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRFV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCCAG GCCGCCGCGC TAGAAGTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCCGGCGT
451  CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQ EGFAQGEEPG LVVGGGVLQ FAARQGDFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNV	LNPAAGRGTAV	VVVGVFAV	PHAACV	GKQAQADGAR	VFRAGHREEQLGGDVGF
			:			
g571	MRVFRVNR	FVTVFVG	GGIGSAV	PHAACV	GKQAQADGAC	VFRTHREEQLGGDVGF
	10	20	30	40	50	
	70	80	90	100	110	120
m571.pep	FVAAVADFFAV	FVIDFRTERAA	FVSAHRTQAA	AVEVFKEGDF	FGSAVAARNAD	FAAEHQ
g571	FVAAVADFFAV	FVIHFRAERAA	FVAHRTQAA	AVEVFKEGDF	FGSAVAARNAD	FAAEHQ
	60	70	80	90	100	110
	130	140	150	160		
m571.pep	EGFAQGE	EPGLVVGG	GVVLQFAAR	QDGFVHAR	QVAARRPX	
g571	EGFA					
	119					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTGCGCG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTTT CAAAGAAGGG
301 GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNV LNPAAGRGTAV VVVGVFAVPHA ACVGKQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQGDFGV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNV	LNPAAGRGTAV	VVVGVFAV	PHAACV	GKQAQADGAR	VFRAGHREEQLGGDVGF
a571	MGIAGAVNV	LNPAAGRGTAV	VVVGVFAV	PHAACV	GKQAQADGAR	VFRAGHREEQLGGDVGF
	10	20	30	40	50	60
	70	80	90	100	110	120
m571.pep	FVAAVADFFAV	FVIDFRTERAA	FVSAHRTQAA	AVEVFKEGDF	FGSAVAARNAD	FAAEHQ
a571	FVAAVADFFAV	FVIHFRTERAA	FVSAHRTQAA	AVEVFKEGDF	FGSAVAARNAD	FAAEHQ
	70	80	90	100	110	120
	130	140	150	160		
m571.pep	EGFAQGE	EPGLVVGG	GVVLQFAAR	QDGFVHAR	QVAARRPX	
a571	EGFAXGE	EPGLVVGG	GVVLQFAAG	QDGFVHAR	QVAARRPX	
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

1	atgtgcgccca	tctgtcggggc	ggcggggcgtg	ccttcgcgcg	tgcgacggcg
51	gcaaaaaaggc	aaaaccatttt	atctggcaaaa	caaagaaaacg	ctgggtgggtt
101	ccggcgcgctt	gtttatggaa	accgcgccgcg	caaacggcgcg	ggcagtggttg
151	cccgctcgaca	gcgaacacaaa	cgcatttttct	caagtttttgc	cgcgcgatta
201	cacagaccgtg	ctgaacgcgaac	accgcatcga	ttcgattatc	ctgaccgctt
251	cggcgggccc	gttttttaaca	accgatttaa	gcacgttcga	cagcattacg
301	cccgagcagg	cgggtcaaaaa	ccccatttgg	cgtatggggc	gcaaaattctc
351	cgtcgatttca	gccactatgg	caaacaaagg	cttgggaactg	attgaagcgc
401	attggtctgtt	caactgtccg	cccgaacaaa	tccaagtctg	catccattcc
451	caatccgtga	tacacagtat	gggtgcgtac	cgcgacggct	ccgtgctggc
501	gcaactggggc	aatcccgcata	tgcgaacgcc	catcgccctat	tgtttgggct
551	tgcccgagcg	catcgattcg	gggtctcggca	aactcgattt	cggcgcattg
601	tccgcctctga	ccttccaataa	gcccgaattc	ggcgcgcttc	ctcgctcgaa
651	gttcgcctat	gaaaccataa	acgcaggcgg	agccgcgccc	tgcgtattga
701	acgcgcgcaa	cgaaaccgcc	gtcgcgcgct	ttttggacgg	acagattaag
751	tttaccgcaca	ttgcctaaaa	cgctcgccac	tgtcttgcac	aagacttttc
801	aaacggcatg	ggcgatatag	aaggactgtt	ggcgcaagat	gcccgacac
851	gcgcacaaagc	gcgggcattt	atcggcacac	tgcgctga	

g572.pap..

1	1	MCAIVGAAGL	PSALAAQKG	KTIYLANKET	LUVSGALFME	TARANGAAVL
51	1	PVDSEHNAIF	QVLPRDYTDR	LNEHGIDSII	LTASGGPFIL	TDLSTFDSIT
101	1	PEQAVKHPNW	RMGRKISVDS	ATMANKGLYL	IEAHWLFNCP	PDKLEVIHP
151	1	QSVIHSVMRY	RDGSLVALQS	NPDMRTPIAL	CLGLPERIDS	GVGKLDFGAL
201	1	SALTFOKPDF	GRFPCLKFAY	ETINAGGAAP	CVLNAANETA	VAAFLDGQIK

m572.seq.

seq.	1	ATGTGCGCCA	TCGTGCGGGC	GGTGGGGCTG	CCTTCCGCGC	TCGCAGCGGC
51	GCAAAAAGGC	AAAACCATTT	ATCTGGCAAA	CAAAGAAACG	CTGGTGGTTT	
101	CCGGCGCGTT	GTTTATGGAA	ACCGCCCGTG	CAAACGGCGC	GGCAGTGCTG	
151	CCCGTCGACA	GCGAACACAA	CGCCGTTTTC	CAAGTTTTGC	CGCGCGATTA	
201	CGCCGGCCGT	GTTAACGAAC	ACGGCATTCG	TTCCATTATC	CTGACCGCTT	
251	CCGGCGGCCC	GTTTCTGACC	GGCGATTAA	ACACGTTTCA	CGCGATTACG	
301	CCCGCCCAAG	CGGTCAAACA	CCCCAATTGG	CGTATGGGAC	GCAAAATCTC	
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGAGAGTG	ATTGAAGCGC	
401	ATTGGCTGTT	CAACTGTCCG	CCCGACAAAC	TCGAAGTCGT	CATCCATCCG	
451	CAATCCGTGA	TACACAGCAT	GGTGCGCTAC	CGCAGCGGCT	CCGTGCTGGC	
501	GCAACTGGGC	AATCCCAGAT	TGCGAACGCC	CATCGCTTAT	TGTTTGGGTT	
551	TGCCCGAGCG	CATCGATTCT	GGGTGCGCGC	ACCTGGATTT	CGACGCATTG	
601	TCCGCGCTGA	CCTTCCAAAA	GCCCCACTTT	GACCGCTTCC	CCTGCCTGAG	
651	GCTCGCCTAT	GAAGCCATGA	ACGCAGGCGG	AGCCCGCGCC	TGCGTATTGA	
701	ACGCCGCCAA	GGAAGCCGCG	GTCGCGCCCT	TTTTGGACGG	ACAGATTAAG	
751	TTTACCGACA	TTTGCAAAAC	CGTCCGCCAC	TGCTTTCGAC	AAGACTTTTC	
801	AGACGGCATA	GCGGATATAG	GGGGGCTCTT	GGCGCAAGAT	CCCCGGACAC	
851	GCGCACAAGC	GCGAGCATTT	ATCGGCACAC	TGCGCTGA		

m572.ppt .

1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LVVSGALFME	TARANGA AVL
51	PVDSEHNAV	QVLPRDYAGR	LNEHGIASII	LTASGGPFLT	ADLNTFDRIT
101	PAQAVKHPNW	RMGRKISVDS	ATMMNKGLEL	IEAHVLFNCP	PDKLEVVIHP
151	QSVIHSVMRY	RDGSPVLAQLG	NPMRTPIAGP	CLGLPERIDCS	GVGDLDFDAL
201	SALTFFQKPDF	DRFCLRLAY	EPDMRTGAAV	CVLNAANEAA	VAAFLDGFQIC
251	FTDIAKTVAH	CLAQDFSDGI	GDIGGLLAQD	ARTRAQARAF	IGTLR*

m572/q572 92.9% identity in 295 aa overlap

```

              10      20      30      40      50      60
m572.pep    MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDSHNAVF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572         MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDSHNAIF
              10      20      30      40      50      60

              70      80      90      100     110     120
m572.pep    QVLPRDYAGRLNEHGIASIIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572         QVLPRDYDRLNEHGIDSIIILTASGGPFLTDTLSTFDSITPEQAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPDPKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDLFDALSALTFOKPDFRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIKTVAHCLAQDFSNMGDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572.seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAGAAAAGGC AAAACCATT TATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGGGCCC GTTTCTGACC GCCGATTTAA ACACGTTTCA CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGCTGTGT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CTTTCCAAA GCGCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCCT TTTGGACGG ACAGATTAA
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGGGCATT ATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFOKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgccctggt  tgtgccgcct  taatcgcaat  atcggcagtt  tccaaatcac
51  gaatctcacc  gaccataatg  atgtccgggt  cctgacgcag  gaaagacttc
101 aaagcagcgg  caaaagtcag  accctgctta  tcattgacgt  taacctgatt
151 gatgcccgcc  aggttaatat  cggcagggtc  ttccgcctgt  gcaatattta
201 ccgactccgt  attcaaaata  ttcaaacagg  tatagagcga  caccgtctta
251 cccgaacccg  tcggacccgt  taccagcacc  atcccgtaag  gacggtgaa
301 cgcttccaac  aacaattttt  tctggaacgg  ctcaaaaccg  agctggtcga
351 tgttcaaaga  cgccgcatcg  gaattcaaaa  tccgcatcac  gaccttttcg
401 ccaaacagcg  tcggcaatgt  gctgacacgg  aaatcgacag  gcttgccgcc
451 cttttgaaag  gtcagctgca  tcctaccgtc  ctgcggtatc  cgtttttcgg
501 aaatgtccaa  acgcgacatt  acctaatcc  gggaagcaag  ctgccccctt
551 accgcaatgg  gcggctgaac  cacctcgagg  agctgcccgt  ccacacggaa
601 acggatacgc  gcattgtgtt  cgtaaaactc  gaaatggatg  tcggatgccc
651 cgctacgcaa  ggcacccgac  aaagttttat  ggataaacct  cggaaacaggg
701 ccgtcttctg  cctcctcgtc  gtcgatatac  aggggtgtgg  tttcctcttc
751 ctcttgcccc  tccccaaagt  cctgaagcag  cgatgtcgaa  cggaaccca
801 cccaatcgag  caaacccgcc  aactggatcat  cctcgacaat  gaccaactca
851 accgcaatcc  ctgcggcaga  aaccgttttc  tgaatttgcg  gcattctgggt
901 cggatcggaa  accgcaaaaa  atactttgtc  gcccccacgg  aaaaccggca
951 cacagtggaa  ctccaccatc  tgctcctccg  tcaacacccc  catcagcacc
1001 ctgtggcgcg  gataatgacg  caaatcaaga  atcgaataac  tgaacaccct
1051 cgcaatcaat  gccgcaagcg  acttgggcga  aatgacaccg  tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCRLNRN  IGSFQITNLT  DHNDVRVLTQ  ERLQSSGKSQ  TLLIIDVNLI
51  DARQVNLGRV  FRCNIYRLR  IQNIQTGIER  HRLTRTRRTG  YQHHPVRTVN
101 RFQQQFFLER  LKTELVDVQR  RGIGIQNPHH  DLFAKQRRQC  ADTEIDRLAA
151 LLKGQLHPTV  LRYPPFGNVQ  TRHYLNPGSK  LPPYRNGRLN  HLAELPVHTE
201 TDTRIVFVKL  EMDVGCPATQ  GIRQSFMDKP  RNRAVFCLLV  VDIQGVAFLE
251 LLPLPKLLKQ  RCRTRTHPIE  QTRQLVILDN  DQLNRNPGCR  NRFLNLRHLG
301 RIGNRKKYFV  APTENRHTVE  LHLLLRQHP  HQHPVARIMT  QIKNRITEHP
351 RNQCRKRLGR  NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT  TGTGCCGCCT  TAATCGCAAT  ATCGGCAGTT  TCCAAATCAC
51  GAATCTCACC  GACCATAATG  ATGTCCGGGT  CCTGACGCAG  GAAAGACTTC
101 AAAGCAGCGG  CAAAAGTCAG  GCCCTGCTTA  TCATTGACGT  TAACCTGATT
151 GATGCCCGGC  AGGTAAATCT  CGGCAGGTC  TTCCGCCGTT  GCAATATTTA
201 CCGACTCCGT  ATTCAAAATA  TTCAAACAGG  TATAGAGCGA  CACCGTCTTA
251 CCCGAACCCG  TCGGACCGGT  TACCAGCACC  ATCCCGTAGG  GACCGTGAAT
301 CGCTACCAAC  aCaw.TTTT  TCTGAAACGG  CTCAAACCG  AGCTGGTCGA
351 TGTTCAAAGA  CGCGGCATCG  GAATTCAAAA  TCCGCATCAC  GACCTTTTCG
401 CCAAACAGCG  TCGGCAATGT  GCTGACACGG  AAATCGACAG  GCTTGCCGCC
451 CTTTGAAG  GTCAGCTGCA  TCCTGCCGTC  CTGCGGTATC  CGTTTTTCGG
501 AAATGTCCAA  ACGCGACATT  ACCTTAATCC  GTGAAGCAAG  CTGCCCCCTT

```

882

```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACCGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLPNCPGR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
g573	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573.pep	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	250	260	270	280	290	300
	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLPNCPGRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLPNCPGRNGFLNLRHLC					
	250	260	270	280	290	300
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq

```

1 ATGCCCTGTT TGTGCCGCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCGGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCTGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CAGATGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPBH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCFAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT	DHNDVRVLTQERLQSSGKSQ	ALLIIDVNLI	DARQVNLGRV		
a573	MPCLCRLNRNIGSFQITNLT	DHNDVRVLTQERLQSSGKSQ	TLLIIDVNLI	DARQVNLGRV		
	70	80	90	100	110	120
m573.pep	FRRCNLYRLRIQNIQTGIER	HRLTRTRRTGYQHHPVGT	VNRYQHFFLKR	LKTELVDVQR		
a573	FRRCNLYRLRIQNIQTGIER	HRLTRTRRTGYQHHPVGT	VNRFQQQFFLKR	LKTELVDVQR		
	130	140	150	160	170	180
m573.pep	RGIGIQNPBHDLFAKQRRQC	ADTEIDRLAALLKGQLHP	AVLRYPPFGNVQ	TRHYLNPGSK		
a573	RGIGIQNPBHDLFAKQRRQC	ADTEIDRLAALLKGQLHP	AVLRYPPFGNVQ	TRHYLNPGSK		
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHT	TETDTGIVFVKLEMDVRC	FAAQGIRQSLMDKPR	NRRAVFCLLV		
a573	LPPYRNGRLNHLAELPVHT	TETDTGIVFVKLEMDVRC	FAAQGIRQSLMDKPR	NRRAVFCLLV		
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLK	QRCRTRTHPIEQTRQLV	ILDNDQLNLNPGCR	NGFLNLRHLC		
a573	VDIQGVAFLELLPLPKLLK	QRCRTRTHPIEQTRQLV	ILDNDQLNLNPGCR	NGFLNLRHLC		

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tgccgcccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgcgcgccaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgcggggttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtagaagc agacagcacc tgctcaatat
501 ctaccagcag gacagggtt gggaaaaagc ggttgaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgctt
651 caatgtcggc aaggcactcg aagccaaca aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgcgctc
751 gaagcctatg ccgccatcga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaaggcg agaaagaagc
951 cgcgcaaac gcgctcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttgaaaa
1051 gccgatgccg acatgatgctg ttcggttatc ggacggcagc tccagcgctg
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTIGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEAMARE RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAPW
351 ADADMMSRVI GRQLQRSVMY RCRNCHFKSQ VFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCgAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGT GGCgAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTTGGGG
451 CTGCAAGACG GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG TCGCGCGTTT

```

m574 . pep . .

1	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA
51	KSIPSGFYKS	LDALVDRNSG	RAARELAEV	DGRPQSYDLN	LTLGKLYRQR
101	GENDKAINIH	RTMLDSPDTV	GKRAARVLFE	LAQNYQSAGL	VDRAEQIFLG
151	LQDGKMARE	RQHLLNIYQQ	DRDWEKAVTE	ARLLSHDDQT	YQFEIAQFYC
201	LQAQAALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE	HRQGNFPAAV
251	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
301	INVVYEKSL	LKCEKEAAQT	AVELVRKPD	LNGVYRLLGL	KLSDMNPWKI
351	ADADMMSVI	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFTPNKI
401	EV*				

	10	20	30	40	50	60
m574 . pep	MRPNL	PNLSKKADMDNELWI	ILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS			
g574	MLPNL	PNLSKKADMDNELWI	ILLPIILLPVFFFTMGWFAARVDMKTVLKQAKSIPSGFYKS			
	10	20	30	40	50	60
m574 . pep	70	80	90	100	110	120
	LDALVDRNSGRAARELA	AEVVDGRPQSYDNLNLT	LGKLYRQRGENDKAINI	HRTMLDSPDTV		
g574	LDALVDRNSGRAARELA	AEVVDGRPQSYDNLNLT	LGKLYRQRGENDKAINI	HRTMLDSPDTV		
	70	80	90	100	110	120
m574 . pep	130	140	150	160	170	180
	GEKRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGKMA	REARQHLLNIYQQDRD	WEKAVET		
g574	GEKRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGEM	AREARQHLLNIYQQDRD	WEKAVET		
	130	140	150	160	170	180
m574 . pep	190	200	210	220	230	240
	ARLLSHDDQTYQFEIAQFY	CELAAALFKSNFDVARF	NVGKALEANKKCTRAN	MILGDIE		
g574	AQLLSHDEQTYQFEIAQFY	CELAAALFKSNFDAARF	NVGKALEANKKCTRAN	MILGDIE		
	190	200	210	220	230	240
m574 . pep	250	260	270	280	290	300
	HRQGNFPAAVEAYAAIEQQN	HAYLSMVGEKLYEAYAAQ	GKPEEGLNRLTGYMQTF	PELDL		
g574	HRQGNFPAAVEAYAAIEQQN	HAYLSMVGEKLYEAYAAQ	GKPEEGLNRLTGYMQTF	PELDL		
	250	260	270	280	290	300
m574 . pep	310	320	330	340	350	360
	INVVYEKSLLLKCEKEAAQ	TAVELVRRKPDINGVYRL	LGLKLSDMNPAWKADADM	MRSVI		
g574	INVVYEKSLLLKGEKEAAQ	TAVELVRRKPDINGVYRL	LGLKLSDLPAWKADADM	MRSVI		
	310	320	330	340	350	360
m574 . pep	370	380	390	400		
	GRQLQRSVMYRCRNCHFKS	QVFFWHCPACNKWQTF	TPNKIEVX			
g574	GRQLQRSVMYRCRNCHFKS	QVFFWHCPACNKWQTF	TPNKIEVX			
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1   ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATA CCGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GCGGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTTCGAT CCGCGCGTTT
651 CAATGTCCGG AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGCTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CCGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAG
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCTT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1   MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLDSPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSLDLPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWI	ILLPIILLPVFFAMGWFAAR	VDMKTVLKQAKSIPSGFYKS			
a574	MRPNLPNSLEKADMDNELWI	ILLPIILLPVFFAMGWFAAR	VDMKTVLKQAKSIPSGFYKS			
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEV	DGRPQSYDLNLTGKLYRQR	GENDKAINIHRTMLDSPDTV			
a574	LDALVDRNSGRAARELAEV	DGRPQSYDLNLTGKLYRQR	GENDKAINMHQTLDSPDTT			
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEV	DGRPQSYDLNLTGKLYRQR	GENDKAINIHRTMLDSPDTV			
a574	LDALVDRNSGRAARELAEV	DGRPQSYDLNLTGKLYRQR	GENDKAINMHQTLDSPDTT			
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGKMAREAR	QHLLNIYQQDRDWEKAVET			
a574	GAKRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGEMAREAR	QHLLNIYQQDRDWEKAVET			
	130	140	150	160	170	180
m574.pep	GEKRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGKMAREAR	QHLLNIYQQDRDWEKAVET			
a574	GAKRARVLFELAQNYQSAGL	VDRAEQIFLGLQDGEMAREAR	QHLLNIYQQDRDWEKAVET			
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFDVARFNVG	KALEANKKCTRANMILGDIE			
a574	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFDVARFNVG	KALEANKKCTRANMILGDIE			
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFDVARFNVG	KALEANKKCTRANMILGDIE			
a574	ARLLSHDDQTYQFEIAQFYCE	LAQAALFKSNFDVARFNVG	KALEANKKCTRANMILGDIE			

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTGYMQTFPELDDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTGYMQTFPELDDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDDLPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCFACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCFACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtaaaaca gtccgcttcc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggtctgt tccgcaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tcggcggtgc gatggcagaa
201 gcggcggtct cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttgacag ggttacaggt ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt gggttcgggt cgaacggccg gtttttccgc
351 ttttgcttcg ggcgcggaac cttttgcttc aggtttttca accgggtttt
401 cgacaggttt ctctatcggg ttctccacag ttgcctgttt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttgcgcgttt gcggtttggg
501 ttgttcgctt ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1  ..MPCLRRQAAR CTNRRTDRQT VFRFRLLRQK PVRQVRQVR RQLHWLFPPQ
51  VRKRCYRFRR SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSF RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq ..
1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTCCCGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTAACGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGAATCGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCCCGCG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCG GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACGCCCGA ACAGACCGTC AACAGTCCG CTTTCGGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCCGTCG CCGTGTTCGAT GGCAGAAAGC GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGCGCGGCG AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCGGAA TGTGA

```

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This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

```
m575.pep
  1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
  51  VWATDSGSGV SMTISTGLYG LKVSGSYTLS VDSMAFQSAS ARFWVSSSCV
 101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201  RKSSSRAINA APPPASSKVY EPPNRPSNSP LSVSSSAETC STGSETALPV
 251  SSVGVSMAEA AASWGADSA VSDAAVFAAG TSGRGTAGFS AFASGAATFA
 301  SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM*
```

m575/g575 70.2% identity in 114 aa overlap

```

      240      250      260      270      280
m575.pep  SSAETCSTGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTG-----
                        |||||
g575      LHWLFPPQVRKRCYRFRRSACRWQKRRLGGADSAAVSDAAVFAAGTGPGRSVAEAGVS
              50      60      70      80      90     100

      290      300      309      310      320
m575.pep  -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
                        |||||
g575      DTAGLGSGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
              110     120     130     140     150     160

      330      340
m575.pep  VCGLGCSALI-----LFRFGMX
                        |||||
g575      VCGLGCSALIFLGAAALILFRFGMX
              170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

```
a575.seq
  1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
  51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
 101  GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
 151  GTTTGGGCGA CAGATTCGGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
 201  GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCCA
 251  TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
 301  AGTGCGCCGG ATAAATGCC GTTTTGC GCGTATCGGT TTCGACATCG AACGTTTGTT
 351  CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
 401  TTGCCGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
 451  ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
 501  AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
 551  CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
 601  CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
 651  CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
 701  AAACCTGTTC GACAGGTTTC GAAACGGCGT TACCGGTTTC GTCGGTCGGC
 751  GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
 801  TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTTCTGGG CGAACGCGCC
 851  GTTTTTCGCG TTTTGCTTCG GGCGCGGCAA CTTTGTGCTC AGGTTTTTCA
 901  ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
 951  GGTTCGGCT TTGGGTTTCG CCGTTTGGCG TTTGGGTTGT TCCGCTTTGA
1001  TCCTGTTTCA ATTCCGAATG TGA
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
  1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
  51  VWATDSGSGV SMTISTGLYG LKVSGSYTLS VDSMAFQSAS ARFWVSSSCV
 101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201  RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
 251  VSMAEAAASW GADSAAVSDA AVFAAGTSG RTAGFSAFAS GAATFASGFS
 301  TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

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m575/a575 98.8% identity in 344 aa overlap

m575.pep	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVST	VSGLFS	SAVWATDSGSGV
a575	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVST	VSGLFS	SAVWATDSGSGV
m575.pep	70	80	90	100	110	120
	SMTISTGLYGLK	VSGSYT	LSVDSMAFQ	SASARFWVSS	SCVSAPDKMP	FCAAARLSKSKSM
a575	70	80	90	100	110	120
	SMTISTGLYGLK	VSGSYT	LSVDSMAFQ	SASARFWVSS	SCVSAPDKMP	FCAAARLSKSKSM
m575.pep	130	140	150	160	170	180
	RLEGVSVSTSN	VCFADNSSD	SPSKASVS	SFTSFFGAG	SGVAGVST	SAKVISMPS
a575	130	140	150	160	170	180
	RLEGVSVSTSN	VCFADNSSD	SPSKASVS	SFTSFFGAG	SGVAGVST	SAKVISMPS
m575.pep	190	200	210	220	230	240
	SGSSSGTDSS	VRRARLDW	ARRKSSSR	AINAAPP	PASSKVY	EPNRPNS
a575	190	200	210	220	230	240
	SGSSSGTDSS	VRRARLDW	ARRKSSSR	AINAAPP	PASSKVY	EPN----SPLSVSS
m575.pep	250	260	270	280	290	300
	STGSETALP	VSSVGVS	MAEAAAS	WGADSA	AVSDAAV	FAAGTGSGRTAGF
a575	240	250	260	270	280	290
	STGSETALP	VSSVGVS	MAEAAAS	WGADSA	AVSDAAV	FAAGTGSGRTAGF
m575.pep	310	320	330	340		
	SGFSTGFST	VACLDGSD	GMDAVS	ALGFAVC	GLGCSAL	LILFRFGMX
a575	300	310	320	330	340	
	SGFSTGFST	VACLDGSD	GMDAVS	ALGFAVC	GLGCSAL	LILFRFGMX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atggcggtgg acatcggacg ctcctgaaa caaatgaagg aacagggcgcg
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101  gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151  ttcttcgagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201  gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgcgc
251  aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301  caggggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351  cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401  gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451  ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501  caaccttgcc taccgcgaac aggtgcgagg cgaaaaaatc ggtccgaacg
551  ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaaac
601  gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRSLK QMKEQGAID LKVFTDAMQA VYDGKEIKMT EEQAEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101  QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151  GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201  APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

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```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC  CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGCGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMKFLQ  EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITQGE  GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ					
g576	MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQGE GKOPTKDDIV					
g576	EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITKQGE GKOPTKDDIV					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID GTVFDSSKAN GGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE					
g576	TVEYEGRLID GTVFDSSKAN GGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
g576	QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC  CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
  51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101  AQEVMKFLQ  EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151  LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201  VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251  KIGAPENAPA KQPAQVDIKK VN*

m576/a576    99.5% identity in 222 aa overlap

                                10      20      30
m576.pep                                MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                |||||
a576      CGKKEAAPAS ASEPAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
              30      40      50      60      70      80

                                40      50      60      70      80      90
m576.pep      FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                |||||
a576      FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
              90      100     110     120     130     140

                                100     110     120     130     140     150
m576.pep      KDGVKTTASGL QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
                                |||||
a576      KDGVKTTASGL QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
              150     160     170     180     190     200

                                160     170     180     190     200     210
m576.pep      VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
                                |||||
a576      VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
              210     220     230     240     250     260

                                220
m576.pep      KQPAQVDIKK VN
                                |||||
a576      KQPAQVDIKK VN
              270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
  1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
  51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101  CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTCAAT CGGCAGCAGC
 151  ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
 201  ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
 251  CCATGCAGGC AGTGTATGAC GGCAAGAAAA TCAAATGAC CGAAGAGCAG
 301  GCCCAGGAAG TGATGATGAA ATTCTGCGAG GAGCAGCAGG CTAAAGCCGT
 351  AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
 401  TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
 451  CTGCAGTACA AAATCACCAG ACAGGGTGAA GGCAAAACAG CGACAAAAGA
 501  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
 551  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
 601  GTGATTCGGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
 651  AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701  GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASAA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTDAMQAVYD  GKEIKMTEEQ
101 AQEVMMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA  KDGVKTTASG
151 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPATFPLSQ
201 VIPGWTEGVR  LLKEGGEATF  YIPSNLAYRE  QGAGEKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPDQVDIKK  VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA  TTTTCAAAAT  CAGCGCACTG  ACCCTTTCCG  CCGCTTTGGC
51  ACTTTCCGCC  TGGCGCAAAA  AAGAAGCCGC  CCCCGCATCT  GCATCCGAAC
101 CTGCCGCCGC  TTCTTCCGCG  CAGGGCGACA  CCTCTTCGAT  CGGCAGCAGC
151 ATGCAGCAGG  CAAGCTATGC  GATGGGCGTG  GACATCGGAC  GCTCCCTGAA
201 GCAAATGAAG  GAACAGGGCG  CGGAAATCGA  TTTGAAAGTC  TTTACCGAAG
251 CCATGCAGGC  AGTGTATGAC  GGCAAAGAAA  TCAAAATGAC  CGAAGAGCAG
301 GCTCAGGAAG  TCATGATGAA  ATTCCTTCA  GAACAACAGG  CTAAGCCGT
351 AGAAAAACAC  AAGGCGGACG  CGAAGGCCAA  TAAAGAAAAA  GGCGAAGCCT
401 TTCTGAAAGA  AAATGCCGCC  AAAGACGGCG  TGAAGACCAC  TGCTTCCGCG
451 CTGCAATACA  AAATCACCAC  ACAGGGCGAA  GGCAACAGC  CGACCAAGA
501 CGACATCGTT  ACCGTGGAAT  ACGAAGGCCG  CCTGATTGAC  GGTACGGTAT
551 TCGACAGCAG  CAAAGCCAAC  GCGGCGCCGG  TCACCTTCCC  TTTGAGCCAA
601 GTGATTCCGG  GTTGGACCGA  AGGCGTACAG  CTTCTGAAAG  AAGGCGGCGA
651 AGCCACGTTT  TACATCCCGT  CCAACCTTGC  CTACCGCGAA  CAGGGTCCGG
701 GCGACAAAAT  CGGTCCGAAC  GCCACTTGG  TATTTGATGT  GAAACTGGTC
751 AAAATCGGCG  CACCCGAAAA  CGCGCCCGCC  AAGCAGCCGG  CTCAGTCGA
801 CATCAAAAAA  GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASSA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTEAMQAVYD  GKEIKMTEEQ
101 AQEVMMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA  KDGVKTTASG
151 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPVTFPLSQ
201 VIPGWTEGVQ  LLKEGGEATF  YIPSNLAYRE  QGAGDKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPAQVDIKK  VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACATTCCGCG TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCGCGCCG TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALS CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

a576-1.pep	10	20	30	40	50	60
	MNTIFKISAL T L S A A L A L S A C G K K E A A P A S A S E P A A S S A Q G D T S S I G S T M Q Q A S Y A M G V					
m576-1	MNTIFKISAL T L S A A L A L S A C G K K E A A P A S A S E P A A S S A Q G D T S S I G S T M Q Q A S Y A M G V					
	10	20	30	40	50	60
a576-1.pep	70	80	90	100	110	120
	D I G R S L K M K E Q G A E I D L K V F T E A M Q A V Y D G K E I K M T E E Q A Q E V M M K F L Q E Q Q A K A V E K H					
m576-1	D I G R S L K M K E Q G A E I D L K V F T E A M Q A V Y D G K E I K M T E E Q A Q E V M M K F L Q E Q Q A K A V E K H					
	70	80	90	100	110	120
a576-1.pep	130	140	150	160	170	180
	K A D A K A N K E K G E A F L K E N A A K D G V K T T A S G L Q Y K I T K Q G E G K O P T K D D I V T V E Y E G R L I D					
m576-1	K A D A K A N K E K G E A F L K E N A A K D G V K T T A S G L Q Y K I T K Q G E G K O P T K D D I V T V E Y E G R L I D					
	130	140	150	160	170	180
a576-1.pep	190	200	210	220	230	240
	G T V F D S S K A N G G P V T F P L S Q V I L G W T E G V Q L L K E G G E A T F Y I P S N L A Y R E Q G A G D K I G P N					
m576-1	G T V F D S S K A N G G P V T F P L S Q V I P G W T E G V Q L L K E G G E A T F Y I P S N L A Y R E Q G A G D K I G P N					
	190	200	210	220	230	240
a576-1.pep	250	260	270			
	A T L V F D V K L V K I G A P E N A P A K Q P A Q V D I K K V N X					
m576-1	A T L V F D V K L V K I G A P E N A P A K Q P A Q V D I K K V N X					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1  atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaaaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggtt
151 tttattttacg gagcaaacat gaaacttata tataccgtca tcaaaatcat
201 tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgccctgtt
351 cgggcggctg ctgtccctgc gcggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaaa tgccgcgttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1  MERSGVFGKI VGNRILRMPS EHAAFYPKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPQ QSVNPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAAESAKQP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1  ATGGAAGGA ACGGTGTATT TGGTAAATT GTCGGAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCTTA CTGCGCGGGG CAAAATTCG ATTTGCCGCT GATTGTCTGA
301 TTGTTGCGCG CATTTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGKV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m577/g577 88.1% identity in 160 aa overlap

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGKVFIYGANMKLI
          |||:|||||
g577       MERSGVFGKIVGNRILRMPSEHAAFYPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI
          10      20      30      40      50      60

          70      80      90     100     110     120
m577.pep  YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGRL
```

895

```

|||||
g577      YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
          70          80          90          100          110          120

          130          140          150          160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||
g577      LSLRGENSRLRAEVKKKSARLSGQKLTAPPIQNAESAQKQPX
          130          140          150          160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAAATT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAAACTAGC  GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAAATCAT
201 TATCCTGCTG  CTCTTCCTGC  TGCTTGCTGT  CATTAATACG  GATGCCGTTA
251 CCTTTTCCTA  CTGCGCGGGG  CAAAATTTCG  ATTTGCCGCT  GATGTGCGTA
301 TTGTTTCGCG  CGTTTGTCGT  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401 TAAAGAAAAA  TGC GCGTTT  ACGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSFKLAQSW  FRVRSCPGGV
51  FIYGANMKLI  YTVIKIIILL  LFLLLAVINT  DAVTFSYLPG  QKFDLPLIVV
101 LFGAFVVGIV  FGMFALFGRL  LSLRGENGRL  RAEVKKNARL  TGKELTAPPA
151 QNAPESAKQP  *

```

m577/a577 98.1% identity in 160 aa overlap

```

          10          20          30          40          50          60
m577.pep  MERNGVFGKIVGNRILRMSSSEHAAASYPKPKSFKLAQSWFRVRSCLGGVFIYGANMKLI
          |||||
a577      MERNGVFGKIVGNRILRMSSSEHAAASYPKPKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          10          20          30          40          50          60

          70          80          90          100          110          120
m577.pep  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
          |||||:|||||
a577      YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
          70          80          90          100          110          120

          130          140          150          160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||
a577      LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          130          140          150          160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1  atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101 acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcg
151 gcggatttcg  ctttcgctgt  atttcaggtt  gttgtagcct  tcgtgttcgc
201 cgttttccaa  aacacggatg  ccgcgcggtt  cgccgaataa  aatatcgccg
251 gtaagtctgc  gcacaatcaa  aatatccaaa  ccggcaacga  tttcaggctt
301 gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF  ADFPKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGDA
51  ADFAFVVFHG  VVAFVFAVFQ  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDFRL

```

896

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTCT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TGCCTTTTTC GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNGMNT
51  ADFAFAVFG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNGMNTADFAFAVFGH					
		:	:	:	:	:
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFGH					
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGVGX			
		:	:	:
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTCT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TGCCTTTTTC GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNGMNTADFAFAVFGH					
		:	:	:	:	:
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFGH					
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGVGX			
		:	:	:
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

897

```

51   TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101  CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151  GGCGCGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201  TGCCGCCGGC GCGCTGATTA TCCTGTTCCTG CCCGTTCAAA GTCGGCGACT
251  TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301  CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351  CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401  GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGCGC
451  AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501  CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551  TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601  CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651  CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCTG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGCGC
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAABEHPLSVQNEERQAAAYITALG					
	: : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAABEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : :				
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTGG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCGG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCGCAAC GCGACATACA CATCATCAAT TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTTNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAABE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60

	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTTNEEVVLPNSVVM					
	: : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTTNEEVVLPNSVVM					
	70	80	90	100	110	120

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAABEHPLSVQNEERQAAAYITALG					
	: : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAABEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : :				
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

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```

1  ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGCG GTTGGGCGGT GCGGTTGTCC TTAAGAACG AGCTGTCCAA
351 TTTTGGCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCGGGA AATCAAAATG
451 GTGCAGACTT CTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCAGC CTGCCGCTTT
551 GCCGCGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQFDLHL LISVSGWGH L AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKQQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGCG GTTGGGCGGT GCGGTTGTCC CTGAAGAACG AGCTGTCCAA
351 TTTTGGCGCC GCGCACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGGAGA GATTAAATG
451 GTGCAGACTT CTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQFDLHL LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKQQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
m579-1.pep  MDFKQFDLHL LISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||
g579-1      MDFKQFDLHL LISVSGWGH LAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m579-1.pep  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKQQLSNFAA
          |||
g579-1      VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKQQLSNFAA
          70      80      90     100     110     120

          130     140     150     160     170     180
m579-1.pep  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPSNVVMGNSIVNRST

```

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

a579-1.seq

```

1  ATGGACTTCA AACAAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGGGTC GGAAATGGG CGGCGAAACG CATGTGCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATGGGG CAGATTGGGC GTTTCACAA CATCCGTAAC CGCCTTAATC
301 GGCGGCGCGG GTTGGCGGT GCGGTGTCC TTGAAAGACC AGCTGTCCAA
351 TTTTGGCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAGATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCGCCG AACCGGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

a579-1.pep

```

1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVLPNSV MGNISVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKA AV EHLPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

901

```

|||||
m579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag cccatttcga tggcaaggca gacttcgccc atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatcgccgc gggttcggca
151 tcgaaaatca gcttggtaaa gcggtgtcgc caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcggtt tcaccgaccc atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep..
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATCGCGCC GGTTTCGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS					
g580	MDSPKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX					
g580	QPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATCGCGCC GGTTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTTCGGT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```


902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPFVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPFVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt ggggtcaaacc ggtatagaac aaaatacgtt
51 ctgtcgtcgt ggttttaccc gcatcgatat gggcggaat accgatgttg
101 cggtagacggc tgatcggggc cttacgagcc atttatttag cctttcaaaa
151 ttagaaacgg aagttagaga atgctttgtt ggcttcagcc atacgggtga
201 cttcttcacg ttttttcaac gcaccgccac ggccttcgga cgcataatc
251 aactcgcctg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAVQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRANPAHCQSQTAX					
g581	GFSHTVYFFTFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTCACG GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCCGCTG CCAAACGCAG GTCCATGGAT TTCTACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGN TDVTVQADRG LTSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV					
a581						
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLLTFAGRIANPAHCQSQTAX					
a581						
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcgagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggtat aagggcgagg cggcatttgt tgttgaaaaa ggcgggggatg
251 cgcttcctgc cgacagtgcg ggcgaaaccg ccgatattcta tacgcctttg
301 agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaaccgc cgcggatctg tgggtcggct
551 acacccaaag atccgatttg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa attttcctga ccagcctgt
651 gaagggcggt ttgcccgttc gcggcaggct cgtatgctc ggtgcggggt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751 aggatttatg ccatggcagg catggaatgg ggcaaatgga cggtgattcc
801 gcgcgtgttg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatatggc acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggatgc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMFPWY NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GCGGGGGATG
251 CGCTTCCTGC CGACAGTGC GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TAAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGCGCGAT TTGCCGTTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGTACGGC GCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFASKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGTGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

```

      10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
g582      MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
      10      20      30      40      50      60
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
g582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
      70      80      90     100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
g582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
      70      80      90     100     110     120
m582.pep  NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAEDLFKTRADL
g582      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAENLFKTRADL
      130     140     150     160     170     180
m582.pep  NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAEDLFKTRADL
g582      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAENLFKTRADL
      130     140     150     160     170     180
m582.pep  WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
g582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
      190     200     210     220     230     240
m582.pep  WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
g582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
      190     200     210     220     230     240
m582.pep  QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
g582      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
      250     260     270     280     290     300
m582.pep  QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
g582      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
      250     260     270     280     290     300
m582.pep  QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
g582      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
      310     320     330     340     350     360
```

905

```

m582.pep  LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
g582      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          ||||| |||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TAAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLEKTRADL WFGYTQRSWQ QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVVKLYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

m582/a582  100.0% identity in 370 aa overlap

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

              190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
              190      200      210      220      230      240

              250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
              250      260      270      280      290      300

              310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
a582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

              370
m582.pep      GLMFNDLDGIX
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacagcgt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcat cgctcatcgc cgcgcccggt ttgtcggcgg
351 ttacgccggt tactgcgacc aaccgcgacg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSOIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGCGCGG
351 TTACGCCGGT TACTGCGACC AACCAGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAGGGC GCACAATACT GCGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583 . pep . .

1	MIVDQSQIFI	HLAFCACFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRGNQSQQ
51	QFGKSETVTD	AQRFSSKNGD	KQISDTHPPQ	CFEQTARNHN	CDGNQPNQRI
101	GERTQRIahr	RARFVGGYAG	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG
151	QQRPSRLRDP	VGYGQCQNQG	AQYCGNGEGY	RFETQFHID	LRRKDRPEKS
201	EK*				

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583 . pep	MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNQSQQQFGKSETVTD					
	:					
g583	MIIDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNQSQQQFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583 . pep	AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG					
g583	AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583 . pep	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGGQRPRLRLDPVGYGQCQNQGAQYCGNGEGY					
	:					
g583	YCDQPDGNNRQRAQRHNLADNGGNHTDKHSQRPRLRLDPVGYGQCQNQGAQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583 . pep	RFETQFHHDLRKKDRPEKSEKX					
g583	RFETQFHHDLRKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1	ATGATAGTTG	ACCAAAGCCA	AATATTTACC	CATCTTGCCT	TCTGTGCCTT
51	TTGCGGGATT	GGAGCCGTAA	CTGCCGGCAA	TCGACTGCAT	AATCGGATGT
101	ATAATGCCGC	CGCCGCGCGC	GGTAT'TGGAA	GGGGTAACGG	GAGCCAGCAG
151	CAGT'TCGGAA	AGAGCGAGAC	TGTAACCGAT	GCCCAGCGTT	TTTCTTCCAA
201	AAACGGCGAT	AAACAATAT	CCGATACGCA	TCCCCAGCCC	TGTTT'GAGC
251	AAACCGCGCG	AAATCATAAC	TGCGAT'GGCA	ATCAGCCAAA	TCAACGGATT
301	GGCGAACGCA	CTCAACGCAT	CGCTCATCGC	CGCACCCGGT	TTGTCGGCGG
351	TTACGCCGGT	TACTGCGACC	AACCCGACGG	CAATAATCGA	CAGCGCACCC
401	AACGGCATGG	CCTTGCCGAT	AATGGCGGCA	ATCACACCGA	TAAACATGGC
451	CAGCAGCGTC	CAAGCCTGAG	GCTTGACCCC	GTCCGGTACG	GGCAGTGCCA
501	AAACCAAGGC	GCACAATACT	GCGGCAATGG	CGAGGGGTAT	CGGTTTGAAA
551	CCCAATT'TCA	TCATATTGAC	CTCCGTAAAA	AAGACCGTCC	CGAAAAATCG
601	GAAAAATAAA				

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pap

1	<u>MIVDQSQIFT</u>	<u>HLAFC AFCGI</u>	<u>GAVTAGNRLH</u>	<u>NRMYNAAAAR</u>	<u>GIGRGNSSQQ</u>
51	<u>QFGKSETVTD</u>	<u>AQRFS SKNGD</u>	<u>KQISDTHPQP</u>	<u>CFEQTARNHN</u>	<u>CDGNQPNQRI</u>
101	<u>GERTQRI AHR</u>	<u>RTRFVGGYAG</u>	<u>YCDQPDGNNR</u>	<u>QRTQRHGLAD</u>	<u>NGGNHTDKHG</u>
151	<u>QQRPSLR LDP</u>	<u>VGYGQCQNQG</u>	<u>AQYCGNGEGY</u>	<u>RFETQFH HID</u>	<u>LRKKDRPEKS</u>
201	EK*				

m583/a583 99.0% identity in 202 aa overlap

m583.pep MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQQFGKSETVTD

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQQFGKSETVTD
           10          20          30          40          50          60

           70          80          90          100         110         120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
           |||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG
           70          80          90          100         110         120

           130         140         150         160         170         180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           |||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           130         140         150         160         170         180

           190         200
m583.pep  RFETQFHHIDLRKKDRPEKSEKX
           |||
a583      RFETQFHHIDLRKKDRPEKSEKX
           190         200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgctgcgtt ctattttggc ggcttcctcg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcgccgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttggtt aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggttcg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgcy ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtg cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acgggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNVANA EFVKKFNNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTGCGTC TTGTTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTTCATC AGAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGmAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATcATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAAAGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CCGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTcAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

909

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNVNA
              ||| : |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVAAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90      100     110     120
m584.pep      EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ TGWEERAEFK VEGRDFDELN
              ||||| : | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ TGWEERAEFK AEGRDFDALN
              70      80      90      100     110     120

              130     140     150     160     170     180
m584.pep      RFIADIQADA ALXYTDFHVS RERRNEVIXQ VSKDAVLRFK ARAEKLAVL GASGYKIVKL
              ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           RFIADVQTDASLEDTF SVSRERRNEVIDQ VSKDAVLRFK ARAEKLAVL GASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep      NLGHIGSHIAGGGAAQAKML RAMPMAASVNM EGADSAAPG VEEISISVNG TVQFX
              ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           NFGQIGSHIAGDGAVRAKML RAMPMAASVNM KGTD SAAPGV EEEISISING TVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTT CAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTCACC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGC GTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

```

a584.pep
1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTA EGRDKNVNA
              ||| : |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584           MLRSILAASL----- IVEFS ESAGVEAVQDTMSARFQVTA EGRDKNVNA
              10      20      30      40

```


910

	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNGRRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPYQYTNGRRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgccgcg  ttatcgctcg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctgggtcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattatgt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gcccggtctc  atccgctgtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaac  gctatatcga  caattacacc
301  atagaacgcg  cccggctgtt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcatcgaa  tacgaccggt  tcggcggaag  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggcttgccgc  ttgcccgat  ttggcacgaa  ttcacatccc  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aacccatcag  aatcttaggc  aacggcatgg  acaggggtgg  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFKTRG DNGAREILTE WKNSPVSSAV YVIQGDKKD IILNRYIDNYT
101  IERARLFAAN NPHSNLVRIE YDRFGEEYLF FIKGWDNHQA QRLPSPLFIP
151  GLPLAPIWHE FIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVAERE
201  LEDRVCCQVR DRDELADVA MQFDTMVEKL E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCGG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAGACA  GCCCGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTT  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCCTGC  CCAGCCCCCT  GTTGATCCCC
451  GGCCTGCCGC  TCGCCCGGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AAACGGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTGCAG  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCG  ACAAATGGT  GGAAAACTC  GAAAACTCG
701  TTGCCAAAGA  ACGCCACCTG  CTCCATCAG  TCTCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCGGA  CTGATTACAG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAATG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACTG  TTAACCTGT  CCGTCTCGA  AACTTCCAAT
901  ATGGCTTGG  AAAAAGAAAG  CCTGAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGTCTGCCGA  CGGAAAATC  CCCGAAAACA  CAACCATCCT  TGCCAACGAA

```

911

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

```

m585.pep..
  1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
 51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGEL LTLSRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSPG GSTILINIGQ DHKHWIIDVT DNGPGVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

```

              10      20      30      40      50      60
m585.pep      MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFRARG
               |||||
g585           MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFKTRG
               |||||
              10      20      30      40      50      60

              70      80      90      100     110     120
m585.pep      DAGAREILTEWKDSPVSSGVYVIQGDEKDDILNRYIDSYTIERARLFAAGHPHNSNLVHIE
               |||||
g585           DNGAREILTEWKNSPVSSAVYVIQGDEKDDILNRYIDNYTIERARLFAANNPHNSNLVRIE
               |||||
              70      80      90      100     110     120

              130     140     150     160     170     180
m585.pep      YDRFGEEYLFITKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
               |||||
g585           YDRFGEEYLFIFKWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG
               |||||
              130     140     150     160     170     180

              190     200     210     220     230     240
m585.pep      NIAKPIRILGNMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHL
               |||||
g585           NIAKPIRILGNMDRVAERELEDRCVQVDRDDELADVAMQFDTMVEKLEX
               |||||
              190     200     210     220     230

              250     260     270     280     290     300
m585.pep      LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELLTLSRLETSN

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

```

a585.seq
  1 ATGAAACTGT TCCAACGCAT CTTCGCCACA TTTTGCGCGG TTATCGTCTG
 51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCCTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTATATC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCACATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

```

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTACCAGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGTGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCAAGAA AAAAACCAGG TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```

1 MKLFQIRIFAT FCAVIVCAIF VASFSEWLVO NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQDEKDD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQVDD DRDDELSHLA IQFDKMVEKL EKLVAERHL LHHVSHMRS
251 PLARMQAIVG LIQAQPQKQE QYLRLELGE TRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHIIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFRARG					
a585	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFRARG					
	10	20	30	40	50	60
m585.pep	DAGAREILTEWKDSPVSSGVYVIQDEKDDILNRYIDSYTIERARLFAAGHPHNSLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQDEKDDILHRYIDSYTIERARLFAAGHPHNSLVHIE					
	70	80	90	100	110	120
m585.pep	YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
m585.pep	NIAKPIRILGNMDRVANGELETRISQVDDRRDDELSHLAIQFDKMVEKLEKLVAKERHL					
a585	NIAKPIRILGNMDRVANGELETRISQVDDRRDDELSHLAIQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
m585.pep	LHHVSHMRSPLARMQAIVGLIQAQPQKQEYQYLRLELGE TRMDTLAGE LTLRLETSN					
a585	LHHVSHMRSPLARMQAIVGLIQAQPQKQEYQYLRLELGE TRMDTLAGE LTLRLETSN					
	250	260	270	280	290	300
m585.pep	MALEKESLKLPLFLGNLVEDNQSIQKNGQTVTSLADGKI PENTTILANESYLYRAFDNV					
a585	MALEKESLKLPLFLGNLVEDNQSIQKNGQTVTSLADGKI PENTTILANESYLYRAFDNV					
	310	320	330	340	350	360

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

g586.seq.

seq1	atggcagccc	atctcgaaga	acaacaagag	ttagacaact	ttaaatattt
51	ttggaaaacc	acgggcaa	ggctgtttgc	cctgctgact	ttggcggcac
101	tcggtactt	gggatacacg	gtttaccaaa	accgtgcggc	tcaccaaaat
151	caggaagacc	cggcgggtgc	ggcaaacatc	gtggaaaagg	cgcaaaaaca
201	agcccgcaa	agcgaatca	atgccgaact	gtccaaactc	caacaaagct
251	acccccattc	catttccgcc	gcccaagcca	cgctgatggc	ggcggcaacc
301	gaatttgacg	cgcagcgta	cgatgtttgc	gaaggtcatt	tgaattgggt
351	gttggtccaac	caaaaagaca	gctgtattcc	ggcggtggcg	gcgcagctgc
401	tggggcttgt	gttgttgcaa	caaaaaaat	acgatgccgc	gcttgccgca
451	ctcgacacgc	cgggtgaggc	ggacttcgcc	ccctgctga	tggaaaactaa
501	agggcatggt	tatgccgcac	agggaaaag	ccaggaagcc	ttaaaaaact
551	acggcagacc	tttgaaaaca	atgctcaag	attctgcgg	tcgcgaattg
601	cttcaaatga	aactcgattc	gctgaaataa		

g586 . pep . .

1	MAAHLEEQQE	LDNFKYFWKT	TGKWL Falli	<u>LAALGYLGYT</u>	VYQNRAASQN
51	QEA AAVLANI	VEKAQNKA PQ	SEINAELSKL	QQSYPHSTSA	AQATLMAAAT
101	EFDAQRYDVA	EGHLKWVLSN	QKDSL I QALA	AQRLGVVLLQ	QKKYDAALAA
151	LDT PVEADFA	PLL METKG DV	YAAQEKSQEA	LKNYQGALEK	MPQDSVGREL
201	LQMKLDSLK *				

m586.seq

1	ATGGCAGCCC	ATCTCGAAGA	ACAACAAGAG	TTAGACAAC	TTAATATTT
51	TTGGAAGAAC	ACGGGCAAA	GGCTGTTGC	CTTGCTGAT	TTGGCGGCAC
101	TCGGCTACTT	GGGATACAG	GTTTACCAA	ACCGTAAAG	TCCCCAAAT
151	CAGGAAGCGG	CGGCGTGCT	GGCAAAACG	GTAGACAAAG	CGCAAGGCAA
201	AGCCCCGCAA	AGCGAAATCA	ATGCCGAATT	GACCAAAC	CAACAAAGCT
251	ACCCGCATT	CATTTCCGG	GCCCAGCCA	CACGTGATG	GGCGGCAACC
301	GAATTTGACG	CGCAGCGTT	CGATGTTGCC	GAAAGCCATT	TGAAATGGGT
351	GTTGTCCAAC	CAAAAAGACA	GCGCTGATCA	AGCGTTGGCG	GGCAGCGCTC
401	TGGGCGTTGT	GTTGTTGCAA	CAAAAAAAT	ACGATGCCGC	GCTTGCCGCG
451	CTCGATACGC	CGGTGTAAGC	GGACTTCGCG	CCCCTGCTGA	TGGAACCAA
501	AGGCGATGTC	TATGCGGCAC	AGGGAAGG	CCAGGAAGCC	TAAAAAAT
551	ACCGACAGGC	TTTAGAAAAA	ATTGCTCAAG	ATTCTGTCG	TGCGGAATTG
601	GTTCAAATGA	AACTTGATTC	GCTGAAATAA		

m586.pcp

1 MAAHLEEQQE LDNFKYFWKT TGKWL~~FALLI~~ LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAE~~LTKL~~ QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGH~~LK~~WVLSN QKDSL~~I~~QALA AQR~~L~~GVVLQ QKKYDAALAA
151 LDTPEADFA PLLMETKGDV YAAQ~~G~~KSQEA LKNY~~G~~QALEK MPQDSVGREL
201 VMK~~L~~DSLK*

m586 / q586 97.1% identity in 209 aa overlap

m586.pep MAAHLEEQQELDNFKYFWKTTGKWLFAILLI AALGYLGTYVYQNRKVSQNQEAAAVLANI
||||| : |||||

914

```

g586      MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAALGYLGYYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPOSEINAELSKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGRELVMKLDLKLX
           |||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELLQMKLDLKLX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAACT TTAAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCGCC GCGCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 ATTGTCCAAC CAAAAGACA GCCTGATCCA GCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACGATGCCGC GCTTGCCGA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAACCAA
501 AGGCGATGTC TATGCCGAC AGGGAAAAAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYY VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPO SEINAELAKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLKWLVLN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDLKLX*

```

m586/a586 97.6% identity in 209 aa overlap

```

           10      20      30      40      50      60
m586.pep  MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAALGYLGYYVYQNRAASQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPOSEINAELAKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLVLN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

```

915

	190	200	210
m586.pep	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
a586	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
	190	200	210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```
g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaaactc acggcaacgg
351 caaaaaccgc aacaaacgga tgtccgacat atccgcgggc atcagccaca
401 ctttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataaact taaggataaa ttatgaatat taa
```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```
g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSNR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKD GK NPALISFLES
151 TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```
m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGC GC TACGGACTGA CCGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCGCCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGTC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTCG GCGCAGGTTT CGGTTTCAAC AAAACACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTG
851 GCGTACAGCA TACATTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```
m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KKTALNASAR FNVSGQSSSE LKFGVQHTF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10

20

30

40

50

60

m587.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGGKWKLETSLTYLNSENRAELAAPVYIQ
g587	: :
	10 20 30 40 50 60
m587.pep	70 80 90 100 110 120
g587	TGATSFIPITEIQENGSDMLVGLTGLRYGLTGNTDIYGGSYLWHEERKLDGNSKTR
	: :
	70 80 90 100 110 120
m587.pep	130 140 150 160 170 180
g587	NKRMSDVSGLISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
	:
	130 140 150 160 170 180
m587.pep	190 200 210 220 230 240
g587	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
	X

```
a587.seq
1 ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAACATTCC CTTACTGACC TGAACACGGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACGCT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA
```

```
a587.pep
1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTG DMLVGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVS LG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*
```

	10	20	30	40	50	60
m587.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLSENENRAELAAPVYIQ					
	:					
a587	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLSENENRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m587.pep	TGATSFIPIPTEIQENGSTMDLVGTLGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
	:					
a587	TGATSFIPIPTEIQENGSTMDLVGTLGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cggtcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaaaaacg gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCTG TTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGGAAATA TTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLKPNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGKPKGKTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKPSGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90     100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAAGREVLFEPNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90     100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
  1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
 51  CGCCGCGTCC GCCGTTCTGA CTTCTATCA AGAACCCGGC TGCACCTACG
101  AAGGCGATGT CGGCAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151  TGCCAAGACG GCGCAACTA TACCGGTTCC TTTAAAAATG GCAAATTCGA
201  CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251  CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACA
301  TTCAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351  AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401  TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
  1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
 51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101  FKKGLAHGRF TVSQNGETLF IMKCENGMKEVKLPKNK*

```

m588/a588 96.4% identity in 138 aa overlap

```

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGKPKGKTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKD GKPAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90     100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90     100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
a588        IMKCENGMKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
  1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
 51  tgcttcgcgc attgaaaaag tggtgaacaa aaaagatttt gtcgaatcgg
101  cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151  aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201  cgcggaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251  atatcggctg gcggttgtgg cttttgctga ccatcaatat cccgttcctt

```

```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgctgtat ggagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgta tgggtgatcg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcacaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttctc
751 cgcaccaacc acggcgaaac catcgctgcc gacggcatta tcgaaagcgg
801 cagcgggttg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcgcaaaa gtgttgccg gcgcgctgat gaccgaaggc
901 agcgtgggtg accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggtcg attaagggcg attggacggt
1101 cgcactgatg cacgccgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tcgcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaagcgaggc
1301 cgcaggttgc cgccgtttat tacgttccc acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgcgc cccaccgcgt
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaaac gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttgggtga atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaaccc atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggg
1851 cggcgacggc atcaacgacg cgcccgccgt tgccgccgcc aacgtcagct
1901 tcgccatgaa aggcgggtcg gcggttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatcgcga
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg cattccgctc gccgcgctcg gcttttttaa tcccgtcata
2101 gcaggcgccg caatggcgcc aagctcggtt tcggtatttg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAI PF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIA C PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFAISDAL
551 KADTAEAIGR LKKNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCCCGAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTT

```

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTACAA AAGCGCGTGG GCGAGCATTG AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCGGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTGG TGCTACTGGG TAAATTTTGG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GGCGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GGCGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGC GCGCGTA GCCGATAAAG
1001 CCGCTGCGGT ATTCGTGCCT GCCGTCGTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CCGTTAAACA CGGTATTTGG
1201 TTTAAAGACG CCGCAGCAAT GGAGGAAGCC GCCCAGTCTG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCGCGAG GTTGGCGCCG
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCGCCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TGCGGTCTCA GTCGATAACA
1601 AACCATCGG CGCATTGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAATCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTC
2051 CTCTCGCCGC GCTTGGCTTT TTAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

```

m589.pep..
1  MQQKIRFQIE  GMTQCACASR  IEKVLNKKDF  VESAGVNFAS  EEAQVVFDDSD
51  KTSVADI AKI  IEKTGYGAKE  KTEDTLPOPE  AEHHIGWRLW  LLFTINVPFL
101 IGMAGMMIGR  HDWMIPLWQ  FALASVVQLW  LAIPFYKSAW  ASIKGGLANM
151 DVLVTIGTVS  IYLYSVYMLF  FSPHAAYGMA  HVEFEVGV MV  IGFVSLGKFL
201 EHRTKKSSLN  SLGLLKLTP  TQVNVQRNGE  WKQLPIDQVQ  IGDILIRANHG
251 ERIAADGIE  SGSGWADESH  LTGESNPEEK  KAGGKVLAGA  LMTEGSVVYR
301 ATQLGSQTQL  GDMMNALSEA  QGSKAPIARV  ADKAAAVFVP  AVVGIALLTF
351 IVTWLIKGDW  TVALMHAVAV  LVIACPCALG  LATPAAIMVG  MGKAVKHGIW
401 FKDAAMEEA  AHVDAVLDK  TGTLTGESPQ  VAAVYCV PDS  GFDEDALYRI
451 AAVEQNAAH  PLARAIVSAA  QARGLDIPAA  QNAQTVVGAG  ITAEVEGVGL
501 VKAGKAEFAE  LALPKFLDGV  WDIASIVAVS  VDNKPIGAFA  LADALKADTA
551 EAIGRLKKHN  IDVYIMSGDN  QGTVEYVAKQ  LGIAHAFGNM  SPRDKAAEVQ
601 KLKAAGKTVA  MVGDGINDAP  ALAAANVSFA  MKGGADVAEH  TASATLMQHS
651 VNQLADALLV  SQATLKNIQ  NLFFAFFYNI  LGIPLAALGF  LNPVIAGAAM
701 AASSVSLSN  ALRLKRVKID  *

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

m589.pep      10      20      30      40      50      60
MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADI AKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIAICPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIAICPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSAGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEIAGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEIAGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

a589.seq

1	ATGCAACAAA	AAGTCCGTTT	CCAAATCGAA	GGCATGACCT	GCCAGGCATG
51	TGCTTCGCGC	ATTGAAAAAG	TGTTGAACAA	AAAAGATTTT	GTGGAATCGG
101	CGGGGGTAAA	CTTCGCCAGC	GAAGAGGCTC	AGGTAGTGTT	TGACGACAGC
151	AAAACCTCAG	TAGCCGACAT	TGCCAAAATC	ATTGAGAAAA	CCGGTTACGG
201	CGCGAAGGAA	AAAACGGGAA	ATACATTGCC	GCAACCCGAA	GCAGAACACC
251	ATATCGGCTG	GAGGTTGTGG	CTTTTGCTGG	CCATCAATAT	CCCGTTCCTT
301	ATCGGTATGG	TAGGGATGAT	GCTAAAAGGG	CTGAATTGGA	CACGGCATGA
351	TTGGATGTTG	TCGCCCTTGT	TGCAGTTTGC	ATTGGCGAGT	GTGGTGCAGC
401	TTTGGCTGGC	GGTGCCATTT	TACAAAAGCG	CGTGGGCGAG	CATTAAAGGC
451	GGGCTGGCGA	ATATGGACGT	ACTCGTTACC	ATCGGCACGG	TCTCGATTTA
501	CCTGTATTCC	GTCTATATGC	TGTTTTTCAG	CCCGCACGCG	GCGTACGGTA
551	TGGCGCATGT	GTATTTTGAA	GTAGGCATAA	TGGTGATTGG	TTTTGTGTCA
601	CTGGGTAAAT	TTTTTGAACA	CCGCACCAAA	AAATCCAGCC	TGAACAGCTT
651	GGGCTTGCTG	CTCAAACCTA	CGCCAACCCA	AGTCAACGTG	CAACGCGATG
701	GCGAATGGCG	GCAGCTACCC	ATCGACCAAG	TGCAAATCGG	CGACCTAATC
751	CGCGCCAATC	ACGGCGAACG	CATTGCCGCC	GACGGCATCA	TAGAAAGCGG
801	CAGCGGCTGG	GCGGACGAAA	GCCATCTTAC	CGGCGAATCC	AATCCCGAAG
851	AGAAAAAGGC	AGGCGGCAAA	GTATTGGCGG	GCGCGCTGAT	GA CTGAAGGC
901	AGCGTGGTGT	ACGCGCGCCG	GCAGCTCGGC	AGCCAAACCC	TGCTCGGCGA
951	CATGATGAAC	GCGCTCTCCG	AAGCGCAAGG	CAGTAAAGCA	CCGATTGCCG
1001	GTGTGGCGGA	CAAGGCGGCG	GCGGTATTTC	TGCCTGCCGT	TGTGGGCATC
1051	GCACTTTTGA	CTTTTATCGC	TACTTGCGTG	ATTAAGGGCG	ATTGGACGCT
1101	CGCATTGATG	CACGCCGTCG	CCGTTTTGGT	GATTGCCTGC	CCGTGTGCAC

```

1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGCAAGC
1301 CGCAGGTGCG CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGGTTTG GAGATCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTGCGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACCTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
1  MQQKVRFAQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLAQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKQPQAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAIEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGA DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

              10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
a589           MQQKVRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
              10      20      30      40      50      60
              70      80      90     100     110
m589.pep      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
a589           IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMLKGLNWTRHDWML
              70      80      90     100     110     120
              120     130     140     150     160     170
m589.pep      PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
a589           SPLAQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
              130     140     150     160     170     180
              180     190     200     210     220     230
m589.pep      AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
a589           AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
              190     200     210     220     230     240

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924

	240	250	260	270	280	290
m589.pep	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
	300	310	320	330	340	350
m589.pep	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VPVAVGIALLT	FIVTWL		
a589	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VPVAVGIALLT	FIVTWL		
	310	320	330	340	350	360
	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIACPC	ALGLATPAAIMVGMGKAVKH	GIWFKDAAAMEEAAHVDA			
a589	IKGDWTVALMHAVAVLVIACPC	ALGLATPAAIMVGMGKAVKH	GIWFKDAAAMEEAAHVDA			
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTGEGSPQVA	AVYCVPSGFD	EDALYRIA	AAVEQNA	AHPLARA	IVSAAQARGL
a589	VVLDKTGTLTGEGSPQVA	AVYCVPSGFD	EDALYRIA	AAVEQNA	AHPLARA	IVSAAQARGL
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVV	GAGITAEVEG	VLVKAGKAE	FAELALPK	FLDGVWD	IASIVAVSVDNKP
a589	DIPAAQNAQTVV	GAGITAEVEG	VLVKAGKAE	FAELALPK	FLDGVWD	IASIVAVSVDNKP
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAE	IGRLKKHNIDVYIMSGDN	QGTVEYVAKQLG	IAHAFGNMSPRDK		
a589	IGAFALADALKADTAE	IGRLKKHNIDVYIMSGDN	QGTVEYVAKQLG	IAHAFGNMSPRDK		
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAM	VG	GDINDAPALAAANVS	FAMKGGADVAEHTASATLMQHSVNQLA		
a589	AAEVQKLKAAGKTVAM	VG	GDINDAPALAAANVS	FAMKGGADVAEHTASATLMQHSVNQLA		
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQN	LFFAFFYNILGIPLAALGFLNP	VIAGAAMAASSVSVLSNALRLK			
a589	DALLVSQATLKNIKQN	LFFAFFYNILGIPLAALGFLNP	VIAGAAMAASSVSVLSNALRLK			
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcgga gtattgctcg gcgttgcttt
51  gggtagacct tattatttgg gtgtcaaac agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctgggttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcaaaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtaa accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaataa
351 cgcgccctgaa acggaaaaag ttttggaaacg ctttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

```

```

501 ctgggaagggc ctgacggggg aaacgggttta tcaaaaaggt ttcaaaaagct
551 accgcaacag ctatgatgcg cccttggttca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatcttc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatctt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaat gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcgcg gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaaaaatac ggcccgtgg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcaaaagg cgatgcttcc ggattattta ccatgacccc
1101 ggtactaaat atcaaaatct tccgtttcac cctgcctcag ggaataattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattggggc tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgcggtt aagtcaggct ggaatatctt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgctt gatggtggac agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaacacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

```

g590.pep..
1 MKKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKEPE LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKkte ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

```

m590.seq (partial) ..
1 ..TGGTTACCT CTATGGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAAACA GTGTGGAAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGCGGTACAT TGAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCC GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTCCC
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATc AG.CTGCACT GGGAAGGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCGA TTCGAAAAC TCAAGCGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACATCCCG TATTGGACAT
951 TAAAACCTTC CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGCGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590 / g590 93.1% identity in 462 aa overlap

m590.pep
g590
30 40 50 60 70 80

m590.pep
g590
90 100 110 120 130 140

m590.pep
g590
150 160 170 180 190 200

m590.pep
g590
210 220 230 240 250 260

m590.pep
g590
270 280 290 300 310 320

m590.pep
g590
330 340 350 360 370 380

m590.pep
g590
390 400 410 420 430 440

m590.pep
g590
450 460 470 480 490 500

m590.pep
g590
460
FDEGGMVS-EPQXX
510
FDEGDMVSGQPHX

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

m590/a590 97.8% identity in 462 aa overlap

m590.pep
 WFTSMETTVIRLKPPELLNNARKYLPDNLKT
 ||||| ||||| ||||| ||||| : ||||| |||||
 a590
 VKAEESLTQQQKILQEAGFLTVESHQYERGWFSTSTETTIVIRLKPPELLHNAQKYLPDNLKT
 30 40 50 60 70 80
 m590.pep
 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| ||||| |||||
 a590
 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
 90 100 110 120 130 140
 m590.pep
 GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFSYRNGYDAPLFKIKLADKGDAA
 100 110 120 130 140 150

928

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|||||
a590  GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSyrNGYDAPLFKIKLADKGDAA
      150      160      170      180      190      200

      160      170      180      190      200      210
m590.ppep FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVdYNVKLNELVNLVTDLQIGAFIN
|||||
a590  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVdYNVKLNELVNLVTDLQIGAFIN
      210      220      230      240      250      260

      220      230      240      250      260      270
m590.ppep PNGSIAPSKIEVGKLAfstKTGESGAFINSEGQFRFDtlVYGDEKYGpLDIHIAAEHLDA
|||||
a590  PNGSIAPSKIEVGKLAfstKTGESGAFIDSEGQFRFGtlVYGDEKYGpLDIHIAAEHLDA
      270      280      290      300      310      320

      280      290      300      310      320      330
m590.ppep SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPsgKID
|||||
a590  SALTVLKRKFARISAKKMTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPsgKID
      330      340      350      360      370      380

      340      350      360      370      380      390
m590.ppep VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEg
|||||
a590  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEg
      390      400      410      420      430      440

      400      410      420      430      440      450
m590.ppep RASLDDINETLRLMVDSTVQSMAREKYLTlNGDQIDTAISLKNnQLKlNGKTLQNEPEpD
|||||
a590  RASLDDINETLRLMVDSTVQSMAREKYLTlNGDQIDTAISLKNnQLKlNGKTLQNEPEpD
      450      460      470      480      490      500

      460
m590.ppep FDEGGMVSEPQqX
|||||
a590  FDEGGMVSEPQqX
      510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGCTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCGGAT AACCTGAAAA
251 CAGTGTGTGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTGCGCCGCG GATTCCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTGGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGCATGCCG CGTTTGAAAA AGTGCATTTT GATTGCGAAA CTTACAGACG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACGT
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAATAACT TCCGATTACG GCTGCCATCG GAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATGGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

```

m590-1.pep
1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHQ
51 YERGWETSME TTVIRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG QVVPASLANT VFYNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFERVHF DSETSDGINP LALGSSNLT EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRMLVD STVQSMAREK YLTNLNGDQID TAISLKNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*

m590-1/g590 93.6% identity in 516 aa overlap

m590-1.pep      10      20      30      40      50      60
m590-1.pep      MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWETSME
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             MKKPLISVAAVLLGVALGTPYYLGVKAESLTQQQKILQKTGFLTVESHQYDRGWFTSTE
m590-1.pep      10      20      30      40      50      60
g590             10      20      30      40      50      60

m590-1.pep      70      80      90      100     110     120
m590-1.pep      TTVIRLKPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             TTVIRLKPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIEEFKYAPE
m590-1.pep      70      80      90      100     110     120
g590             70      80      90      100     110     120

m590-1.pep      130     140     150     160     170     180
m590-1.pep      TEKVLERFFGQVVPASLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             TEKVLERFFGQVPSLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG
m590-1.pep      130     140     150     160     170     180
g590             130     140     150     160     170     180

m590-1.pep      190     200     210     220     230     240
m590-1.pep      FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             FKSyrNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
m590-1.pep      190     200     210     220     230     240
g590             190     200     210     220     230     240

m590-1.pep      250     260     270     280     290     300
m590-1.pep      VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGQFRF
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGRFRF
m590-1.pep      250     260     270     280     290     300
g590             250     260     270     280     290     300

m590-1.pep      310     320     330     340     350     360
m590-1.pep      DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKMTEEQIRNDLIAAVKGEAS
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKMTEEQIRNDLIAAVKGDAS
m590-1.pep      310     320     330     340     350     360
g590             310     320     330     340     350     360

m590-1.pep      370     380     390     400     410     420
m590-1.pep      GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             GLFTHDPVLNIKIFRFTLPQGGKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK
m590-1.pep      370     380     390     400     410     420
g590             370     380     390     400     410     420

m590-1.pep      430     440     450     460     470     480
m590-1.pep      MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRMLVDSTVQSMAREKYLTNLNGDQID
g590             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g590             MLEDLAVSQAGNIFSVNAEDEAEARASIADINETLRMLVDSTVQSMAREKYLTLDGNQID
m590-1.pep      430     440     450     460     470     480
g590             430     440     450     460     470     480

m590-1.pep      490     500     510
m590-1.pep      TAISLKNQLKLNGKTLQNEPEPDFDEGGMVS-EPQQX

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930

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g590      |:||||| |:||||| |:||||| |:| |:|
          TVISLKNNAKLNKLTQNEPDPDFDEGDMVSGQPHX
          490      500      510

a590/m590-1 98.3% identity in 516 aa overlap

a590.pep      10      20      30      40      50      60
MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      10      20      30      40      50      60
MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFTSME

a590.pep      70      80      90      100     110     120
TTVIRLKPPELLHNAQKYLDPNLTQVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      70      80      90      100     110     120
TTVIRLKPPELLNARKYLPNLTQVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE

a590.pep      130     140     150     160     170     180
TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      130     140     150     160     170     180
TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG

a590.pep      190     200     210     220     230     240
FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      190     200     210     220     230     240
FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG

a590.pep      250     260     270     280     290     300
VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFASTKTGESGAFIDSEGQFRF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      250     260     270     280     290     300
VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFASTKTGESGAFINSEGQFRF

a590.pep      310     320     330     340     350     360
GTLVYGDEKYGPLDIHIAAEHLDAASALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEAS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      310     320     330     340     350     360
DTLVYGDEKYGPLDIHIAAEHLDAASALTVLKRKFQISAKKMTTEEQIRNDLIAAVKGEAS

a590.pep      370     380     390     400     410     420
GLFTHNPVLDIKTFRFTLPSPGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      370     380     390     400     410     420
GLFTNNPVLDIKTFRFTLPSPGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK

a590.pep      430     440     450     460     470     480
MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNGDQID
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      430     440     450     460     470     480
MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNGDQID

a590.pep      490     500     510
TAISLKNNAKLNKLTQNEPDPDFDEGDMVSEPPQXX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m590-1      490     500     510
TAISLKNNAKLNKLTQNEPDPDFDEGDMVSEPPQXX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1   TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TGCGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTGCATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCGCGC AAGCGCATCG CCATCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTGCTG TACGGACTION gctTttcctt
351 cggcgtaaCC GAACTGCGGC CCTatgtcgg cacagtcgaA cccgacaccg

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401 ttgccgCCCC CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtgc ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcacccgtgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAacagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACC GTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTcAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTCGCGT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

```

g591.pep..
1  LQTLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG
51  DTEWCLAPIP LGGYVKMVDL REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLALMM LMMAAAFFND VTRLIG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

```

m591.seq
1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCTATGGCA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACC GTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTcAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGGT
1251 CCAAAACATC GGTTCGCGT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

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This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

1	<u>LHTLLAFIFA</u>	<u>ILILVSLHEF</u>	<u>GHIIVARLCG</u>	<u>VKVVRFSVGF</u>	<u>GKPFSTRKRG</u>
51	<u>DTEWCLAPIP</u>	<u>LGGYVKMVD</u>	<u>REGEVSEADL</u>	<u>PYAFDKQHPA</u>	<u>KRIAIIVAAGP</u>
101	<u>LTNLALAVLL</u>	<u>YGLSFSFGVT</u>	<u>ELRPYVGTV</u>	<u>PDTIAARAGF</u>	<u>QSGDKIQSVN</u>
151	<u>GTPVADWGSA</u>	<u>QTEIVLNLEA</u>	<u>GKVAVGVQTA</u>	<u>SGAQTVRTID</u>	<u>AAGTPEAGKI</u>
201	<u>AKNQGYIGLM</u>	<u>PFKITTAVAG</u>	<u>VEKGSFAEKA</u>	<u>GLKPGDRLTA</u>	<u>ADGKPIASWQ</u>
251	<u>EWANLTRQSP</u>	<u>GKKITLNYER</u>	<u>AGQTHTADIR</u>	<u>PDTEVQSDHT</u>	<u>LIGRVGLRPQ</u>
301	<u>PDRAWDAQIR</u>	<u>RSYRPSVURA</u>	<u>FGMGWEKTVS</u>	<u>HSWTTLKFFG</u>	<u>KLISGNASVS</u>
351	<u>HISGPLTIAD</u>	<u>IAGQSAELGL</u>	<u>QSYLEFLALV</u>	<u>SISLGVNLNL</u>	<u>PVPVLDGGHL</u>
401	<u>VFYTAEWIRG</u>	<u>KPLGERVQNI</u>	<u>GLRFGALMM</u>	<u>LMMAVAFFND</u>	<u>VTRLG*</u>

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRF	SVSGFGKPFFFTRKRGDTEWCLAPIP				
g591	LQTLAFIFAILILVSLHEFGHYIVARLCGVKVVRF	SVSGFGKPFFFTRKRGDTEWCLAPIP				
	10	20	30	40	50	60
m591.pep	70	80	90	100	110	120
	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
g591	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
	70	80	90	100	110	120
m591.pep	130	140	150	160	170	180
	ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA					
g591	ELRPYVGTVEPDTVAARTGFGSGDKIQSVNGVSVQDWSSAQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
m591.pep	190	200	210	220	230	240
	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSAPAEKAGLKPGDRLTA					
g591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSAPAEKAGLKPGDRLTA					
	190	200	210	220	230	240
m591.pep	250	260	270	280	290	300
	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
g591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
m591.pep	310	320	330	340	350	360
	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
g591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
m591.pep	370	380	390	400	410	420
	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
g591	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLVFYTVIEWIRGKPLGERVQNI					
	370	380	390	400	410	420
m591.pep	430	440				
	GLRFGALMMLMMAVAFFNDVTRLLGX					
g591	GLRFGALMMLMMAAFAFFNDVTRLIGX					
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>>:

933

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TCGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTCGACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT GGCCTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGCT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGE
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTFVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMMAVAFEND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

```

m591.pep      10      20      30      40      50      60
LHTLLAFIFA I LILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG DTEWCLAPIP
|||||
a591          10      20      30      40      50      60
LHTLLAFIFA I LILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG DTEWCLAPIP

m591.pep      70      80      90      100     110     120
LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAG PLTNLALAVLL YGLSFSFGVT
|||||
a591          70      80      90      100     110     120
LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAG PLTNLALAVLL YGLSFSFGVT

m591.pep     130     140     150     160     170     180
ELRPYVGTV EPDTIARAGF QSGDKIQSVNGT PVADWGSAQTEIVLNLEAGKVAVGVQTA
|||||
a591         130     140     150     160     170     180
ELRPYVGTV EPDTIARAGF QSGDKIQSVNGT PVADWGSAQTEIVLNLEAGKVAVGVQTA

m591.pep     190     200     210     220     230     240
SGAQTVRTID AAGTPEAGKI AKNQGYIGL MPFKITTVAGG VEKGSPEAKA GLKPGDRLTA
|||||
a591         190     200     210     220     230     240
SGAQTVRTID AAGTPEAGKI AKNQGYIGL MPFKITTVAGG VEKGSPEAKA GLKPGDRLTA

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934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tggggcgcgt tcaaattcga
51  cgcggcagca ggcggttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcgccctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgcgc ccgcccgcgc cgaagtgaac caccctgttt cgcaaggat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcac catcttgatt taccaacagc cttatggcga ttgagcggg
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 ggggttcctc gccgtcatcc tgtttatggt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcggtgg tctatttcgg
501 gcgggttgcc aatgtgcctt tggctcggga tatggcggtt atggcgatgg
551 gcatcatggc gtggatcaac ctgctcgcca tcctgctgct ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFQQIF SGAFKFDAAG GLLGGLISQ TMMGIKRL YSNEAGMGSA
51  PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFILI YQPYGDLG
101 AALTQAIAVS QVGQWAGFL AVILEMFAFS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGCCTG TATTCCAACG AGGCGGGTAT GGGTCCGCG
151 CCGAACGCCG CCGCCGCCG CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTATTGTTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTGTGCGCCA TCCTGCTGCT CTCGCCCTTG

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935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGATTG AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDLG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRLYSNEAGMGSAPNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWGAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCAGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTCCCGC
 151 CCGAACCCG CCGCGCCGC CGAAGTGAAA CACCTGTGT CGCAAGGTAT
 201 GATTCAAATG CTGGCGGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTATTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCCG TATGCTGGT TTGGCGTGGG TCTATTTCGG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGATTG AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDLG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

```

g593.seq..
1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcgggcg aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgccct
451 tccctgctgt tgctggatga atcgttttcc agtttggaca cgcatttgcg
501 cgaccggctg cgccgatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcac tcgccgaag aggcctgcac ggcggcgac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtgca ggtcgcccg ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801 ctcgctccgg ctttcggccg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcgtc
901 cgcacccggc tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

```

g593.pep..
1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLRL LSAVHPEHGE LTLNLTVGQH TDGISNGNTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

```

m593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAATACTC GCCGTTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TCGGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

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201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCG CTGGAAAATG CGGCATTTCGG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep  ..
1  MLELNLCKR  FGNKTVADNI  CLTVGRGKIL  AVLGRSGCGK  STLLNIIAGI
51  VRPDGGEIWL  NGENITRMPP  EKRRISLMFQ  DYALFPHMSA  LENAAGFLKM
101 QKMPKAEAE  LAMAALAEVG  LENEHRKPE  KLSGGEKQRL  ALARALVVRP
151 SLLLLDESFS  SLDTHLRGTL  RRMTAERIRN  GGIPAVLVTH  SPEEACTTAD
201 EIAVMHKGRI  LQYGTPELTV  KTPSCVQVAR  LMGLPNTDDN  RHIPQHVRV
251 DQDGMECRVL  SRTCLPESFS  LSVLHPEHGI  LWLNLDMRHA  GAVSGKDTVR
301 IHIEEREIVR  FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGEIWL					
	:					
g593	MLELNLCKCFGGKTVDNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEAEERLAMAALAEVG					
	:					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	:					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRI LQYGTPELTVKTPSCVQVARLMGLPNTDDN					
	:					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPELTIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	: : :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
101 GCGGGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TCGCGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCTGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCA  TATGAGTGCA CTGGAATATG CGGCATTTCG TTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAATATG AGGCGCACCG CAAGCCTGAN AAACCTTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GGCGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCGAAG AGGCCTGCAC GGCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTCAATGCG GTACGCCCGA
651 AACCTTGTTT CAAACGCCTG CCGGCGTGCA GGTCCGCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLKLM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DQDGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICTLVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	: : : : :					
a593	MLELNLCKRFGGKTVADDICTLVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEERLAMAALAEVG					
	: : : :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGT LRRMTAERIRN					
	: : : :					
a593	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIIVMHKGRILQYGT PETLVKTPSCVQVARLMGLPNTDDN					

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	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRKCQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTTTCCG AAGGGAAAAA ACTGGCCACA AACCGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTCAAG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GCGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggtttt
51  gaccgctgac cagccgccgg aggcggagaa agccgcgcgc gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac

```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgtgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggg ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgc gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcgcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg caaaaaaca agccttggtg gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcacaaa
```


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1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggctt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIADV
 51 DNACEPMNLT VPSGQVFN I KNSGRKLEW EILKGMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTAGGTTT
 51 GACCGCGTGC CAGCCGCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACC GCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTC AAC
 151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGAAGTGGC
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGTGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTGTTTGC CGACACCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAAGTCCA CCGGTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
 51 DNACEPMELT VPSGQVFN I KNSGRKLEW EILKGMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN	DNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGIADV	DNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

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m595 . pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595 . pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
g595	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
	130 140 150 160 170 180
m595 . pep	KAKSLFADTRVHYERIEPIAELFSELDVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
g595	KAKSLFAATRVHYERIEPIAELFSELDVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595 . pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m595 . pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFEYDCLKG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFEYDCLKS
	310 320 330 340 350 360
m595 . pep	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380 389

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595 . seq
1  ATGAGAAAT TCAATTGAC CGCATTGTC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAACGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGAATTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595 . pep
1  MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTN EGGSVSIADV
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPGLS

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
a595	MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQVVFNIKNNNGRKLWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNNNGRKLWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFEYDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFEYDKLG					
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1 ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51 atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat tttggaactc
151 gaccgcggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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451   ttccggcgata aagtgtctgat tgacgggtttg agcttcaaag tgccggcgagg
501   cgcgattgtc  ggcattcatcg gcccgaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat  tgccgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacgg  tgaaaatgag cttgattgac caaagccgag aagggtttgca
651   aaacgacaaa  accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca  gtttgaaatc cccgcccggc aatatttggg acgcttcaac
751   tttaaaggca  gcgaccaaag caaaatcgca aggcagcttt ccggcggcga
801   acgcggccgt  ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
851   tgctgctgga  cgaaccgtcc aacgatctcg acgtggaac cctgcgcgag
901   ttggaagacg  cattgttggg atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg  tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa  atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac  gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg  gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKE
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLDDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTC CCTTCTTTTC TCCCCGGCG
101 CGAAATTCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGATGACC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TTGCCTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTGTC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAA GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGCAGGTT GGTCAGTTTG AAATTCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGSC
1351 GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CTTGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTTCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTCTTCTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAVRK AMQOELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

	160	170	180	190	200	210
m596.pep	LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPQTV					
g596				MLLLDEPTNHLDAESVEWLEQFLVRFPQTV		
				10	20	30
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAVRKAMKQE					
g596	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAVRKAMKQE					
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGRQAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS					
g596	LEWVRQNAKGRQAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS					
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLSEFKVPAGAIVGIIPNGAGKSTLFKMISGKEQPDGGEVKIGQTVKMSLID					
g596	FGDKVLIDGLSEFKVPAGAIVGIIPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID					
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR					
g596	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR					
	220	230	240	250	260	270

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLGGGNVLLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX				
	:				
g596	ACEGDSKWVFFDGNVQEYADKKRRLGKEGAKPKRIKYKPVTRX				
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```
a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTT TCCTCCCGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAGCG GTTTGGGCGA AGTGCGTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGCT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAACG TTTGGAAAAC GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGCG
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCAAATGGG GTTCTTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```
a596.pep
1  MSQQYVYSML RVSKVPPQK TTIKDISLSF FPAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSQ QSKITGQLSG
451 GERGRHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGTPKPR
551 IKYKPVTR*
```

m596/a596 99.3% identity in 558 aa overlap

948

	10	20	30	40	50	60
m596.pep	MSQQYVYSMLRVSKVPPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVPPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m596.pep	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m596.pep	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSSGGEKRRVALCKLL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m596.pep	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m596.pep	IPWKGNYSSWLEQKEKRLNEAKSEAARVKAMQLEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSSWLEQKEKRLNEAKSEAARVKAMQLEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m596.pep	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m596.pep	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m596.pep	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLLDPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLSGGNVLLLDPSNDLDV					
	430	440	450	460	470	480
	490	500	510	520	530	540
m596.pep	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
	490	500	510	520	530	540
	550	559				
m596.pep	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq
 1 ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
 51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
 101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAAC TAACACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TGCGCCGGA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TTcaggAtgc ggAagcaaAA agaAAATTGG CTGAagCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggC GATGTTTGA AAGGCGTGT CTATTCCACT
901 GCGCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCACG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNRKLT EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISYIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAAGTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGAAAAACGC CGAACCAGGT CAGAAAAACC GCTTTTTCG TTTATACCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGTT AAAAACAGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAA TCAGGCAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGC AGACAGAATG CCAAATCGC
501 CAAAGATGCC CGAAAACTGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAA AGGCCGAACA CCGCATTCAG
601 GATCGCGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCGATAT TTGAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCC ATCAGGCGGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATAA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKRKLA ERLAAAEKAR KEAAQKAEK RRAEMSNLTA EDNRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDDYGVK VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVDHGENYISIIYAGLSEISVKGKYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSGWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTGCC CGTTTCGTAT CGGGGAAC TAACAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCGCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCACGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACGT TTGAAAAAAC CGTTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGGCGGC GATGTTTGGA AAGCGTGTT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA

```

951

```

951  CGAGTTGGAC  GGCTACGGCA  AAGTGGTCGT  GGTTCGATCAC  GGCGAGAACT
1001 ACATCAGCAT  CTATGCCGGT  TTGAGCGAAA  TTTCCGTCGG  CAAGGGTTAT
1051 ATGGTCGCGG  CAGGAAGCAA  AATCGGCTCG  AGCGGGTCGC  TGCCGGACGG
1101 GGAAGAGGGG  CTTTACCTGC  AAATACGTTA  TCAAGGTCAG  GTATTGAACC
1151 CTTTCGAGCTG  GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK  QLQEERIRQE  RIRQERIRQA  RGNLASVNRK  QREAWDKFQK
51  LNTLNLRLKT  EVAATKAQIS  RFVSGNYKNS  QPNAVALFLK  NAEPGQKNRF
101 LRYTRYVNAS  NREVVKDLEK  QOKALAVQEQ  KINNELARLK  KIQANVQSLL
151 KKQGVTDAAE  QTESRRQNAK  IAKDARKLLE  QKGNEQQLNK  LLSNLEKKKA
201 EHRIQDAEAK  RKLAEARLAA  AEKARKEAAQ  QKAEARRAEM  SNLTAEDRNI
251 QAPSVMGIGS  ADGFSRMQGR  LKKPVDGVPT  GLFGQNRSGG  DVWKGVFYST
301 APATVESIAP  GTVSYADELD  GYGKVVVDH  GENYISIIYAG  LSEISVGKGY
351 MVAAGSKIGS  SGSLPDGEEG  LYLQIRYQGG  VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTLNLRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTLNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
a597.pep	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
a597.pep	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
a597.pep	SGSLPDGEEGLYLQIRYQGGVLNPSSWIRX					
m597	SGSLPDGEEGLYLQIRYQGGVLNPSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTGCGCGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CCGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGCGCCGC aaagcggta
551 tgaCGCCGAG CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAAGTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGACG GCCACCAAAG
551 CGGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

|||||
g601  TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
|||||
g601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
      130     140     150     160     170

      190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCC GCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCGGTACGCG TGGTCAACCT TGCCCGAGGC
451 GCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
|||||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
|||||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
|||||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
      130     140     150     160     170     180

      190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CCGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA TgcgagattA TATCACTTGC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGO INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQIAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 CLQMRDYITC FWRLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: : : : : :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHVIIVEMCAWYGVSA-GEYTVN---LQMRDYITRF*QLHX					
	: :: : : : :: :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLAAQLQMRDYITCFWRLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CCGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRRTLLGRQVNRHGQTGNCGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNIVIVEMCAWYGVVSAGEYTVNLQMRDYITRFXLHX					
a602	AGLHVCNSVHELFFLNIVIVEMCAWYGVSTGEYTVNLQMRDYITRFXLHX					
	70	80	90	100	110	

q603.seq

1	ATGGGATTCCC	GCCTGCGTGG	GAATGACGCT	AGGAAATACG	GCATACGCTT
51	TGCCCCAAGA	GGCCGTCTGA	AACACACTCC	GCCCAACGCC	CATCCTTTTT
101	CAGACGGCCC	CGCACCAAAA	AAACAACCAC	AAACTACAAG	GAGAAACATC
151	ATGTCCGACC	AACCTATTCT	TGTCCTGAAC	TGCGTCAGTT	CATCGCTCAA
201	AGGCGCCGTT	ATCGACCGCA	AAAGCGGCAG	CGTCGTCTTA	AGCTGCCTCG
251	GGGAACGCCT	GACTACGCCC	GAAGCCGCTA	TTACCTTCAA	CAAAGACGGC
301	AACAAACGCC	AAGTTCCTCT	GAGCGGCGCG	AACTGCCACG	CGGGCGCGGT
351	GGGTATGCTG	TTGAACGAAC	TGGAAAAACA	CGGACTGCAC	GACCCGCATCA
401	AAGGCATCGG	CCGCCGCATC	GCCACGCGCG	GCGAAAAATA	TCACGAGTCC
451	GTCCTCATCG	ACCAAGACGT	CCTTGACGAA	CTGAAAGCCT	GCATCCCGTT
501	CGCCCCGCTG	CACAACCCCG	CCAACATCAG	CGGCATCTTC	GCCGCGCAGG
551	AACACTTTCC	CGGCCTGCCC	AACGTGCGCG	TGATGGACAC	CTCGTTCCAC
601	CAAACCATGC	CGGAGCGGGC	CTACACTTAT	GCCGTGCCGC	GCGAATTGCG
651	CAAAAAATAC	GCCTTCCGCC	GCTACGGTTT	CCACGGTACC	GGTATGCGTT
701	ACGTGCCCC	TGAAGCCCGA	CGCATCTTGG	GCAAACCTct	ggaaGACATC
751	CGCATGGATA	TTGCCCACTT	AGGCAACGCG	GCATCTATTA	CCGCCGCTCA
801	AAACGGAATA	TCCGTCGATA	CCGGTATGGG	TTTCACGCCG	ATCGAAGGTT
851	TGGTAATGGG	TACACGTTGC	GGCGACACCG	ATCCGGGCGT	ATACAGCTAT
901	CCGACTTTCC	ACGCAGGGAT	GGATGTTGCC	CAAGTTGATG	AAATGCTGAA
951	CGAAAAATCA	GGTTTCCCGG	GTATTTCCga	actTCCCAAC	GACTGCCGCA
1001	CCCTCGAAAT	CGCCGCCGAC	GAAGGCCGCG	AAGGCGCGCG	CCTCGCCCTc
1051	gaAGTCATGA	CCTGCCGCCT	CGCCAAATAC	ATCGCTTCGA	TGGTGTGGC
1101	CTGCGGCAGT	GTTGACGCAC	TCGTGTTTCA	CGGCGGTATC	GGCGAAAAAT
1151	CGCGTAATAT	CCGTGCCAAA	ACCGTTTCCT	ATCTTGATT	CTTGGGTCTG
1201	CACATCGACA	CCAAAGCCAA	TATGAAAAAA	CGCTACGGCA	ATTCGGGCAT
1251	TATCAGCCCG	ACCGATTCTT	CTCCGGCTGT	TTTGGTCGTC	CCGACCAATG
1301	AAGAACTGAT	GATTGCCTGC	GACACTGCCG	AACTTGCCGG	CATCTTGTA

g603.ppt

1	MDSRLRGNDA	RKYGIRFAQR	GRLKHTPPNA	HPFSDGPAPK	KQPQTRRNI
51	MSDQLILVLN	<u>CVSSSLKGAV</u>	IDRKSQSVVL	SCLGERLTPP	EAVITFNKDG
101	NKRQVPLSGR	NCHAGAVGML	LNELEKHGLH	DRIKAIGRRI	AHGGEKYHES
151	VLIDQDVLDE	LKACIPFAPL	HNPAITSGIL	AAQEHFPGLP	NVGVMDTSFH
201	QTMPEAYTY	AVPRELRKKY	AFRRYGFHGT	GMRYVAPEAA	RIILGKPLEDI
251	RMIIAHLGNG	ASITAVKNKG	SVDTGMGFTP	IEGLVMGTRC	GDTPDGVVSY
301	PTFHAGMDVA	QVDEMLNEKS	GFPGISELPN	DCRTLAIARD	EGREGARLAL
351	EVMTCKRLAKY	<u>IASMAVACGS</u>	VDALVFTEGI	GENSRNIRAK	TVSYLDLFLGL
401	HIDTKANMEK	RYGNSGIISP	TDSSPAVLVV	PTNEELMIAC	DTAELAGIL*

m603.seq

1	CTGTCTCTCGC	GTAGGCGGGG	ACGGAATAAC	GATAGAAAAT	GCGGCATACG
51	CTTTGCCCAA	AGAGGCCGTC	TGAAACACCT	TGCGCTGAT	GTCTGC . CTT
101	TTTCAGACGA	CCCCACACTA	AAAAACAAC	CACAACTAC	AAGGAGAAAC
151	ATCATGTCCG	ACCAACTCAT	CCTCGTTCTG	AACTGCGGCA	GTTCATCGCT
201	CAAGGCGCC	GTTATCGACC	GAmAAAGCGG	CAGCGTCGTC	CTAAGCTGCC
251	TCGGGCAACG	cCtGACCACG	CCCCAAGCCG	TCATTACGTT	CAACAAAGAC

956

```

301  GGCAACAAAC  GCCAAGTTCC  CCTGAGCGGC  CGAAATTGCC  ACGCCGGCGC
351  GGTGGGTATG  CTTTTGAACG  AACTGGAAAA  ACACGGTCTG  CACGACCGCA
401  TCAAAGCCAT  CGGCCACCGC  ATCGCCCACG  GCGGCGAAAA  ATACAGCGAG
451  TCTGTTTTGA  TCGACCAGGC  CGTAATGGAC  GAACTCAATG  CCTGCATTCC
501  GCTTGCGCCG  CTGCACAACC  CCGCCAACAT  CAGCGGCATC  CTTGCCGCAC
551  AGGAACATTT  CCCCAGTCTG  CCAATGTCG  GCGTGATGGA  TACTTCGTTC
601  CACCAAACCA  TGCCGGAGCG  TGCCTACACT  TATGCCGTGC  CGCGCGAGTT
651  GCGTAAAAAA  TACGCTTTCC  GCCGCTACGG  TTTCCACGGC  ACCAGTATGC
701  GTTACGTGTC  CCCTGAAGCC  GCACGCATCT  TGGGCAAACC  TCTGGAAGAC
751  ATCCGCATGA  TTATTGCCCA  CTTAGGCAAC  GGCGCATCCA  TTACCGCCAT
801  CAAAAACGGC  AAATCCGTCG  ATACCAGTAT  GGGTTTCACG  CCGATCGAAG
851  GTTTGGTAAT  GGGTACACGT  TGCGGCGACA  TCGATCCGGG  CGTATACAGC
901  TATCTGACTT  CCCACGCCGG  GATGGATGTT  GCCCAAGTGG  ATGAAATGCT
951  GAACAAAAAA  TCAGGTTTGC  TCGGTATTTC  CGAACTTTCC  AACGACTGCC
1001 GCACCTCGA  AATCGCCGCC  GACGAAGGCC  ACGAAGGCGC  GCGCCTCGCC
1051 CTCGAAGTCA  TGACCTACCG  CCTCGCCAAA  TACATCGCTT  CGATGGCTGT
1101 GGGCTGCGGC  GCGTTGACG  CACTCGTGTT  CACCGCGGGT  ATCGGCGAAA
1151 ACTCGCGTAA  TATCCGTGCC  AAAACCGTTT  CCTATCTTGA  TTTCTGGGT
1201 CTGCACATCG  ACACCAAAGC  CAATATGGAA  AAACGCTACG  GCAATTCGGG
1251 CATTATCAGC  CCGACCGATT  CTTCTCCGGC  TGTTTTGGTT  GTCCCGACCA
1301 ATGAAGAACT  GATGATTGCC  TGCGACACTG  CCGAACTTGC  CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

```

m603.pep
1  LSSRRRGRNN DRKCGIRFAQ  RGRLKHLAPD  VCXFSDDPTL  KKQPQTTRRN
51  IMSDQLILVL  NCGSSSLKGA  VIDRXSGSVV  LSCLGERLTT  PEAVITFNKD
101 GNKRQVPLSG  RNCHAGAVGM  LLNELEKHGL  HDRIKAIGHR  IAHGGEKYSE
151 SVLIDQAVMD  ELNACIPLAP  LHNPNANISGI  LAAQEHFPGL  PNVGVMDTSF
201 HQTMPERAYT  YAVPRELRKK  YAFRRYGFHG  TSMRYVAPEA  ARILGKPLED
251 IRMIIAHLGN  GASITAIKNG  KSVDTSMGFT  PIEGLVMGTR  CGDIDPGVYS
301 YLTSHAGMDV  AQVDEMLNKK  SGLLGISELS  NDCRTLEIAA  DEGHEGARLA
351 LEVMTYRLAK  YIASMAVGCG  GVDALVFTGG  IGENSRRNIRA  KTVSYLDLFLG
401 LHIDTKANME  KRYGNSGIIS  PTDSSPAVLV  VPTNEELMIA  CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

```

          10      20      30      40      50      60
m603.pep  LSSRRRGRNNDRKCGIRFAQRGRLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
          ::||| ||: || ||||| ||||| ||:: ||| |: ||||| ||||| |||||
g603      MDSRLRG-NDARKYGIRFAQRGRLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
          10      20      30      40      50

          70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNKQVPLSGRNCHAGAVGM
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      NCVSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNKQVPLSGRNCHAGAVGM
          60      70      80      90      100     110

          130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHHGGEKYSESVLIDQAVMDDELNACIPLAPLHNPNANISGI
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603      LLNELEKHGLHDRIKAIGRRIAHHGGEKYHESVLIDQDVLDELKACIPAPLHNPNANISGI
          120     130     140     150     160     170

          190     200     210     220     230     240
m603.pep  LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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g603      LAAQEHFPLPNVGVMDSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
          |||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISELPNDCRTLEIAADEGREGARLALEVMTCLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

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a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGA AAA ACACGAAGT CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCTTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAATTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RRLKHTPPN AHPFSDDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHN PANISGI LAAQEHFPL PNVGVMDSF

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201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGNSRNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQGRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL					
a603	LSSRRRGRNDRKCGIRFAQGRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL					
	10	20	30	40	50	60
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNRQVPLSGRNCHAGAVGM					
a603	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDGKNRQVPLSGRNCHAGAVGM					
	70	80	90	100	110	120
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHHGGEKYESVLDQAVMDELNACIPLAPLHNPANISGI					
a603	LLNELEKHELHDRIQAVGHRIAHHGGEKYESVLDQAVMDELNACIPLAPLHNPANISGI					
	130	140	150	160	170	180
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSFHTQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
a603	LAAQEHFPGLPNVGVMDSFHTQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
	190	200	210	220	230	240
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
	310	320	330	340	350	360
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGNSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	YIASMAVGCGGVDALVFTGGIGNSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
m603.pep	430	440	450			
	PTDSSPAVLVVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GGCGGGTTTC GGCGTGCGCG CGCGGGCGGC GGCTTCGGAT

g604 . pep

m604.seq

m604 . pep

m604/g604

a604.seq

1	ATGCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCTGCG	GCAAGGTTGA
51	CCAGCGTACC	GGGCACGGCG	GCGGCGGTGCG	CAATGGCAAC	AGAGGCGGTA
101	CCCATCATCG	CGTGGTGCAA	TTTGCCCATG	CTCAGGGCGC	GTACCAGCAA
151	ATCGATGTCG	GCGGCATTCA	CGGTTTTGCC	ACTGGAGGCG	GTGTAATCGG

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201  CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGCGAGCT
251  TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301  TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGAT TCGTCTTGCA
351  ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTACAGGAA AACGGTCGGA
401  ATGCCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451  AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501  CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551  TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601  ATGGGCAATA ATGGTTTTCG CGATGTTTTT CTGCCAGATT TTGACTGTGC
651  AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNC AVLHRY
201 MGNNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
	: : : : : : : : : :					
a604	MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA					
	: : : : : : : : :					
a604	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSCGIVVDVVLQLFA					
	70	80	90	100	110	120
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI					
	: : : : : : : : :					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKKFDLYFGCRE					
	130	140	150	160	170	180
	190	200	210	220		
a604	RYAVELKIACFQNC AVLHRYMGNNGFADVF LPDFDCADAVX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGcta tGCCGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCTCC GGCTAcccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTCCGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCcgCAAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACC GAAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNKLKE IFTAIESSAS GYPSEQGIK LFDDFDFTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKQF DEHIIIEGFF
251 GQEINHHTYN LARMNMFHVN VNYNKFHIEL GDTLTNPCLK DSKPFDVVS
301 NPPFISDWIG SDDPTLIND RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVP
451 IAQNAAQQTV KONGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCCTCG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGACAG
201 CATCATCAGC CCGGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCGCA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACCTG ATTTGCGCAA
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCTGCCAAC GCAGGCAAAT CCGGCGCGCA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCAGA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEINHHTYN LARMNMF LHN VNYNQFHIEL GDTLTNP KLD SKPFDAIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGA EQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNN NVL IEEHIAEIVK LFADKADVP H
451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng)

from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQQAQLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQQAQLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIIIEGFFGQEINHHTYNLARMNMF LHN VNYNQFHIELGDTLTNP KLD SKPFDAIVS					
g605	DEHIIIEGFFGQEINHHTYNLARMNMF LHN VNYNQFHIELGDTLTNP KLD SKPFDAVVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGA EQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNI LVLSKHKDNTDIQFIDASGF					
g605	FYRGGA EQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNI LVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNN NVL IEEHIAEIVKLFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					
g605	FKKETNN NVL TEEHIAEIVKLFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					

963

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	: : : : : :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIEIX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```

a605.seq
1  ATGATGACCG AAATACAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTCAAACAAT
101 ACGTCTCTCG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCACG CCCGAAATCA AAGACGATGC CGTCAAAGTC AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCGCGCTCC GGCTATCCGT CCGAACAAGA CATTAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT AAAAGGCGTG GCGGAACTCG ATTTTCGGCAG
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCTAATA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTAAAC AAAATCTACG ACCAGCTTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAATCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTTTCC
901 AATCCGCCCT ATTCCATCAA CTGGATAGGC AGCGGCGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CTGCAGGCGT ACTCGCCCCG AAATCCAAG
1001 CCGATTTTGC CTTCAATTCT CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTCA
1151 TCGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATA
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AGCGGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTTG AACCCGAAGA CACCCGCGAA ATTATCGACA
1451 TCAAACAGCT TAACGCCGAA ATCAGCGAAA CCGTTGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```

a605.pep
1  MMTEIQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51  YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTHLKE IFTAIESSAS GYPSEQDIKG LFDDFDFTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGSFED HHIDLFGBAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEINHHTYN LARMNMFLHN VNYNKFHIEL GDTLTNPCLK DSKPFDVVVS
301 NPPYSINWIG SGDETLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KDNQYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER
501 LRREIDEVIA EIEA*

```

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQRQLHRQIWKIAD EVRGAVDGWD FKQYVLGTLFYRFISENFTD YMQAGDSSID					
	: : : : : :					
a605	MMTEIQQRAQLHRQIWKIAD EVRGAVDGWD FKQYVLGTLFYRFISENFTD YMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKV KGYFIYPGQLFCNIAAEAHQ NEELNTHLKEIFTAIESSAS					

a605	Y A A M P D S I I T P E I K D D A V K V K G Y F I Y P G Q L F C N I A A E A H Q N E E L N T K L K E I F T A I E S S A S	70	80	90	100	110	120
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAE LDFGNFENHHIDLFGDAY	130	140	150	160	170	180
a605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAE LDFGSFEDHHIDLFGDAY	130	140	150	160	170	180
m605.pep	EY L I S N Y A A N A G K S G G E F F T P Q S V S K L I A R L A V H G Q E K V N K I Y D P A C G S G S L L L Q A K K Q F	190	200	210	220	230	240
a605	EY L I S N Y A A N A G K S G G E F F T P Q S V S K L I A R L A V H G Q E K V N K I Y D P A C G S G S L L L Q A K K Q F	190	200	210	220	230	240
m605.pep	D E H I I E E G F F G Q E I N H T T Y N L A R M N M F L H N V N Y N Q F H I E L G D T L T N P K L K D S K P F D A I V S	250	260	270	280	290	300
a605	D E H I I E E G F F G Q E I N H T T Y N L A R M N M F L H N V N Y N K F H I E L G D T L T N P K L K D S K P F D A V V S	250	260	270	280	290	300
m605.pep	N P P Y S I N W I G S D D P T L I N D D R F A P A G V L A P K S K A D F A F I L H A L N Y L S G R G R A A I V S F P G I	310	320	330	340	350	360
a605	N P P Y S I N W I G S G D P T L I N D D R F A P A G V L A P K S K A D F A F I L H A L N Y L S G R G R A A I V S F P G I	310	320	330	340	350	360
m605.pep	F Y R G G A E Q K I R Q Y L V E G N Y V E T V I A L A P N L F Y G T G I A V N I L V L S K H K D N T D I Q F I D A S G F	370	380	390	400	410	420
a605	F Y R G G A E Q K I R Q Y L V E G N Y V E T V I A L A P N L F Y G T G I A V N I L V L S K H K D N T D I Q F I D A G G F	370	380	390	400	410	420
m605.pep	F K K E T N N N V L I E E H I A E I V K L F A D K A D V P H I A Q N A A Q Q T V K D N G Y N L A V S S Y V E A E D T R E	430	440	450	460	470	480
a605	F K K E T N N N V L T E E H I A E I V K L F A D K A D V P H I A Q N A A Q Q T V K D N G Y N L A V S S Y V E P E D T R E	430	440	450	460	470	480
m605.pep	I I D I K Q L N A E I S E T V A K I E R L R R E I D E V I A E I E A X	490	500	510			
a605	I I D I K Q L N A E I S E T V A K I E R L R R E I D E V I A E I E A X	490	500	510			

q606.seq

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep
 1 MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNFATGAS RNSSLIAVST GLLDHMTRE VEAVALHEMA HVGNGDMVTL
 101 TLIQGVNTF VVFLSRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSSL STHPSLDNRI ARLKSL*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq
 1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGC GCGGAAG TTATCGACAC
 51 GCCGCGCACC GAAGAAGAAAG CCTGGGCTTT GAACACTGTC GAAGCCCAAG
 101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
 151 GAACCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
 201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
 251 TATTGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
 301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
 351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCAGGGGAA
 401 CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
 451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
 501 GGGCGCGGCA AAACCTGGTCG GCGCGCCGAA AATGATTTCC GCCCTGCAAA
 551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
 601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACCC CTTGCTGGA
 651 CAACCGTATC GCGCGCTCA AATCGCTTTA A

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep
 1 MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNFATGAS RNSSLIAVST GLLDHMTRE VEAVALHEMA HVGNGDMVTL
 101 TLIQGVNTF VVFLSRIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSSL STHPSLDNRI ARLKSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng)
 from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIQKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
g606	MSKFIQKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNNGDMVTLTLIQGVNTFVVFLSRIAN					
g606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNNGDMVTLTLIQGVNTFVVFLSRIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCG GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTTCAGCAT GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNFATGAS RNSSLIAVST GLLDHMRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
a606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
	10	20	30	40	50	60
	/					
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTcgACCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGTGTGGGC
351 GGCGATTACG CCGTTCGCGA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCGC
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

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601 GGTTCGGCG TGGCGACAAT GCGGGTGT TT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAgccaGcg cGTTTTCGTT
801 TATCGTGT TTGATTGCGC CTttcggCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTTA AGCATCGCCT CCACCGTCTT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFLGILGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRAHAYSA SSLNRPRILIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAAPWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCGT CGGTTTGTGTC GATACTGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCGA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGTGTGTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTCTT CCGCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTCC AACCAGCAGA CTTCACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCGCCTT TTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF PVFLKEVRLL TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

101 IWFGFLGLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRALHAYT SSLNRPRILIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPOSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFRSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAAPFWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	: : : : : : : : : :					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGLGVFGMVLMWAAIT					
	: : : : : : : : :					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLGLGIFGMILMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILIMLVSFAAFVLN					
	: : : : : : : : :					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYASSLNRPRILIMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
	: : : : : : : : :					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV					
	: : : : : : : : :					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNNDDPAVL					
	: : : : : : : : :					
g607	GSAGTVRIGFSLGRREFSRRARYISGVSLVSGWVLAVITVLSLVLFRSPLASMYNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
	: : : : : : : : :					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
	: : : : : : : :					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMEVLKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1   ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTCGGGAC TGGCGACGAT GCGGTTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTATG ATCGCCAAGG AAAATTCTT CCGCCCATTC GGAAGTACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTTC TTGATTGCGC CTTTCGCGCA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGGTGC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTATA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTCC AACCAGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCCT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATTT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1   MLLDLNRFSF SVFLKEVRL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHREALHAYA SSLNRPRLIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVEFKQIWKI
251 GAPIGLSYFL EASAFSIVE LIAPFGEDYV AAQQVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFHIH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCSR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTALPMLLAQVAQVGIGFVDTMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFSVFLKEVRLLTALPMLLAQVAQVGIGFVDTMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGVLMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLHAYTSSLNRPRLIMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRLHAYASSLNRPRLIMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
|||||
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
|||||
a607          WAVFKQIWKIGAPIGLSYFLEASAFSIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMMLAVITVLSLVLFRSPLVSMYNNDAVL
|||||
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNNDAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIIHAAAFWGCGLLPGYLLAYRFN
|||||
a607          SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIIHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
|||||
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1  ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTcaaa caaATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1  ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGCCG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGDILIG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRSELT SFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
m608.pep	70 80 90 100 110 120					
	TFRNSAVQKILQGGEPEGAGDIGLEGDILIGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGDILIGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
m608.pep	130 140 150 160 170 180					
	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
m608.pep	189					
	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
 51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
 101 TTGCCGGGTT GAACTTGCCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
 151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT
 201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGGCTCG
 251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
 301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
 351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
 401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
 451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
 501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGDILIG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep      MSALLPIINRLILQSPDSRSELAAGKTTLNIAGLKLAGRITEDGLLSAGNGFADTEI
|||||
a608          MSALLPIINRLILQSPDSRSELAAGKTTLNIAGLKLAGRITEDGLLSAGNGFADTEI
              10      20      30      40      50      60

              70      80      90      100     110     120
m608.pep      TFRNSAVQKILQGGEPGAGDIGLEGLDILGIAVLSLLGSLRSRASDELARIFGTQADIGS
|||||
a608          TFRNSAVQKILQGGEPGAGDIGLEGLDILGIAVLSLLGSLRSRASDELARIFGTQADIGS
              70      80      90      100     110     120

              130     140     150     160     170     180
m608.pep      RAADIGHGIKQIGRNIAEQIGGFSRESEANIGNEALADCLDEISRLRDGVERLNERLDR
|||||
a608          RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
              130     140     150     160     170     180

              189
m608.pep      LERDIWIDX
|||||
a608          LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GGCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTGGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCCTCTTT CATTTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRV FV GLFGNVFFIG
51 AFEQAVELAA RLRFHIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GGCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCGTAT TGGGAAATTT CTTGGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCCTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRV FV GFEGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

              10      20      30      40      50      60
m609.pep      MVVDRLEILALDDETLDFAFVGNQRSSDIAHHIFHEFRV FVGFEGNVFFIGAFEQAVELAA
|||||
g609          MVVDRLEILALDDETLDFAFVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m609.pep      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRVAVLGNFFGT RAKRGYGNHDLHTVAVCPVF
|||||

```

973

```

g609      RLRFHIIIDNFLDITDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF
           70          80          90          100          110          120

           130
m609.pep  DFARETDIIIX
           |:|:|:|:|:|
g609      HFTREADIIIX
           130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```

a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TGCCTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTCG GGTTCGTA GGCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGCGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGCTTTT CATTCGCCC GTGAGGCTGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

```

a609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101 RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*

```

m609/a609 96.9% identity in 131 aa overlap

```

           10          20          30          40          50          60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFEVGGFFGNVFFIGAFEQAVELAA
           |||
a609      MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFEVGGFFGNVFFIGAFEQAVELAA
           10          20          30          40          50          60

           70          80          90          100          110          120
m609.pep  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           |||
a609      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
           70          80          90          100          110          120

           130
m609.pep  DFARETDIIIX
           |:|:|:|:|:|
a609      HFAREADIIIX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1937>:

```

g610.seq
1  ATGATTGGAG GGCTTATGCA ATTCCTTAC CGCAATGTTC CGGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATATGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG
151 GCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGCTGAAG CTCGGTATTC
251 CGATGTTGGC ACTCTTCCC GTGGTTACGG CAAACAAAC CGGGCGTGCG
301 CAGGAGGCGT ACATCCCGA AGGACTCGTG CCGTCAACTG tccgagccTT
351 GCGCGAGAGG TttcCgaac tggggattat gacggatgtc gcgctcgAtc
401 cttatacggg gcacGGTCAG GACGGACTGA CGGACgaaaa cggttaCGTG
451 ATGAatgAtg aaaCCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCATGC
501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CGATATGATG GACGGGCGTA
551 TCGGCGCCAT CCGCAGGCT TTGGAGGATG CCGGACATAT CCATACGCGG
601 ATTATGGCAT ATTCCGCCAA ATATGCTTCT GCATTCTACG GCCCTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG AAAGGCAGAT AAAAAGACCT
701 ATCAGATGGA TCCTGCAAAT ACCGATGAGG CGCTGCATGA AGTGGCGCTC
751 GATATTCAGG AAGGTGCGGA TATGGTGATG GTGAAGCCCC GTTGCCGTA

```



```

801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep

```

1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51 AAREEDVPSM PGVKRQSLDR LLFTAEAEVAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSSE YAMLAQAVAN
301 GWLDGGKVVVL ESLLAFLKRA ADGILTYAI EAAKMLKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq

```

1 ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGCGGAAGA GCGGTAAG CTCGGTATTC
251 CGATGTTGGC ATGTTCCTCC GTGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTATATGTG
451 ATGAACGATA AAACCGTAGA GGTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCGCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGCGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGTAATG GTCAAGCCCG GTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep

```

1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51 SAREEDVPSM PGVKRQSLDR LLFTAEAEVAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AOVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSSE YAMLAQAIAN
301 GWLDGGKVVVL ESLLAFLKRA ADGILTYAI EAAKMLKR*

```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEAEVAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEAEVAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPGLGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM					
g610	FPGLGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLKGADKKTYQMDPAN					

975

```

g610      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTATATGT
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVASRMRR MRRDDFSRRL MREHTLTADD LIYPVVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTQYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVV L ESLLAFKRAG ADGILTYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHTLTADDLIYPVVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHTLTADDLIYPVVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

```

976

```

m610.pep    FPELGIMTDVALDPYTVHQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
|||||
a610        FPELGIMTDVALDPYTVHQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
|||||
a610        DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
|||||
a610        TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
|||||
a610        GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatectTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctga
251 TcgcgGTCTa tggtttcCca ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTTGTA ggcaacCTGA TACTgtctgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGtc gCTCAtgcCG TAGCGCGTTA
501 CCATTTCCGC TGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTTTGTG GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCGTCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGgttac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFH FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||:|||||
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||:|||||
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
               |||||:|||||
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X
               |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTG TGTTTCCCA TTCCATCAGG GCTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GCTCATGCCG TAGCGCGTTA
501 CCATTTCGCG CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLGLCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFL
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

               10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
               |||||:|||||
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X

```

978

a611 |
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGGcttctg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51  AGCCTttgac tttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGCATTTCCG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGCATTTCCG TCATCATCGA
301 AATCCATATA .AAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIAKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
	: : : :					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAGVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
	: : : :					
g612	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGTATTTCCG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTT.AC GGGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVFDGFR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVFDGFRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612           MGFGGNIAKKLAGVDEIAFDGIVFDGFRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep      KCAENVLFKVP AIHRAAYFVG NFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a612           KCAENVLFEVPAIHRAAYFVG NFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep      GHSNX
              ||||
a612           GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGaggcagtc ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTG TCGGCGATG
151  TTCTGCCGA TTTgtttGAT GCCGTGTCCG ATGTCGGTGG CACGgtgccc
201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCTG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGCGGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLP SR DSTAMP RMR
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCGGA CTCGATTTCG CGGGAAAATC CGCCGATTG TCGGCGATG
151  TTCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCTGTC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCTG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGCGGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPSA  CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KFFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLP SRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLP SRDSTAMPRMRSPSSLMSPAPGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	PAKAASSERLSGL	LCRIRRLMMG		
g613	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	PAKEVSSERLSGL	LCRIRRLMMG		
	130	140	150	160	170	180

	190	200
m613.pep	RRADIFSDRGGECLLLLLPLILQAX	
g613	RRADIFSDWGGECLLLLLPLILQAX	
	190	200

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCTG  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTCGCGGA  CTCGGGTTTC  CGGGAAAATC  TGCCGATTTC  TTCGGCGATG
151 TTCTGCGCA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCGGA  AGGTGATTTT  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501 GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTTCT  GTTGACGCTT
601 ATTTTACAGG  CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPMSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101 PSSPMSAPAG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFNP
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*

m613/a613    98.0% identity in 204 aa overlap

m613.pep
10  20  30  40  50  60
MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP
|||||
a613
10  20  30  40  50  60
MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP
|||||

m613.pep
70  80  90  100  110  120
MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSPMSAPAGSPPWRIFCTA
|||||
a613
70  80  90  100  110  120
MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSPMSAPAGSPPWRIFCTA
|||||

m613.pep
130 140 150 160 170 180
LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLP
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq
 1 AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
 51 cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
 201 TCAAACCTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
 251 AACCGAGCGC GCTGACTGCC CTGTTTACAC GCCTGCTGCC CGTCCTGCTG
 301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
 351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
 401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
 451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCTa
 501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
 551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCGGCG
 601 GTGCCGTTCT TCAGCATTTT CCGTTCCGAT TTTGTGCGAA TGTTCTGTCGG
 651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
 701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
 751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
 801 ATTATTGGTT GAAATGGACG GTTTTGAAG CAATCAGACT GTAATTGTGA
 851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
 901 GGCCGTTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGAGCA TCCGGGGCGG
 951 CGAACAGatn ttGAACGTCC ATTCTaaAAA AGTGCcttTG gacgaATCTg
 1001 tggatTTTATT GTCCCTCGCG CGCGGCACGC ccggtttTTc cggcgcggat
 1051 tTggcgaac tggtaacga agccccctg tttgccggcc gccgcaacaa
 1101 agtgaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
 1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIEGSV VSGYLIKGER
 51 TDKSTFFTNA PLDDNLIQTL LKNVVRVKVT PEEKPSALTA LFYSLLPVLL
 101 LIGAWFYFMR MQAGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVVP LPDIRGREQX LNVHSHKVP L DESVDLLSLA RGTPTGFSAD
 351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51 CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
 151 ACCGACAAAA GCACTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
 201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
 251 AACCGAGCGC GCTGGCTGCC CTGTTTACAC GCCTGCTGCC CGTCCTGCTG
 301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
 351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
 401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
 451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
 501 TCAAAGCCTG GCGGGCGCGG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
 551 CGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
 601 GTGCCGTTCT TCAGCATTTT AGGTTCGAC TTTGTGCGAA TGTTCTGTCGG
 651 TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
 701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
 751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
 801 ATTGTTGGTT GAAATGGACG GTTTTGAAG CAATCAGACT GTAATTGTGA
 851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
 901 GGCCGTTTCG ACCGCCAAGT GGTGTGCCCC CTGCCGAGCA TCCGAGGCGG
 951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
 1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGTTTTTTC GGGCGCGGAT
 1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGAATAA
 1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
 1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

m614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
 51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
 101 LIGAWFYFMR MQTGGGKGG AFSFGKSRRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIIAGEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTPGFGSAD
 351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
	: : : : : :					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
	: : : : : :					
g614	PLDDNLIQTLLNKNVRVKVT PEEKPSALTALFYSLLPVLL LIGAWFYFMR MQAGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSFGKSRRAR LLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	: : : : : :					
g614	AFSFGKSRRAR LLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	: : : : : :					
g614	AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	: : : : : :					
g614	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGTPGFGSADLANLVNEAAL					
	: : : : : :					
g614	GRFDRQVVVPLPDIRGREQLNVHSHKKVPLDESVDLLSLARGTPGFGSADLAKLVNEAPL					
	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	: : : : :					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

a614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51 CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
 201 TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
 251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCTGCTG

984

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301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTAAGTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GGCGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTCGAAA TGTTTCGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATGTTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTGTCCT CTGCCGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
  1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
  51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLPVLL
 101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIEGAG
 201 VPFFSISGSD FVEMFVGUGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD
 351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

      10      20      30      40      50      60
m614.pep MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA
      10      20      30      40      50      60

      70      80      90     100     110     120
m614.pep PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLPVLL LIGAWFYFMRMQTGGGGKGG
a614      PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLPVLL LIGAWFYFMRMQTGGGGKGG
      70      80      90     100     110     120

      130     140     150     160     170     180
m614.pep AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
a614      AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
      130     140     150     160     170     180

      190     200     210     220     230     240
m614.pep AGSPGTGKTL LAKAIEGAGVPFFSISGSD FVEMFVGUGASRVDRMFQAKKNAPCIIFI
a614      AGSPGTGKTL LAKAIEGAGVPFFSISGSD FVEMFVGUGASRVDRMFQAKKNAPCIIFI
      190     200     210     220     230     240

      250     260     270     280     290     300
m614.pep DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
a614      DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
      250     260     270     280     290     300

      310     320     330     340     350     360
m614.pep GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL
a614      GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDKSVDLLSLARGTPGFSGADLANLVNEAAL

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985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGCGCGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACAC  AATGCCGAAa  gcaggCtgaa  gcGGTTgcgC
101 GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151 aggcgcAGga  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201 cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251 aatcaggggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301 ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351 gAaagggctt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401 cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451 gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501 agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGGtgggc  GATGCCGAGG
551 CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601 GCCGTTGTGT  CgcgcGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651 AAGGGATGTC  GAGTTCGTCG  TGGACACGA  GGATTCTTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801 CAACTTCGCC  GAAGAATTT  TTTTCTTCTT  TAAACGAAGC  CTTCCATTTC
851 CACGCCAGTT  CGTCGAGGAA  CCAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901 GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951 acatgataTT  TtccgtgTTT  CTgTCGaatg  cggTctgaAG  GCTTCAGacg
1001 gcatggTtaT  TCTTCTTgaT  TttgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051 GGTGCATCAA  CAGCGGGCGG  TACACTTCGA  TGCGGTGCGC  GTCGCGCAGC
1101 GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101 LSSFMTVRIR  KSGKCRKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151 ATASSICRRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201 AVVSAVAAAE  FEFDPSARDV  EFVVDDEDF  GFDFVELCKR  GNRLSGTVHE
251 RGRFEQPNIA  VGQGGAGNFA  EEEFFFKRS  LPFPRQFVEE  PKARIAGLF
301 VFFARVAQAD  NHFDCVRHDI  FRVSVCEGLK  ASDGMVILLD  FERVCALLW
351 GRSTAGGTLR  CGRRRAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAA  GCGGTGGCG  CGGTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101 GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGGAT
151 AGGCGCAGGA  ATTTCCGCC  GCGTGGCGCC  AGCATATCGC  GCCAAACGGC
201 AATTTCTTCG  GCGGAGGGG  CATCGTCTAT  GCTGCATTTC  TAGAGCAGGA
251 AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCGGTTTG  GATAAGCTGC
301 TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351 GAAAGGGCTT  CAGACGGCAT  CGGGTCAATT  GCTGTGCAGG  AAGCGGGTTG
401 CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTC
451 GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTACTG  GGTTTGTTCA
501 GGACATAGCC  GACGACGAGG  TTGCGTTCGC  CCGGTTGGCC  GATGCCGAGG
551 CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601 GCCGTTGTGT  CCGCCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651 AGGGAATGTC  GAGTTCGTCG  TGGACACGA  GGATTCTTTC  GGGTTTGATT
701 TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751 CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

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986

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801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTCGA TCGGGTCGCC GTCGCGCAGC
1101 GCGTGTCTG CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
  1 MRKRRWRGFG SFEKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
 51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAAAAAE FEFDPAGNV EFVDDDEFF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDFE EEEEEFFKXS LPFPQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECCCK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

```

              10      20      30      40      50      60
m615.pep      MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS LDRRRNFPPRAA
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g615           MWKRRRRGVGSFEEQRIDAAGKPCGKQAEAVARQLHAASSSSHVWQILDRRRNLPPRAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m615.pep      SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
              | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g615           SMSRHCA TSSADGASSMLHSYSRKS RVSSMTGMDSVWISCLSSFM TVRIRKSGKCR LKGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m615.pep      QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA
              | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g615           QTALDYLLCRKRVASSHLPEMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA
              130     140     150     160     170     180

              190     200     210     220     230     240
m615.pep      DAEAQAVIVCRAEFCLNVFQAVVSAAAAAEFEFDPAGNV EFVDDDEFFGFDFVELCKR
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g615           DAEAQAVIVCRAEFCLNVFQAVVSAAAAAEFEFDPAGNV EFVDDDEFFGFDFVELCKR
              190     200     210     220     230     240

              250     260     270     280     290     300
m615.pep      GNCLSGTVHERGRFEQPNVAVGQGGTGDFAE EEEEEFFKXSLPFPQFVEEPKTRIVACLF
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g615           GNRLSGTVHERGRFEQPNVAVGQGGAGNFA EEEEEFFKXSLPFPQFVEEPKTRIVAGLF
              250     260     270     280     290     300

              310     320     330     340     350     360
m615.pep      VFFARVAQADNHDFCVXHDI FRVSVECCCKASDGMVILLDFERVCGALLWGRSTAGGTLR
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g615           VFFARVAQADNHDFCVRHDI FRVSVECCCKASDGMVILLDFERVCGALLWGRSTAGGTLR
              310     320     330     340     350     360

              370
m615.pep      CGRRRAAACRLX
              | | | | | | | | | |
g615           CGRRRAAACRLX
              370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GGC GCGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGCGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTCTG TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTTCG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CCGGTGATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCTG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCCTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TCGGTTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPSAGNV EFVVDDEDFG GFDPIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VQGSGTGDFE EEEEEFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECLRK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSSHVWHS	SLDRRRNFPPRAA				
a615	MRKRRRRGVGSFEEQRIDAA	GKPQCGKQAEAVARQLHAAS	SSSHVWQILD	RRRNLP	PPRAA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIW	KSGTCRLKGL				
a615	SMSRHCATSSADGASSMLHSY	SRKSRVSSMTGMDSVWISCLSSVMTVRIW	KSGTCRLKGL			
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRX	FRTGFVQDIADDEVAVARVA				
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRX	FRTGFVQDIADDEVAVARVA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPSAGNVEFVVDDEDFG	FDFVELCKR				
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPSAGNVEFVVDDEDFG	FDFIKLRKG				
	190	200	210	220	230	240
	250	260	270	280	290	300

988

```

m615.pep      GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFKXSLPFPQFVEEPKTRIVACLF
                |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615           GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFKXSLPFPQFVEEPKTRIVACLF
                250      260      270      280      290      300

                310      320      330      340      350      360
m615.pep      VFFARVAQADNHFDVCVXHDI FRVSVECKLKASDGMVILLDFERVCGALLWGRSTAGGTLR
                |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615           VFFARVAQADNHFDVCVXHDI FRVSAECLRLKASDGMVILLDFERVCGALLWGRSTAGGTLR
                310      320      330      340      350      360

                370
m615.pep      CGRRRAAACRLX
                |||||
a615           CGRRRAAACRLX
                370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

g616.seq

```

1  atgtcgaaCA CAATCAAAAT GGTGTGTCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGC GGATCAAATT CAAACTCGGC GcgggcaaCG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGC GCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGaagcaccg CcgggcaaTC gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTTCGGg caaatgggaa
551 gaggcaacgc gcTTCCTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg catTTtcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaacctc
701 gatttctgc tGTACGAATG cagcAtcgac gaagCAccgt ccgccgaaga
751 agtggcacaT TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGCtGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgcaA CgcttcaGc ctgctTTCCG CATTTGTGGT TGCCGGCGGc
901 atctATtCgc tgctcttcaa AGCTGccgaC ACCGCGCCG CGCCGTTTCC
951 ACATTTcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAA AC CGGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

g616.pep

```

1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSAEAP PANRRCRROI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PNSHRTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFP PHFD KAHLALFFA QILFLAKAFK TGKLPIPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGSLGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

m616.seq

```

1  ATGTCAAACA CAATCAAAAT GGTGTGTCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAATGGGAA

```

989

```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGGCCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATGTGGTGT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTCAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCCCT TCCAGCGAAT GCGCGCAGGC
1101 ATGTTTACG GCAACGAGAA CCGCAGTTT GGCAGATGC CTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTACC GCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
  1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
 51 VARAALPDGD VWLLKPATFM NRSGQAVAAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRRI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHDRTQAA YPNRIHPRHR RNPFRPALRM QHRRCLRRR
251 NCRLARYAGR TRRKIPAPIQ TMPDAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGSGLDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQAVAAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHHNGLK					
g616	VWLLKPATFMNRSGQAVAAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRRCRRI PASHTRHPCR					
g616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSAEAPPANRRRCRRI PAGRTRHHFR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRNPRFPALRM					
g616	QMGRGNALPAQIIQCRLKPFQTAFSRFPYPNSHRTQAAYPNGIHPRHRNPRFPAVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCLRRRNCRLARYAGRTRRKIPAPIQTMPDAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRSTVRRRSGTMRHTCRTRRQIPAPVQNLPNVAGRGGGMKLPNRNRFSLLSALWFAGG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAAETAPPPFPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAADTAPPPFPHFDKAAHLALFFAQILFLAKAFKGLPIPYRSLIAFAFCFAV					
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFTATRTGSGLGDLADLTGAALALFTARAACRPDX					
g616	GSECAQAWFTATRTGSGLGDLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1   ATGTCAAACA CAATCAAAAT GGTGTGTCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCTG CTACCCTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCGG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCTCGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGCGGCG AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTTCG CATTGTGGTT TGCCGGCGGC
901 ATCTATTCGC TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCGCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTTCGCA CTCTTTGCCG CCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1   MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARATLPDGD VWLLKPTTFM NRSGQVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GGNGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QOMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPVRM QHRRRTIRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPRNRF LLSALWFAG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLLTKAFK TGKLPYPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSGQVAALAQAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNLK					
a616	VWLLKPTTFMNRSGQVAALAQAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRRNPRFPALRM					
a616	QMXRGNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRRNPRFPVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

991

```

m616.pep    QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPD MAXRGTS MNLPNRNFILLSALWFAGS
              ||||  :|||:  :|||:  ||||:||||:|:|:|:|  ||  :|||:||||  |||||:|:|:|
a616        QHRRRTIRRRSGT MARHTCRTRRQIPAPVQNL PNVAGRGGGMKLPNRNFSLLSALWFAGG
              250      260      270      280      290      300

              310      320      330      340      350      360
m616.pep    IYSLLEKAAETAPPPFP HFDKVAHLALFFAQIWLLTKAFRTDNRP IPIYRSLMVFALCFAL
              |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a616        IYSLLEKAAETAPPPFP HFDKAAHLALFFAQIWLLTKAFKTGKLP IPIYRSLMVFALCFAL
              310      320      330      340      350      360

              370      380      390      400
m616.pep    FSECAQAWFTATRTGSLG DVLADLTGAALALFTARAACRPDX
              |||||  |||||  |||||  |||||  :|:|:|:|:|:|:|:|  ||||  ||||
a616        FSECAQAXFTATRTGSLG DVLADMAGTVLALFAARAADRPDX
              370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

g619.seq

```

1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTGCGCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTCCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtcgGC
301 GCGGTGGGCT ATAcatccct gccgttgacg gCAAATTCG GCTTTGAACT
351 GGTGTGTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTTGCCG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTC GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGATTTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TCGTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGGT TGTGCGCCCG
751 GTGAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
801 gtCCGTGCGC CATTCCGTCC GCCTGCgat gacggttGC gtcgGcggCA
851 TCCTCTTggt cggCggacaA ACCGTATTCC AACACTTCTT GGGCATGAag
901 gCggTATTAA GCGTGGTGGt cgAATTGCG ggcggactcG TTTTCTCTA
951 TCTCGTTTAA AAACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

g619.pep

```

1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTLVFTFG
101 GVGYTSPLPT GKFGFELVVM MGGSLLL FYT LIRQGGRLP HMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

m619.seq

```

1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCGTT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTCCGT GTATGTGTTT TTGCAGACCT TGCTGGTGT TACGTTGCGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
351 GGTGCTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTTGTCT CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGATTTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCGGT GGTGCGCCCC
751 GTAAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAA CATTCCGTCC GCCTGCCGAT GACGGTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTCC AACACCTGCT CGGTATGCAG

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992

901 GCAGTGTGA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTTCCTCTA
 951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
 101 GVGYSASPLT GKFGFELVVM MGSLLLFYT LIKQGGRLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMO
 301 AVLSVVVEFA GGLVFLYLVL KHKK*

m619/g619 95.1% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGSLLLFYTLIRQGGRLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMO					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTCG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
 151 CTTGCGCGCG TGCTGATGGT CGCCTATGCG GTCGCGGTTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
 251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGGC
 301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
 351 GGTCTGTATG ATGGGCGGCT CGCTGCTGCT GTTTACACG CTCATCAAAC
 401 AGGGCGGGCG CGATTGCGCG CGTATGATTT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTG AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTTT TGGGGCGCGA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG

993

```

751  GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801  GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851  TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901  GCGGTATTAA GCGTGGTGGT CGAATTTGCG GCGGACTCG TTTTCCTCTA
951  TCTCGTTTAA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
  1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
 51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTL LVFTFG
101  GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGG RDLP RMILIGVIFG
151  ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201  VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG P
251  VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301  AVLSVVVEFA GGLVFLYLV L RHKK*

```

m619/a619 97.2% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA					
a619	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSL YVF LQTL LVFTFGGVGYASLPLTGKFGFELVVM					
a619	VGVSTQLFQTLTNNPILTPSILGFDSL YVF LQTL LVFTFGGVGYASLPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGSLLLFYT LIKQGG RDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
a619	MGSLLLFYT LIKQGG RDLP RMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVG PVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVG PVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLRHKKX					
a619	AVLSVVVEFAGGLVFLYLVLRHKKX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
  1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
 51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101  gttecggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151  aaagcccaga ttttttgaa cGGCAAACCC GATCAGCCCG TTTGTTCTC
201  CACCGTcaaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251  GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301  AATCCTAATG CCCACACGGA GTGGATAGAT GCGAAAAAG CCTTTTACGT
351  CATCGACAGC GCGTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401  TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGCGGCAAG
451  GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
  1 MKKTLLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	: : : : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTDNPNADTEWMDAKKAFYVIDS					
g620	: : : : : : : : :					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	: : : : : : : :					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a620						
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFYTKLPPEEPKIRVIYVTDMGNVTDWTPNPADTEWMDAKKAFYVIDS					
a620						
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a620						
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  ccgctgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCCG  CGTTGCCTGC
301 GGCTTGGATT  CGATGGTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTTG  CTAAAGAGT  CCGTACCGAT
451 ACCGCTGTGC  GCGAAAATTC  GGTTCGATG  GCTTCCGCGT  CCGTCAAGTT
501 GCGGGAACAG  ATTTTCCCG  ACATCGGCGA  TTTGAACGTA  TTGTTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCC GGCTGA  TGACGGTTGC  CAACCGGACG  CTGGCGCGTG  CACAGGAGTT
651 GTGCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTAAC  GGCAGGCCAG
751 CTTCCGATAG  TCGGCAAAGG  CATGGTCGAA  CGCGCATTGA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTATGC  TTGACTTGGC  CGTGCCGCGC  GATATTGAAG
851 CGGAAGTCGG  CGATTGTAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCAACATCG  TCCAAAGCGg  caaggaggca  aggcagaaaag  ccgccgcCgc
951 cgccgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTTTGC  AGGCAGCAGC
1001 AGGGCAGGCA  GagcgttcCG  CTGATTAAGG  CCTTGCGGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAATATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaaCGGCG  GAAGaggttt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGGCGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGATt  tatcatttGG  ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH  QTAPLSIREK  LAFAAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGQIKDAV  RAAQEQESMG  AKLNALFQKT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEQ  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLPAILHDY  DVVVSSTASQ
251 LPIVGKGMVE  RALKQRQSMP  LFMLDLAVPR  DIEAEVGDNL  DAYLYTVDDM
301 VNIVQSGKEA  RQKAAAAAET  LVSEKVAEFV  RQQQGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLRLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHAVAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTCCG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAAG  CTGGCGTTTG  CCGCCGCCGC  CCTGCCATAA  GCCGTCGCGA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCCG  CGTCGCTGC

```

```

301 GGGCTGGATT CGATGGTGTG GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTG GCGAAAACTC GGTTCATG GCTCCGCTT CCGTCAAATT
501 GGGCGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCATTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTGGC AGTGCCCGT GACATTGAAG
851 CGGAAGTCG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGCGGAG
1051 AAAGCGCGCA AACAGGTGTT GGAATGTC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDNL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPLI KALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEESMGKKLNALFQKTF SVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEESMGAKLNALFQKTF SVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMP LFMLDLAVPRDIEAEVGDNLDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMP LFMLDLAVPRDIEAEVGDNLDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAAC TC GTTTCCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCGCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTG TG TTCACGCCGT CGGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLA EQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDIN DAYLYTVDDM
301 VNIVQSKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

m622/a622 98.1% identity in 415 aa overlap

10 20 30 40 50 60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
|||||
a622 MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
10 20 30 40 50 60

70 80 90 100 110 120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
|||||
a622 SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
70 80 90 100 110 120

130 140 150 160 170 180
m622.pep RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
|||||
a622 RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
130 140 150 160 170 180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTA CTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCAtccc cgcgcTTTcA ccgCTGGCTG
151 CACcgGCacc gCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatcctTTtg CattTTCCCC aacnctggtg ggtcGGGGCG
301 GTTTCATCGG TTTTTGTTC CTTGTcacc ATacggatgt gGcacAGacC
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep

```

1  MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWRHPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TACTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTA CTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CTTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
301 GTTTCATCGG TTTTTGTTC CTTGTGCGC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep

```

1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRHPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGGISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	10	20	30	40	50	60

```

301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTTCCGCTT CCGTCAAATT
501 GGGCGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCAGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG CATGGTGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTGGC AGTGCCGCGT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 TCAATATCTT TCCAAAGCGG CAAGGAGGCA AGGCAGAAG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCTT TTGATTAAG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAATATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA AAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTGA ATAAGGCGG GGAAGAAGAT
1201 AAAGATTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILDY DUVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILDY					
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DUVVSSTASQLPIVGKGMVERALKQRQSMP LFMLDLAVPRDIEAEVGD LN DAYLYTVDDM					
g622	DUVVSSTASQLPIVGKGMVERALKQRQSMP LFMLDLAVPRDIEAEVGD LN DAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLRLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLRLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCCTG CCTGCCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 AGTGCCGTCG GCGAAAATC GGTTCCTATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCCA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGCG CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDIN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

m622/a622 98.1% identity in 415 aa overlap

10 20 30 40 50 60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
|||||
a622 MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
10 20 30 40 50 60

70 80 90 100 110 120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
|||||
a622 SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
70 80 90 100 110 120

130 140 150 160 170 180
m622.pep RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
|||||
a622 RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
130 140 150 160 170 180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSSTASQLPIVGKGMVERALKQRQSMPLFMDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSSTASQLPIVGKGMVERALKQRQSMPLFMDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatctTTtgg CattTTCccc aacnctggtg ggtcGGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTCacC ATacggatgt gGcacAGacC
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep

```

1  MIRYLLIACG GISLLGLIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWHRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GTCGGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTCGCC ATATGGATGT GGCAGAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep

```

1  MIRYLLIACG CISLLGLIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACCGISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	: : : : :					
g624	MIRYLLIACCGISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISM	TASCLIMFWQFPQRWWVG	AVSSVFCSLVAIWMWRRPESX			
g624	HNWEQNGAVPRKAKIFAISM	TASCLIMFWQFPQRWWVG	AVSSVFCSLVTIRMWHRPESX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1   ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TGCTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTAAGTC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCCG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
301 GTTTCATCGG TTTTTGTTC CCTTGTGCC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1   MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
a624	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISM	TASCLIMFWQFPQRWWVG	AVSSVFCSLVAIWMWRRPESX			
a624	HNWEQNGAVPRKAKIFAISM	TASCLIMFWQFPQRWWVG	AVSSVFCSLVAIWMWRRPESX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1   ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1   atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtctTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1   MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRSWLAFFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGGCC TTTGGAACCC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCTG TTTCAATcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

```

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CATcgTACAT
601 ACCCTcgTCT TTTTcgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
  51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
  51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCACATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
 201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
 401 CTTGATGAC GGTACCCTG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
  51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

          10      20      30      40      50      60
m627.pep  MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
          |||||:|||||
g627      MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG
          10      20      30      40      50      60

```


1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTCAATAT GCGGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTTG TTTCAATCGC TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGGGCGGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLSILKAG EAGALGGVVS LVHDTAGHP
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFVFKLL *
  
```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
190 200 210

g628.seq

1	ATGTGCGTGC	CACTCAAGCC	GGCAGGATGC	GGGCCGCCAA	ATTCATGTGT
51	TTCGATATTG	GCAGCATTTT	CAGACGGCAC	GTCTGCGCCT	GCTGCTTTAC
101	ACACATGGAT	TTTACGTTTC	GTCAGGCGGC	TCAATACCAA	CAGGCCGCGT
151	TTGAAGTCTT	CGGCGGCTTC	TTTGATGATG	ACCGTAGGGT	CGGCAGCCAG
201	CGGATTGGTG	TCCATCGCAT	TGACGAAGAT	GGCGAACGGC	TCGGCATCTA
251	CGGCAAGGAT	TTTGCTGAAC	GGACGGGTGC	GAAGCGCAGT	CCATAAGCCT
301	GATTGAATCA	GGTTGCGGCG	CACTTTTTCG	CTGCTCAATT	TTGCCAGCGC
351	TTCAGGTacg	TAG			

g628.pep

1	MCVPLKPAGC	GPPNSCVSIL	AAFSDGTSAP	AALHTWILRS	VRLNTNRPR
51	LKSSAASLMM	TVGSAASGLV	SIALTKMANG	SASTAGILLN	GRVRSVHKP
101	D*IRLRRTFS	LLNFASASGT	*		

```
m628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCAGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 AAACATGGAT  TTTGCGTTCG  GTCAAACGGC  TCAATACCAA  CAGGCCGCGT
151 TTGAAATCCT  CGGCGGCTTC  TTTGATAATG  ACCGTAGGGT  CGGCAGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGAAT  TTTGCTGAAC  GGACGGGTGC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GGTTCGGCGC  CACTTCTTCG  CCGCTTAAGT  TTGCCAGCGC
351 TTCAGTGCGC  TAG
```

```
m628.pep
  1  MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRPR
 51  LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101  DWIRLRRTSS PLKFASASGA *
```

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m628.pep		MCVPLKPAGCGPPNSCVSMLA	AFSDGTSAPAA	LQTWILRSVKRLNTNR	PRLKSSAAS	LIM	
g628		MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAA	LHTWILRSVRRLNTNR	PRLKSSAAS	LMM	
		10	20	30	40	50	60
		70	80	90	100	110	120
m628.pep		TVGSAASGLVSI	ALTKMANGS	ASTAGILLNGR	VRSAVHKPDWIR	LRTSSPLKFAS	ASGA
g628		TVGSAASGLVSI	ALTKMANGS	ASTAGILLNGR	VRSAVHKPDXIR	LRTFSLNLFAS	ASGT
		70	80	90	100	110	120
m628.pep	X						
g628	X						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
  1 ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
351 TTCGGGCGCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
  1 MCVPLKPAGC GFPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
 51 LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 DWIRLRRTSS PLKFANASGA *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLN	TNRPR	LKSSAASLIM	
a628	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALHTWILRSVKRLN	TNRPR	LKSSAASLIT		
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
a628	TTGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFANASGA				
	70	80	90	100	110	120

```

m628.pep    X
             |
a628         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
  1 ATGACTGCca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
 51 ggtatTGTTT GCCGTGAGcc tGtcggTCGG cattgccgaT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc
201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta
251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
301 ctgctgcctg CcgcGccgct gccggtcaAA ATGTCGGtag Cgcgccgttgc
351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac
401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
451 GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAT
501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CGGTGTTGC CTACCTGATT
601 CCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
651 GGGTTTGAAC CGGACGGCGG TGTGTGGTGC GGGTTTGATT ATTGTGGCAC
701 TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATCC GTTTATCGGG
751 CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTCGCCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATCC GGTCTCCACG
901 GTTTTTGGTG TGTGGGTAC GCCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCGCGCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
  1 MTAKPFSLNL ANLLLPVLF AVSLSVGIAD FRWSDVFSLS DSQQVMFISR
 51 LPRTFaIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

```

151 VEAVATFVAY EFEMQLMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVPNVIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

```
m629.seq
1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51 GGTGTTGTTT GCCGTGAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CTGATGTGTT TTTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
151 CTGCCCGCGA CGTTTGCATG TGTGCTGACG GGC CGCTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATT TGTATCGCAA CCGTTTGTGC GAACCTCGA
251 TGGTGGGCGC AAGCCAAAGC GCGGCTTAG GTTTGCTGCT GATGACCTG
301 CTGCTGCCGG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCGGTTGC
351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTTT CGGCGGTGTG
451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAA
501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGTG CTGGGCGGCT
551 ACGAGCTGCT TTGGATTACG GCGGCTTGG CCGGTTTTCG CTATCTGATT
601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
651 GGGTTTGAAC CGGACGGCGG GTTGTGGTTC GGGTTTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTTGCGCCA
801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
851 ACATTATCGG ACGCGTGATT GTGTTTCCGT TTGAAATTCC GGTCTCTACG
901 GTTTTGTGGT TATTGGGATC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ATCCCGCTAT GCCGTCTGA
```

m629.pep

1	<u>MTAKPFSLNL</u>	<u>TNLLLLAVLF</u>	<u>AVSLSVGAD</u>	<u>FRWSDVFSLS</u>	<u>DSQQVMFISR</u>
51	<u>LPRTFAIVLT</u>	<u>GASMAVAGMI</u>	<u>MQILMRNRFV</u>	<u>EPSMVGASQS</u>	<u>AALGLLMTL</u>
101	<u>LLPAAPLPAK</u>	<u>MSVAAVAALI</u>	<u>GMLVFMLLIR</u>	<u>RLPPTAQLMV</u>	<u>PLVGII FGGV</u>
151	<u>IEAVATFIAY</u>	<u>ENEMLQMLGV</u>	<u>WQQGFSSVL</u>	<u>LGRYELLWIT</u>	<u>GGLAVFAYLI</u>
201	<u>ADRLTILGLG</u>	<u>ETVSVNLQSL</u>	<u>RTAVLWSGLI</u>	<u>IVALITSLVI</u>	<u>VTVGNI PFIG</u>
251	<u>LVPNIISRL</u>	<u>MGDRLRQSLP</u>	<u>AVALLGASLV</u>	<u>LLCDIIGRVI</u>	<u>VFPFEIPVST</u>
301	<u>VFGVLGTALF</u>	<u>LWLLLRKPAY</u>	<u>AV*</u>		

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	: : : : : : : : : :					
g629	MTAKPFSLNLANLLLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPKMSVAAVAALI					
	: : : : : : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFFGGVIEAVATFIAYENEMLQMLGVWQQGDFSSVL					
	: : : : : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLQMLGVWQQGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					

1006

```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GCGCGCTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTGTGC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCTTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAACGAAA TGCTGCAAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTTG CTCGGACGGT
551 ATGAACGTGT GTGGGCAACG GGGATTTTGG CTTTGTGTGC CTATTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSNLN TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAGMI MQILMRNRFV EPSMAGAGQS AALGLLMLSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMMLIR RLPPTAQLMV PLVGIIFFGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

           10      20      30      40      50      60
m629.pep  MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAGMIMQILMRNRFVEPSMVGASQAALGLLMLTLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAGMIMQILMRNRFVEPSMAGAGQAALGLLMLSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMMLIRRLPPTAQLMVPLVGIIFFGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1007

```

a629      GMLVFMMILIRRLPPTAQLMVLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  gtacaacgtc GGCGCACAGG CATTTCGGTGC CTTAACGCCC GAtttgctgc
101 aacaaagcat cgccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt ccccgaaGc gggcgtgtTg ggcaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCGC
451 GCCTTCCTGT TCTTCGCCTa CCCCGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAGCCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttggtacat ggcacttggT GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQQSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAV VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTCK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVE ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAAAGTC GGCGCGCAGG CATTTCGGTGC GTTAACGCCT GATTGCTGTC
101 AACAAACAT CGCCAACGAC TGGCATTACG CCTTGGCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTCT GACAAAATGC TGTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTTGTG GCGGTTTCT
251 GGGAAGTTTT GTTCGCCACC GTGCGCAAAC ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCTTTCCTGT TCTTCGCCTa CCCTGCCAAc TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAGCCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTtcttgGCG CATTATTGCC GCGTGATGA TCGGTATGAT TGCGATGTCT
751 TCGCTGTTCa ACTTCATCGG TTCGACACC AACGCTATGT TTGCTATGCC

```

1008

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801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTCG CACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

```

m630.pep
  1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLEMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALF	PAMFYGMYNV	GAQAFGALTP	DDLQONIAND	WHYAFANALG	INMSSEAGVS
g630	MMILVWLALF	PPMFYGMYNV	GAQAFGALTP	DDLQOSIAHD	GNALANALG	INMSPEAGVL
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYF	LPIYATVFVV	GGFWEVLFAT	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
g630	GKMLFGAIYF	LPIYATVFIV	GGFWEVLFA	SVRKHEINEG	FFVTSILFAL	IVPPTLPLWQA
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVV	AKEVFGGTG	KNFMNPALAG	RAFLFFAYPA	NLSGDAVWT	AVDGYSGATALA
g630	ALGISFGVVV	AKEVFGGTG	KNFMNPALAG	RAFLFFAYPA	NLSGDAVWT	AVDGYSGATALA
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
g630	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSS	LFNFIGSDTN	NAMFAMPWYW	HLVVGGFAIG	MLEMATDPVS	ASFTNVGKWW
g630	GVMIGMIAMSS	LINFIGSDTK	AMFAM----	HLVHGTWWK	DDYHSLYIK.	
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCV	LIRVVNPAYP	EGMMLAILFA	NLFAPIFDYF	VAQANIKRRK	ARSNGX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

```

a630.seq
  1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GGCACACAGG CATTCGGTGC GTTAACGCCC GATTGCTGTC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTTC GGCAAAATGC TGTTCGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
251 GGGAAGTTTC GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCCA TAACCGGTCA AACCATCACT
601 TGGATGGATG CGTTTATCGG CAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

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1009

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCa ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTTGGCGAT TCTGTTTGCC AACCTGTTG
1001 CCCCATTTCG CACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

a630.pep

```

1  MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQNIANDWHYAFANALGINMSSEAGVS				
a630	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQSIANDWHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
a630	GKMLFGAIYFLPIYATVFIVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMN	PALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA			
a630	ALGISFGVVVAKEVFGGTGKNFMN	PALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWY	WHLVVGGFAIGMLFMATDPVSASFTNVGKWW				
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWY	WHLVVGGFAIGMLFMATDPVSASFTNVGKWW				
	250	260	270	280	290	300
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGGAAG GACAGGGCAT AGCCTTTCGC
151 CTCAAACCCC AATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAG AAGCGTCGCC ACCGAAGCCG CCCCAGAGGA

```


301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
351 TCTGCAATTT GATTTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

1 MTRRRVGKQN RIAIHSQYR KMVVFAVFQI HDDGDFQLRE LFERQGIAGR
51 LKTQIGHNAP HILKRRRAHLF LTQFFQHQFF RQLLPVKIVQ KRRHRSRPAG
101 KIQILLYNIE IPPREFTLQF DFSVNNRRII KHRCSIQTIR QGSVPD*

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATACCGA	GAAATGATCA	TCCTTGCGGT	ATTTCAGATA	CACGATAGCG
101	GGGATTTTGCA	ACTGTGCAAG	CTGCTCGAA	GACAGGGCAT	AGCCTTTTCG
151	TCAAAAACAA	AAATCAGGCA	TAAATGCGCG	CATATCCTCA	AACGACGCGG
201	GCATCTGCTC	CTTATCCAGT	TTTTTTAACA	CGTCCTCTTC	CGTCAGCTTT
251	TGCCCGTAAA	AATTGTTCAA	AAGCGTCAcC	ACCGAAGCGG	CCCCGACAGGA
301	AAAATCCAAA	TCTCTGCTTT	CAATATTGAA	ATCGCGCCTT	TCTTTCCAAc
351	TCTGCACTTT	GATTTTTCcA	TAAGCAACAG	GATTATAGTG	GATTAA

```

1  MTQRRVGKQN RIAVYTAQYR EMIILAVFQI HDDGDLQLCK LLERQGIAPR
51  FKTQIRHNP  HILKRRGHLL LIQFF*HVL  RQLLPVKIVQ KRHHRSRPAG
101 KIOILLYNIE IAPFFPTLHF DFSISNRIIV D*

```

		10	20	30	40	50	60
m635.pep		MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI	AFRFTQIRHNAP				
		::	::				
g635		MTRRRVGKQNRIAIHSAQYRKMMVFAVFQIHDDGDFQLREL	FERQGI	AFRLKTQIGHNAP			
		10	20	30	40	50	60
		70	80	90	100	110	120
m635.pep		HILKRRGHLILLIQFFXHVLF	RQLLPVKIVQKR	HRHRSR	PAGKIQ	ILLYNIEI	APFFPTLHF
g635		HILKRR	AHLFLTQFFQHFF	RQLLPVKIVQKR	HRHRSR	PAGKIQ	ILLYNIEIPPRFPTLQF
		70	80	90	100	110	120
		130					
m635.pep		DFSISNRIIVDX					
		::					
g635		DFS	VNNRIIVK	HRC	SIQTIRQGS	VDPDX	
		130	140				

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATACCGA	GAAATGATCA	TCCTTGCGGT	ATTCAGATA	CACGATGACG
101	GGGATTTGCA	ACTGTGCAAG	CTGCTCGAAA	GACAGGGCAT	AGCCTTTCGC
151	CTCAAAACCC	AAATCAGGCA	TGATGCGCCG	CATATCCTCA	AACGACGCGC
201	GCATCTGCTC	CTTATCCAGC	TTTTTCAACA	CGTCCTCTTC	CGTCAGCTTT
251	TGCCCGTGAA	AATTGTTCAA	AAGCGTCGCC	ACCGACAGCC	CCCCGAGGAA
301	AAAATCCAAA	TCTCGCTTTA	CAATATTGAA	ATCGCGCCTT	TCPTTCCAAC
351	TCTGCACTTT	GATTTTTTCCA	TAAGCAACAG	GATTATAGTG	GATTAA

1 MTQRRVGKQN RIAVYTAQYR EMII LAVFQPI HDDGDLQLCK LLERQGI AFR
51 LKTQIRHDAP HILKRRRAHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
101 KIOILLYNIE IAPFPTLHF DESISNRIIV D*

10 20 30 40 50 60

1011

```

m635.pep      MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
                |||||||||||||||||||||||||||||||||||||||||||||:|||||:|
a635          MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDA
                10      20      30      40      50      60

                70      80      90      100     110     120
m635.pep      HILKRRGHLLLIQFFXHVLFRLQLPVKIVQKRHRSRPAGKI QILLYNIEIAPFFPTLHF
                |||||:|||||:| |||||||||||||||:|||||||||||||||||
a635          HILKRRHLLLIQLFQHVLFRLQLPVKIVQKRHRSRPAGKI QILLYNIEIAPFFPTLHF
                70      80      90      100     110     120

                130
m635.pep      DFSISNRIIVDX
                |||||||||
a635          DFSISNRIIVDX
                130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc attGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTAGCATGTA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcccACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg GcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTGTGTGT
501 CAACACAGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GCGCGGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAGC
851 GCCTTCAAGC ATATACGGAG CGCGGATGTG TGCATAGTGT CCTCTGTTT
901 CGTTCCGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDLI AAADGDIVEH
51  FEFPGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYIERI IKNIVFNQAG ARGGFIEINT GIHCWQAHTG TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGCATATA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTG TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCAGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAGGTcg CGTCGCGGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTGTGTGT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCTGTCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep

```

1  MIGEKFIIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVI VDGETQIAEA VVFGVVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVVFNQG ARGSFEEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVAFDGGCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

```

m638/g638 88.2% identity in 254 aa overlap

m638.pep	10	20	30	40	50	60
	MIGEKFIIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY FEPLGKHQHI					
g638	10	20	30	40	50	60
	MIGGQFIVVG IIVGNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH FEFPKGKHQHI					
m638.pep	70	80	90	100	110	120
	AHIVAHGNIA ADFAVVGVI VDGETQIAE AVVFGVVVRAG IGKNAVPPFG NVVADDLRTG					
g638	70	80	90	100	110	120
	AHIVAHGNIA ADFAVVGVI VDGETQVAE AVVFGVVVRAG IGKNAVPPFG NVVADDLRTG					
m638.pep	130	140	150	160	170	180
	CVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIVVFNQG ARGSFEEINT					
g638	130	140	150	160	170	180
	RVPNGNAIAA LIHAQGRIAD DFILAHHRIG RTMKVYAERI IKNIVVFNQG ARGSGFEINT					
m638.pep	190	200	210	220	230	240
	GIHCGQAHTG TGNGQVAERY VRRVYGYGTP APVAFDGGCT VGRPFNRNRF VNVKFGFIYA					
g638	190	200	210	220	230	240
	GIHCGQAHTG TGNGQVAERY VRRVYGYGTP ALVPFDGGCT VGRPFNRNRF VDIKFGLIYA					
m638.pep	250	260				
	GSQFERIARP GAGKCGIPISIIGSX					
g638	250	260	270	280	290	300
	GSQFDRIARP GAGKNGKVVLRG NVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSPVLPF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq

```

1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201 AAATATTGCC GCTGATTTTCG CTGTCGTTGG TGTACATATA GTGACGCGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCTA ACGGTAACGC CATTGCCGCG CTCGTTCACG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTCTCGA GATAAATACC GGCATCCATT
551 ACGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCC
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep

```

1  MIGGQFIVVG IIVGNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVI VDGETQIAEA VVFIGVVVRAG
101 IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIIVFNQG ARGSFEEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

```

1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLVNVDVNVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIIVGNALARFVDNVDVNVNIGIVDIVEHDAVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
m638.pep	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLDRAG					
	70	80	90	100	110	120
m638.pep	CVPNGNAVAALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQGARGSF FEINT					
a638	RVPNGNAIAALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQGARGSF FEINT					
	130	140	150	160	170	180
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNRNRFVDVKFGLIYA					
	190	200	210	220	230	240
m638.pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIIDSX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CACGCGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGCGGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATATGGG GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTGA
951 TCAGGCGGAT AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GGCGGAAAAC GGTCTTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDINS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFNTS THNTYKNNRF
101 SDLRFVHYHM YTNDSEVSGN ISVGNMGMV LMFSERLKVF DNIAGVSRD*
151 GIMLVYVNYN DIHNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQQA FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGCCTC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGA
201 CGCACCCTGG GCGCAGGTGC TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTACAAAAA CAACCGCTTC
301 AGCGATTGCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAATATTCCG GATATTACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTTGCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTAGCA CGCGCTTCTT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCCGCCG TCTGCGCTGG CGGCGTGGT
901 AEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGD
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAC GGTTCCTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDEISIGN ISVGNMNGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYVNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGD
251 FGDSAYRPNQ IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNISFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
g639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g639-1.pep	ISVGNMNGYVLMFSERLKVF DNIAGVSRDXGIMLNYVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVF DNIAGVSRDQGIMLNYVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTS LHDNSFINNGSQVKYVSTRFLDWS EGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTS LHDNSFINNESQVKYVSTRFLDWS EGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
g639-1.pep	NSPFDLNGDGFSGDSAYRDPGIIIDQIIWRAPVSRLLMNSPAISIVKWAQAF FPAVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAF FPAVLPGGVV					
	250	260	270	280	290	300
	310	320	330	340		
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEATRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```

1  ATGAGCCTGC  CCGCAATGGA  TGCCGGTATT  TATCTCGAAG  AAACTGCCCC
51  GCGCGCCCTG  ATTGAACACA  ATAATATTTT  GGATAATTCG  GTCGCGTCT
101 ATCTGCATGG  TTCTGCCGAT  GCGATGGTGC  GGGAGAATAA  AATCGTCGGC
151 GACGCGACTT  TGCGCGTGAA  CGAGCGCGGC  AATGGCGTTA  CCGTTTGAA
201 CGCGCCCGGC  GCGCAGGTGC  TCGGCAACGA  TATTTCCAAA  GGGCGGGACG
251 GCATTTTTTC  CAATACCAGC  ACGCACACA  CCTATAAAAA  CAACCGCTTC
301 AGCGATTTCG  GTTTCGCCGT  CCACTATATG  TACACCAACG  ACAGCGAAAT
351 CAGCGGCAAT  ATTCCGTGG  GCAACAATAT  GGGCTATGTG  CTGATGTTT
401 CCGAGCGGCT  CAAAGTGTTT  GACAATATCG  CCGTCGGCAG  CCGCGACCAA
451 GGCATCATGC  TCAACTATGT  CAACTATTC  GATATTCACG  ACAACATTAT
501 CAACAAAGCG  GGCAAGTGCG  TTTTTCCTA  CAATGCCAAC  TACGATAAAC
551 TGTCCGCCAA  TCATTTTGAA  AACTGCCAAA  TCGGCATACA  CTTTACCGCC
601 GCCATCGAAG  GCACGTCCTT  GCACGACAAT  TCCTTTATCA  ACAACGAAAG
651 CCAGGTCAAA  TACGTACGCA  CGCGCTTCT  CGACTGGAGC  GAGGGCGGAC
701 ACGGCAACTA  TTGGAGCGAC  AACAGCGCGT  TCGATTGAA  CGGCGACGGC
751 TTGCGAGCAA  GCGGTACCG  TCCCAACGGC  ATCATCGACC  AAATCATCTG
801 GCGCGACCCC  GTATCGCGCC  TCTTGATGAA  CAGTCCCGCA  ATCAGCATCG
851 TCAATGGGC  GCAGGCGCAA  TTCCCGCCG  TTTTCCTGG  CGGCGTGGTG
901 GACAGCAATC  CGCTGATGAA  GCCTTATGCC  CCCAAATTC  AAACCCGTTA
951 TCAGGCGATG  AAGGACGGGC  TGCTCAAAA  AGTCGAAACG  CGGCAGTTGG
1001 AATGGGGCAG  GCGGAAAAC  GGTTCCTTGA  ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI  YLEETAPRAL  IEHNNILDNS  VGVYLHGSAD  AMVRENKIVG
51  DATLRVNERG  NGVTVWNAPG  AQVVGNDISK  GRDGIFSNTS  THNTYKNNRF
101 SDLRFAVHYM  YTNDSEISGN  ISVGNMNGYV  LMFSERLKVF  DNIAVGSRDQ
151 GIMLNYVNYS  DIHDNIINKA  GKCVFAYNAN  YDKLSANHFE  NCQIGIHFTA
201 AIEGTSLDHN  SFINNESQVK  YVSTRFLDWS  EGGHGNYSW  NSAFDLNGDG
251 FGDSAYRPN  IIDQIIWRAP  VSRLLMNSPA  ISIVKWAQQA  FPAVLPGGVV
301 DSKPLMKPYA  PKIQTRYQAM  KDGLLKKVET  RQLEWGRAEN  GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	ISVGNMNGYVLMFSERLKVF DNI AVGSRDQ GIMLNYVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVF DNI AVGSRDQ GIMLNYVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	YDKLSANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKL FANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	NSAFDLNGDGF GDSAYRPNGI IIDQIIWRAPVSRLLMNSPAISIVKWAQQA FPAVLPGGVV					
m639-1	NSAFDLNGDGF GDSAYRPNGI IIDQIIWRAPVSRLLMNSPAISIVKWAQQA FPAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1   ATGATTGATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcgAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGTA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GGCGCCGGGC GACATCATCA GcggtGCGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTG GTCAGCCAGC CTTCCATCGG TAAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCTG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1   MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDISIQR YKVIANQYRL
201 GSDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGSYVRGGI FDRIEMIQGE
351 NSFRFTDAQH ERVVELSAAD APRFKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1   ATGATTGATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGCGCATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1   MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

```

m640.pep      10      20      30      40      50      60
MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
|||||:|||||:|||||:|||||:|||||:|||||:
g640          10      20      30      40      50      60
MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK
|||||:|||||:|||||:|||||:|||||:
m640.pep      70      80      90     100     110     120

```

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
               *
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||||||||||||||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFIFKNPPTPSVAPGDIISGATVTL
               130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq      (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep      (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

               10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
               10      20      30      40      50      60

               70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               ||||| |||||:|||||||||||||||||||||||||||||||||||||||:|:|
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               ||||||||||||| |||||
a640          DGTIAGAKLVDHHEPIMLIGIPH
               130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGCTGT
151 GGTGTCTTCG TGTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CCGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGGCGgc gTAAGTGAT
551 TCCGTGGCGa ggTTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTGCGGGC GTTCGTAATC GACGAATCTG

```


1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGAGCG GATGTATGTT TTGGGGACGA
951 CGAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCTGCCAGT ATTTGCGGGC
1051 GttgACGTAA ATGGTTtgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCgcgcgcg gaggtTtcgg gttcggtAc gcccaaacgg
1151 cggttttcgc ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTGCGcttc
1201 gccgcccgaac tCTTGACAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
  1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADV VQQEGC
 51 GV FVFLLYED KKS GDDFADE DFLQAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFVGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEF LQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 AAFGCEGF AA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGFGFGN AQTA AF AFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
  1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
 51 CTTTGCGGAT GTCGTT CAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTT CAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCA ACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAAT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGC GCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGGCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTGCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GCGGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGA CTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
  1 ACRRICPLPA ISAVQYIFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFVGIK HIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADV SFQI FKDV FHN AV R HADQLQAAAD KDV LERA Q T G
251 SVALGEFHHG GCRHFGIDAV DGVT DGAQAF GCEGFAADV C FGDEQQVDDF
301 GEFVAVFALFG GNEEEVALRV ALPVFRGV DV NGLSVDIFV GLHFACNRR A
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQH QRA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30
				ACRRICPLPAISAVQYIFADV	VQEGCGVFVFR	LYED
g642	MRYPFQSAVLQNAARCLLR	PKSACRRICPLSAISAVQYIFADV	VQEGCGVFVFL	LYED		
	10	20	30	40	50	60
m642.pep	40	50	60	70	80	90
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH				
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN				
	70	80	90	100	110	120
m642.pep	100	110	120	130	140	150
	ACFFFFGGGADKLVVNFGIKHIVRAFKNREGADVDS	DIAGGVSAFKTLRTQEF	LQHLRGG			
g642	ACFFFFGGGADELVVNFGIKHIVRAFKNREGADIDG	DIAGVWSAFKTLRAQEF	LQHLRGG			
	130	140	150	160	170	180
m642.pep	160	170	180	190	200	210
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVK	NLGNLMAAPDFAAFVIDE	FVDVADVS			
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVK	DGNLMAALDFAAFVIDES	DIVADIS			
	190	200	210	220	230	240
m642.pep	220	230	240	250	260	270
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVALGEFHHGGCRHFGIDAVD	GVTDGA			
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVAPGEFHHGGCRHFGIDAVD	GVTDGA			
	250	260	270	280	290	300
m642.pep	280	290	300	310	320	330
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRGVDV	NGLSVDI				
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDV	NGLFVGI				
	310	320	330	340	350	360
m642.pep	340	350	360	370	380	390
	FVVGLHFACNRRAGGFGFGNTQTAALAFENHLQ	TLRDLRFIAELLQWLQHQRAFDAGTQR				
g642	FVAGLHFACNRRAGGFGGNAQTAAAFENHVQ	TLCDLRFAAELLQRLQHQRAFDAGTQR				
	370	380	390	400	410	420
m642.pep	400					
	NGHAVMPRNP					
g642	NGHAVMPRNPX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1   GCCTGCCGCC GTATTTGCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCGGAT GTCGTTGAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCCGGGCA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAATTCA TGCCTGCTTC
301 TTTTTCTTCG GCGGTGGCGC GGACAAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTG TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCAGCGCCG
601 GATTTTCGCG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATATA TGCCGTGCGT CATGCCGATC

```

1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGGC CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
  1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

              10      20      30      40      50      60
m642.pep      ACRRICPLPAISAVQYIFADVQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
              |||||  |||||:|||||
a642           ACRRICPLSAISAVQYVFADVQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
              10      20      30      40      50      60

              70      80      90      100     110     120
m642.pep      LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLVVNFGIKHIV
              |||||  |||||:|||||
a642           LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLVVNFGIKHIV
              70      80      90      100     110     120

              130     140     150     160     170     180
m642.pep      RAFKNREGADVDSDIAGGVSAFKTLRTQEFLOHLRGGVSVFRGEGFDDVRLHQLMGDGGN
              |||||  |||||:|||||
a642           RAFKNREGADVDSDIAGGVSAFKTLRAQEFLOHLRGGVSVFRGEGFDDVRLHQLMGDGCN
              130     140     150     160     170     180

              190     200     210     220     230     240
m642.pep      RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
              |||||  |||||:|||||
a642           GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD
              190     200     210     220     230     240

              250     260     270     280     290     300
m642.pep      KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
              |||||  |||||:|||||
a642           KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
              250     260     270     280     290     300

              310     320     330     340     350     360
m642.pep      GEFVAFALFGGNEEEVALRVALPVFRGVDVNGLSVDIFVVGLHFACNRRAGGFGFGNTQT
              |||||  |||||:|||||
a642           GEFVAFALFGGNEEEVALRVALPVFRGVDVNGLSVGIFVVRHLHFSGNRRAGGFGFGNAXT
              310     320     330     340     350     360

              370     380     390     400
m642.pep      AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
              |||||  |||||:|||||
a642           AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1  ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51 gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTGCGCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCCG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagaTGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAT
351 GACCTGCGCg aGTGtTGCgG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1  MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51 ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPM TAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVW VSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1  ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTGCGCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAT
351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCCGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1  MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51 ATRVSKRTRR LPSAAAVCCG DAEILCSATV SGVPM TAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVW VSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

```

              10      20      30      40      50      60
m643.pep      MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR
              |||
g643           MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR
              10      20      30      40      50      60

              70      80      90      100     110     120
m643.pep      LPSAAAVCCGDAEILCSATVSGVPM TAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA
              |||
g643           LPSAATVCCGDEEMLCSATVSGVPM TAEMVSSACRRRLFRATSCMSSSAAACMSFGGMTCA
              70      80      90      100     110     120

              130
m643.pep      SVAVWVSDGMAVCFSVX
              |||
g643           SVAVWVSDGMAVCFSVX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
  1 ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGCGCAG GTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTTCGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
  1 MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
a643	LPSAATVCCGDEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMAVCFSVX					
a643	SVAVWVSDGMAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
  1 ATGCCGCTCTG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTcCCCCG ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTGTGCTGT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTTG CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGGA CATGATTTTC AAaggcgaaa gccgcgcttt
501 gggcgTtacc gaaccggaAa cctccggcgc gGcgattGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacaAA CCATTTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgcccgaac
651 agagcgcaaa aacGGcaaac tcgccaagt CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAATC TCCCGGGGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCGCGG AAATCCAACG CCGCCATCAG GTTTCGAAA
1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtcgC GCccgTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA AccctCGCCA CGGAATACAC
1101 TTAagcCGCC GCGCAATGT TGCAAAAAC TTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 CGTCCGCGCC ACCGCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgctt tgCCGCCGTT
1351 GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTTGACC GACGCCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644 . pep

1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAAIL REMQSCYEY DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEAGIK LDKNQTLDA VQTDVRFVAV
 451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644 . seq

1 ATGCCGTCTG AAAGGTCGGC GGATTGTTGC CCGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCCGCA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TAAAGCACA TCGAATCCGC
 201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCCG
 251 AAGACAAATG GCTTGCTTGA AAGCAGGCGG GTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGCGCAG CAGTTTGAAG TCCAAGAAGT
 351 CcTGGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT
 501 GGGTGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTACGT CAACGCGCGC
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCTG CAACCGCGCT
 801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CGTCGATTAC GAACGCCGCG AAATCCGCG CCGCCATCAG GTTCCGAGA
 1001 TCTTTTACCG CTACGTCTGC CATTCGTTT CGCCTGTGCG CCCCCTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAAAATG TGCAAAACT CTTGGGTGCG AAGGGTTTTG
 1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCGGAAATTT ACGACCAATT
 1251 TGTCCGCGCC ACCGCGGAAG AAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCCT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGTC
 1351 GCGCGGACT ACACCTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCCGTACC GATCCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCGCCCGACT CTTGTCTTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644 . pep

1 MPSEPADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIL REMQSYEYI DGQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
 451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644 . pep	MPSEPADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

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	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKHGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLPQLEFGDEAQAQGLEMI FKGE GGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
g644	REM QSYYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
g644	EYILENLERVVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTLDLRLQTDARFAAVARDYTLPEDIRSFLOEHTLTDACALQKVFI					
	430	440	450	460	470	480
m644.pep	490	500	510			
g644	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644.seq
1   ATGCCGTCCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCGCCCGC ATTTTGTGAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAATC GCAAAGCGAC TTCTCCTCG TTGCCGCCAA
651 AGAGCGCAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCCGT
801 GATGAAATC TCCAGAGCG ACGCTGCCG TTTGCGCGC TTCCAAAACA

```

1025

```

851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTGTG
1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYET DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HVSVPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGGRKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLQPLQEFQDEAQAQGLEMI FKGEGGGLGVTEPETSGAAIA					
a644	AGHYGVPVXXXXXEGALVLQPLQEFQDEAQAQGLDMVFKGEGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYTDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
a644	EYTLENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a 644						
	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSF LQEHTLT DACALQKVFI					
a 644						
	430	440	450	460	470	480
	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSF LQEHTLT DACALQKVFI					
	490	500	510			
m644 . pep	GKIIARLFV FVQAKHEDTAA FLN DIRKDILDCRYCGX					
a 644						
	490	500	510			
	GKIIARLFV FVQAEHEDTAA FLN DIRKDILDCRYCGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTCCTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TGCGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTGCGCAG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGCGGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcggcgat ggcggcggcC TGGTCTTCGG
851 TTCTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMMVLALGMS MPVSMMEQSS NTLNLCKKKS RMTCSRSSR SCPCATPIRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTL SLNGLTKVET
101 ARRLGAVVI SEKSRPSSA MLRVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCPVITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPI ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTCCTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGCGGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTGCGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTCTCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep
 1 MMVLALGIS IPVSMMEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA
 51 SGRVSSRSR IFSIVSTSLC RKNTCPRLS SRNTASRTLP SLKGLTKVLT
 101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLK
 201 RERLATFTGK SAKRSKFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAMAAA WSSVSS*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMVLALGISIPVSMMEQSNLTNRCCKKS RMTCSSSRSRSCPCATPMRASGRVSSRSR					
	: :					
g645	MMVLALGMSMPVSMMEQSNLTNLCCKKS RMTCSSSRSRSCPCATPIRASGRVSSRSR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPRLSSRNTASRTLP SLKGLTKVLTARRRLGAVVISEKSRSPSNA					
	: :					
g645	IFSIVSTSLCRKNTCPRLSSRNTASRTLP SLNGLTKVFTARRRLGAVVISEKSRPSSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLARRLSCSFRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
	: : : :					
g645	MLRVRGIGVAVMVRMSTLARRLSCSFRTPKRCSSSIINKPKFLNFMSSCTNLCVPITI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLKRERLATFTGKSAKRSKFCAACCSTKSVVGASTATCLPPIT					
	: :					
g645	STVPSAMPSSVALVALLLKRERLATFTGKSAKRSKFCAACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAMAAAWSSVSSX					
	: :					
g645	ATNAARRATSVLPKPTSPHTSRSIGFACVKSLITAMAAAWSSVSSX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq
 1 ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
 51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
 101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
 201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
 251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTGTACG
 301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
 351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGACG
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
 501 TATGTCGTCC TGCACAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAAA
 601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGGGCAAA
 651 ATTTTGC GCG TGTGCTCGA CCAGAAGCGT GGTGGTGGC AGTACGGCAA
 701 CTTGTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
 801 TCGCGTCAA TCTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGC
 851 TTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep
 1 MMVLALGMS IPVSMMEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA

1028

```

51  SGSRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep      MMMVLALGISIPVSMVEQSNLTNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           MMMVLALGMSIPVSMVEQSNLTNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              10      20      30      40      50      60

              70      80      90     100     110     120
m645.pep      IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
              :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90     100     110     120

              130     140     150     160     170     180
m645.pep      ILKVRGIGVAVMVRISTLARRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           ILKVRGIGVAVMVRMSTLARRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep      STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVGDQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGTVAVADTV FRQIVGVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFGKTVGQTE					
	: : : : :					
g647	MQRLAADGIQIFFVGVDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFGKTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVAVADTVFRQIISIVNHADAERTAAAHSRGTRGFYRISLIIX					
	: : : : : : : : : : : : : : : :					
g647	RGTVAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

```
a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGTTT GGTTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCCTGTAGC
201 GGACACCGTT TTTCCGCAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 ATCGAACGGT GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGCAATCT AA
```

```
a647.pep
      1  VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
     51  GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
    101  LII*
```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIIFVSVDDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
a647	: : :: : :					
	10	20	30	40	50	60
	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	70	80	90	100		
m647.pep	RGTVAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
a647	: : :					
	70	80	90	100		
	RGAVAVADTVFRQIIRIVDHADTERTAHSRGTRGFYRISLIIX					

```
g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGT
51 CGACGCTTTG AATGTAGATG GCCTCGGTCC CGGCACGCTC CTGCATCAGC
101 TGTGAAAAAC GGTGCGGCAGC CGGAATGATA CGCTTGCCTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TTGCTCTTGG TCGGACAAAA
201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG CGGAAACAG CCGAATGTG
251 CGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGAGGCTT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGGCAACAA GATTGACCG CGCCCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGCTTCA CCGCCCCGGA
501 TTTCGTGTCT CAGCCGCGCG ATACGTCGGC CATGTATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTTCAA TCAGCACACA GCTTGA
```

q648 . pep

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV QGCRAAAHAT LRTFRDRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGT AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCCGGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTGTACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCCGG CATTTGATGC GATGCCCGCA
551 CGTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
101 IKLTDTVVFH TAVVFQHQQA FGFDMPOGVE QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTL LHQRGKQVGS RNDALADIRVLLVFRIEPLK					
	: : : : : : : : : :					
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGS RNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQA VDLHAVIKLTDTVVFHTAVVFQHQQA					
	: : : : : : : : :					
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQA VDLHAI IKLADTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAA LRTGFDRRLKH FKEGNAAGM PRFAAPDFAVQTADTSGIDA					
	: : : : : : : : :					
g648	FGFNMPOGVEQGCRAAAHAT LRTFRDRLKHLKEGNAAGM PGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	: : : : : : : : :					
g648	DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGT AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCGCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTGTACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCGGA

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501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGA
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGDCRLK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQ	RNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA				
a648	FVLVGKKRFVQSRNLVGRKQ	RNVAALNQAGVQQAVDLHAVIKLTDTVVFHAPVVFQHQQA				
	70	80	90	100	110	120
m648.pep	FGFDMPQGV	EQGCRAAAHATLRTGDCRLKH	HFKEGNAAGMPRFAAPDFAVQTADTSGIDA			
a648	FGFDMPQGV	EQGCRAAAHATLRTGDCRLKH	HFKEGNAAGMPCFAAPDFAVQSADTSGIDA			
	130	140	150	160	170	180
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAGSGVDGIQAVVAFDQYAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAA CATATCAGCA
 101 AGGCAAACAA GCAGATGCTG CACCCGAAT GCAGGAAATA TTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCACCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGCGCTTAT GAGGCTTTCG ATGATTTCGA CGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCRAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCGAAT GCAGGAAATA TTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGCGCTTAT GAGGCTTTCG ATGATTTCGA CGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649          MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649          VQELRENKKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51  CGCTGCCCGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649          MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649          VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAAC TCAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGAG CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGGAAG AAACaccgGT TTACGacgac aggacGacg TtacgcaGc
501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatgga CTGTTGCGCG
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACC CCCCATCTT TCGGCATGAA TATCAGCGAC

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1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCCGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCAATCAAC GTCCCCGCGt tcatCCCCAA AAACaaacgc
901 aaacTGCTGC TTCCTGTCGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcgacatta ccgtcgacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatcccct tgtccgaTt accgaaccg ccctTGCAGC
1351 AGCCGCAGCg CaacctCAA cggAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1  MSKLTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEGNVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSI DI DNTPTD TYRSN
401 MPAGTVNVS IARIQAAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1  ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATCGG CTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TAGCATAATCG CCAACGAAGT CAAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGTACCCG CAGGCATTAC
451 GGCGCTGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCGGCG
551 ACTGGCCGCT TGCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TCGCATAACAT TATTGCCACT CCCCATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCCGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAACCTGCTG TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1  MSKLTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEGNVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSI DI DNTPTD TYRSN
401 MPAGTVNVGI ARIRPAAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKCLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKCLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFMRGGEVNPPELVRRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGFMRGGEVNPPELVRRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
g650	LFGDWPLAFAAYNWGEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSEFGMNSIDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSEFGMNSIDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDITYRNMNPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDITYRNMNPAGTVNVSIARIQPAQAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDHRAVX					
g650	ADITVAPLPQETVRTGTTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

```

1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAA AAACACCGGT TTACGACGGC AGGCACGACA TTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGCG
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCCAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCTATTT TCAGGCAGTC GAACCGGACC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTC AAC GTCCCGCGT TCATCCCAA AAGCAAACGC

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1035

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901  AAACGTGCTGC TTCCTGTGCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCTGCCG
1001 CCAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650.pep

```

1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPTKQ
51  YFQSGSLWSE LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPFY
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFSNYLNAAP DSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

```

m650/a650 99.1% identity in 465 aa overlap

m650.pep	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGF LYAQTSSHQ IGLAIMRLN SSILDLPTKQYFQSGSLWGE					
a650	MSKLKTIALTASGLSVCPGF LYAQTSSHQ IGLAIMRLN SSILDLPTKQYFQSGSLWSE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPFY MYHIANEVKKR NMPAEALLP					
a650	LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPFY MYHIANEVKKR NMPAEALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKA KSHVGASGLWQ FMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
a650	FIESAFVTKA KSHVGASGLWQ FMPATGRHYGLEKTPVYDGRHDIAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFA AYNWEGENVG RAINRARAQGLEPTYENLRMPNETRNYVPK LLAVRNIIAT					
a650	LFGDWPLAFA AYNWEGENVG RAINRARAQGLEPTYENLRMPNETRNYVPK LLAVRNIIAA					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNISD IDNKPYFQAVEPDRPLDNEA IARLAGITQSELLALNPAFN VPAFIPKSKR					
a650	PQSFGMNISD IDNKPYFQAVEPDRPLDNEA IARLAGITQSELLALNPAFN VPAFIPKSKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAP DSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAAP DSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSIL VAKNGKTLQTASESVVSIDI DNTPTYRSNMPAGTVNVGIARIRPAAQT					
a650	NLVNAGRSIL VAKNGKTLQTASESVVSIDI DNTPTYRSNMPAGTVNVGIARIRPAAQT					

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCCGA ATACTTGGA GGCTTGGTTA
551 ACGAATTCCC GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GGCAAAAAAG TCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGCGAGT CGCCACCAAC TGTATGCAGA TTA AAAAccgG TTCTTTGAGc
901 cgTTCGACG GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1  MIELDGTENK GNLGANATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
201 EGWKLLETKL GKKVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAGGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGTAGAG TTCAATTGGT
651 TGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAAACCG TTCTTTGAGC
901 CGTTCGACG GCATGGCGAA ATACAACCA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1  MIELDGTENK GNLGANATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
```

1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              |||||
g652           MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m652.pep      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              |||||
g652           EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              70      80      90      100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              |||||
g652           SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFP IISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              |||||
g652           GLVNEFP IISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTLSETLKAVDLAKRNRYSVM SHRSGETEDSTIADLAVATN CMQIKTGSLS
              |||||
g652           LLVKVNQIGTLSETLKAVDLAKRNRYSVM SHRSGETEDSTIADLAVATN CMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGKX
              |||||
g652           RSDRMAKYNQ LLRIEELAE AAYPGKAAF YQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
51  GACTTTGGCG GTTTCTATGG CGGTGTCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCCG CGGCGCAAAA TCTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCACGG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGCGCAAAG TCCAACTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

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1038

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151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFTVNPILAE EGIKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

```

m652/a652 99.7% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              |||||
a652           MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90     100     110     120
m652.pep      EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              |||||
a652           EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
              70      80      90     100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              |||||
a652           SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEIEKGVANA
              |||||
a652           GLVNEFPIISIEDGMDENDWEGWKLLETKLGGKVQLVGDDLFVTNPKILAEIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTLSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS
              |||||
a652           LLVKVNQIGTLSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAKYNQLLRIEELAEAADYPSKAAFYQLGKX
              |||||
a652           RSDRMAKYNQLLRIEELAEAADYPSKAAFYQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCCA CA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCG GGCAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCACACG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCACAAAAT CTTTCGCCGA AGCGTTGCGC TGGCGTGCGG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCGC ACAGTAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTGC AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGTTAA CGAATTCCTG ATTATTTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCGACGACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 CTCGATCTGG CAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGGCAAAAC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCTACTA
1251 CCGCGCAA GCGCATCTT ACCAATGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMMNVI
151 NGGEHANN S NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKL LT
301 EKLGGKVKLV GDDLFTVNP K ILAEGIEKGV ANALLVKV NQ IGTLS ETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEEE LAEAA YYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACCG GCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA GCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMMNVI
151 NGGEHANN S NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKL LT
301 EKLGGKVKLV GDDLFTVNP K ILAEGIEKGV ANALLVKV NQ IGTLS ETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEEE LAEAA DYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGANATLAVSMAVAR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANN SLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANN SLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDSKGFPTTV	GDEGGFAPNL	NSHKEALQ	LMVEATEA	AGYKAGEDVLFA
g652-1	CGAEIFHALKKL	CDSKGFPTTV	GDEGGFAPNL	NSHKEALQ	LMVEAAEA	AGYKAGEDVLFA
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTN	AEFAEY	LEGLVNE	FPIISIEDGM
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTN	AEFAEY	LEGLVNE	FPIISIEDGM
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQ	LVGDDL	FVTNPK	ILAE	IEKGVAN	ALLVKVNQ
g652-1	EKLGGKVQ	LVGDDL	FVTNPK	ILAE	IEKGVAN	ALLVKVNQ
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHR	SGETED	STIADL	AVATNC	MIKTG	SLSRSD
g652-1	SVMSHR	SGETED	STIADL	AVATNC	MIKTG	SLSRSD
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTTCGCGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTCAACACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGGCGTCCG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGCG TACAAGCGCG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGCAAAAT CCAACTCGTT GGCGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQAL I GIDANEQSYI DQIMIELDGT
101 ENKGNLGA N TLA VSMARV A AAEDSGLP L YRYLGGAGP M SLPVPMNVI
151 NGGEHANNS L NIQEFMIMP V GAKSFREAL R CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEAL Q LMVEATEAG Y KAGEDVLFA LDCASSEFYK
251 DGKYHLEAE G RSYTNAEFA E YLEGLVNEF P IISIEDGMDE NDWEGWKLLT
301 EKLGGKVQL V GDDL FVTNPK I LAEGIEKGV A NALLVKVNQ I GTLSETLKA
351 VDLAKRNRY A SVMSHRSET E DSTIADLAV ATNCMIKTG SLSRSDRMAK
401 YNQLLRIEE E LAEAADYPS K AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
|||||
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
          10      20      30      40      50      60

          70      80      90      100     110     120
m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
|||||
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
          70      80      90      100     110     120

          130     140     150     160     170     180
m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
|||||
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
          130     140     150     160     170     180

          190     200     210     220     230     240
m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
|||||
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
          190     200     210     220     230     240

          250     260     270     280     290     300
m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFPIISIEDGMDENDWEGWKLLT
|||||
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFPIISIEDGMDENDWEGWKLLT
          250     260     270     280     290     300

          310     320     330     340     350     360
m652-1      EKLGGRRQLVGDDLFTVNPKILAEGIEKGVANALLVKVNIQIGTLSETLKAVDLAKRNRYA
|||||
a652-1      EKLGGRRQLVGDDLFTVNPKILAEGIEKGVANALLVKVNIQIGTLSETLKAVDLAKRNRYA
          310     320     330     340     350     360

          370     380     390     400     410     420
m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAADYPSK
|||||
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEAADYPSK
          370     380     390     400     410     420

          429
m652-1      AAFYQLGKX
|||||
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1   ATGGCGGcg g aaccgatgcg gAtgcccggag gtaAcgtaCG GTTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgcccAAG
101 CGGCTTcggc ggctttgcCg gtgaTTTTCA TCGGTTGCAG GtcgacgaGG
151 AAAacgTGGC TTTCGGTGCG GCCGGAaacy atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCACCTGT TTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTACGGCA CAAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGAatggc
451 ACGGGgtagg gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1   MAAEPMRMPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1   ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```


1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
  1 MAAEPMRMPE VTKGFSGSFG MAFLLTMVCA LPKAASAALP VIFIGCRSTR
 51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTMVCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
g653           MAAEPMRMPEVTTYGFSGSFGMAFLLTMVCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
g653           MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLVWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
g653           SWVLSRHKITPPRGPRRLVWVVVVTKSQNGTGLGYSPPATSPAX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
  1 ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
 51 ATCATTCGGG ATGGCGT TTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGG GGCTTTGCCG GTAATTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
  1 MAAEPMRMPE VTKGFSGSFG MAFLLTMVCA LPKAASAALP VIFIGCRSTR
 51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTMVCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
a653           MAAEPMRMPEVTKGFSGSFGMAFLLTMVCAALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
a653           MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLVWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
a653           SWVLSRHKITPPRGPRRLVWVVVVTKSQNGTGLGYSPPATRPAX

```

1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1   ATGCCGCGTT TCTCCGGTTC GATTCTTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGcgggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCTGG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCCGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1   MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTS ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1   ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTGG TAACTTTGAC
201 TTCGCCGGTT TTAATGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTCGCG TCGGACGAGG ATTTCCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1   MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRRTS ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	: : : : : :					
g656	MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPsFKQPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	: : : :					
g656	ILSVTLTSPVLLMRPTSLRPKSISITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLSRRTSISGEEPTMWKSPKSX					
	:					
g656	MTSSRSRRTSISGEEPTMWKSPKSX					
	130	140				

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGCTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
201 TTCGCCGTTT TACTGATGTC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTGCGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTGCGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPs	FRRPSTLETMCITWEYFSIT			
a656.	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPs	FRRPSTLETMCITWEYFSIT			
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLR	PKSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
a656	ILSVTLTSPVLLMRPTSLR	PKSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLR	PKSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
a656	ILSVTLTSPVLLMRPTSLR	PKSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ITSLRSRTRISGEEPTMWK	SPKSX				
a656	MTSSRSRTRISGEEPTMWK	SPKSX				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTGAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCCCCg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCGCG CCACCATACG ATAGATGCCT
851 GCGCCCGAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAACctGCCG
901 cccGccgACA CCAAATTATT aTCCCCttgC TGTATGGCGA ATATTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGCGCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCACAGAAA
1051 GGTCCGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pep
1 MNTPPILPPA MLGILGGGQL GRMFAVAAKT MGYKVTVLDP DPNAPAAEFA
51 DRHLCAPFDD RAALDELAKC AAVTTEFENV NADAMRSLAK HTNVSPSGDC
101 VSIAQNRIQE KAWIRKAGLQ TAPYQAVCKA EDITEASAQF LPGILKTATL
151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRGEI SVIVCRLNDE
201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQQARQTAQR LADELDYVGV

1046

251 LAVEMFVVG D THELLVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSP C CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQS L*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAA G CGCGCAATT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAAC TCAA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
 551 TGGATTTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGCTTATTCC ATCGTCCCGG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GGCGCAACGC TTGGCGGACG AATTGGATTA TGTGCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCGGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCCTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTGA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPAAEFA
 51 DRHLCAPFND QAALDELA KC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASAQF LPGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADEL D YGVV
 251 LAVEMFVVG D THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSS C CMANILGDVW QEDGGEPDWL PLQSHPNAL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQS L*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSP	AMLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA	DRHLCAPFND
	::	:				
g657	MNTPPILP	PAMLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA	DRHLCAPFDD
	70	80	90	100	110	120
m657.pep	QAALDELA	KCAAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
	:					
g657	RAALDELA	KCAAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
g657	TAPYQAVCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
	: : : : : :					
g657	EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
	: : : : : :					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNNAHLHLYGKKTAKHGRKMGHFTVL					
	: : : : : :					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSLX					
	: : : : : :					
g657	TTDSDTAFQEAKKLHQSLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGGCGG
51  CGGACAATTA GGCAGAATGT TTACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTACAGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTCGCGGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCC
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGCGCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNLYGV
251 LAVEMFVVGDT HELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAFPND					

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```

|||||
a657  MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAFAEFADRLHLCAPFDN
      10      20      30      40      50      60
      70      80      90      100     110     120
m657.pep QAALDELA KCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
      :|||:|||||
a657  QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
      70      80      90      100     110     120
      130     140     150     160     170     180
m657.pep TAPYQVVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDLKAFAEHGGVDCVL
      |||||:|||||
a657  TAPYQAICKAEDITEESIQFLPGILKTATLGYDGKGQIRVKTLDLKAFAEHRGVDCVL
      130     140     150     160     170     180
      190     200     210     220     230     240
m657.pep EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR
      |||||:|||||
a657  EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR
      190     200     210     220     230     240
      250     260     270     280     290     300
m657.pep LADEL DYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
      |||||:|||||
a657  LADEL NYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP
      250     260     270     280     290     300
      310     320     330     340     350     360
m657.pep PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHRNAHLHLYGKKTAHKGRKMGHFTVL
      |||||:|||||
a657  PADTKLLSSCCMANILGDVWQEDGGEPDWFLQSRPDAHLHLYGKKTAHKGRKMGHFTIL
      310     320     330     340     350     360
      370     379
m657.pep TTDSDTAFQEAKKLHQSLX
      :|||||
a657  STDSDTAFQEAKKLHQSLX
      370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658.seq
1  ATGGTGGCCG GAATTGTGCG TGC GCGGGGC GGTTCATTG ACGAGCAATT
51  CATGTGTGTC GCCGACAACA AACATTTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAAT CTCGCCGCGC AAGTCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTTGAC GCGGATTGTA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAACC GCCTGATACG GCGCGGTTTG CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTC CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCCGTC GTCAAACGGC GCGCACAAAT GGCGGTCGGC AAATTCGCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTAGCGGCA ACGGCAAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658.pep
1  MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH
51  VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

```

1049

```

101 NAIHAAVFGK RGFEEVQRFQ ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM L CQRAHRVGID
201 VFKEFGRNRR FCQFVQGRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
  1 ATGGTGTCCG GAATTGTGCG GCGCGGGGGC GATTTCGTTG ACGACCAATT
 51 CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTTCG CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGCGACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATACTA TTACGGAAAT TTTACTGCGC AAATCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTTGA CCTTGCCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCCT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCCCTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GGCGGTCGGC AAATTCTGCT
701 GCCGGCGCGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA
```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
  1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLH
 51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG N FTAQIHFFQ
101 NAIHAAVFGK RGFEEVQCFY ADLTFVAVQA RSRFQDAGQK LRACFSDFVS
151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKEFSGHRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENG YFVAHG
251 FGGNGKHS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

      10      20      30      40      50      60
m658.pep  MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHVGTSRGGDDG
      ||:||||| ||:||| |:|||||:|||||:|||||:|||||:|||||
g658      MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHVGTPRGDDG
      10      20      30      40      50      60

      70      80      90     100     110     120
m658.pep  ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY
      ||||||||| ||:||| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
g658      ISQDAVFVDVFGGVEGLHVIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEVQRFQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m658.pep  ADLTFVAVQSRFQDAGQKLACFSDFSLTNHLIRRGLQSRFAYPCFLNAVLCNRHT
      ||||||||| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
g658      ADLTFVAVQSRFQDAGQKLACFSNVFGLANRLIRRGLQACFAYPRFFLNAVLCNGHA
      130     140     150     160     170     180

      190     200     210     220     230     240
m658.pep  IAARGNIGMFCQKAHRIGIDVFKEFSGHRRFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG
      :| ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g658      VAAGGNVGM L CQRAHRVGIDVFKEFGRNRRFCQFVQGRPVVKRRAQMAVGKFRRRRIRVG
      190     200     210     220     230     240

      250     260
m658.pep  VENG YFVAHGFGGNGKHSAX
```


1050

```

      :|||||||:|||||
g658  IENGYFVAHGFSNGKHSAX
      250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
  1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
  51  CATGCGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
 101  TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
 151  GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGCGGAGG ATACCGTTTT
 201  CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTTCTG
 251  CGGCATACGA TAACGGAAAT TTCGCGCGCG AAGTCCACCA TTTTTCCTCAA
 301  AACGCAATCC ACGCCGCGGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
 351  CCGTTTGTAC GCGGATTGG CCTTTCCTG CATAGCCCAA TGTCGCGGTT
 401  TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
 451  TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
 501  ATGCTTTTTC CTGAATGCGG TTTTTCGCGA TGGCAACGCA GTCGCCGCTG
 551  GGGGAAACAT TGGTATGTTT GGCAGAAAA CGCATCGCAT CGGCATTGAC
 601  GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
 651  CGGTTTGGTT GTCAAACGGC GCACACAAAT GCGGTCGGC AAATTCGCT
 701  GCCGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
 751  TTTGCGAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
  1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
  51  VGTQSGWDDG VGEDTVFVNV FGRIESLHVV IVQTAYDNGN FAAQVHHFFQ
 101  NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
 151  FANCLIRRLG QACFAYPCLF LNAVLRDGNA VAAGGNIGMF GEKTHRIGID
 201  VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFRCRIRRVG IEYGYFVAHG
 251  FGSNSKHSAX*

```

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG					
a658	MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLRLLLNVTQSGWDDG					
	10	20	30	40	50	60
m658.pep	ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHHFFQNAIHAHVFGKRGFEFIQCFY					
a658	VGEDTVFVNVFGRIESLHVIVQTAYDNGNFAAQVHHFFQNAIHAHVFGKRGFEFIHRFD					
	70	80	90	100	110	120
m658.pep	ADLTFVAVQSRFQDAGQKLRACFSDVFSLTNHLIRRLQSRFAYPCLFLNAVLCNRHT					
a658	ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLQACFAYPCLFLNAVLRDNGA					
	130	140	150	160	170	180
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRQMAVGKFCRRVRIG					
a658	VAAGGNIGMFGKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFRCRIRRVG					
	190	200	210	220	230	240
m658.pep	VNGYFVAHGFSGNGKHSAX					
a658	IEYGYFVAHGFSGNSKHSAX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

```

g661.seq
  1 ATGCACATCG GCGGTATTTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT GCGGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGAAAAA CCTgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCCcga acaGATGGCG Gatgcggcgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGgcg
401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCcgccg tcgccaaaat cgcgaagat tgcggcattg ccgccCttgc
501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GCGcgGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CGGCGACATC actTCgcccgc AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTa TGCCGAACAC GCGTTTTTAC CGCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGCGGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
  1 MHIGGYFIDN PIALAPMAGI ADKPFRRLLCR AFGAGWAVCE MLASDPTLRN
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTTGA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
  1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAAGC CGTCGTCCGT GCGGCAGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAAACATTa TGCCGAACAC GGTGTTTTGC CGCTGCCTT
751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
  1 MHIGGYFIDN PIALAPMAGI TDKPFRRLLCR DFGAGWAVCE MLTSDPTLRN
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFACIL
251 EFGMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
	: : : :					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
	: : : : :					
g661	ADEGGIVAVQIAGSDPEQOMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
	: : : : :					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFTL					
	: : : : : :					
g661	GALRTHRRDQKPSEHPGLQRRHHFAAKSRRRPQTNRRRRHDRARRARQAVVFPREFAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
	: : : : :					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT ACCGACAAAC CGTTCGCCCG ACTTGCCGA GATTTGGCG
101 CAGGTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTAC CCTCAAAACC CGTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPREFTL RRTRCFTACL
251 EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
	: : : :					

1053

a661	MHIGGYFIDNPIALAPMAGITDKPFRRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
	10 20 30 40 50 60
	70 80 90 100 110 120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
a661	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
	70 80 90 100 110 120
	130 140 150 160 170 180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
a661	VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
	130 140 150 160 170 180
	190 200 210 220 230 240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
a661	SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
	190 200 210 220 230 240
	250 260 270 280 290 299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
a661	RRTRCFACLEFGRMYRHYFEPHSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

g663.seq

1	ATGTGTACCG	AGATGAAATT	TATATTTTTT	GTACTGTATG	TTTTGCAGTT
51	TCTGCCGTTT	GCGCTGCTGC	ACAAGATTGC	CGGCCTGATC	GGTTCGCTTG
101	CCTACCTTCT	GGTCAAACCG	CGCCGCCGTA	TCGGCGAAAT	CAATTTGGCA
151	AAATGTTTTT	CCGAATGGGA	CGAAGAAAAG	CGTAAAACCG	TGTTGAAACA
201	GCATTTCAAA	CACATGGCAA	AACTGATGCT	CGAATACGGC	TTATATTGGT
251	ACGCGTcttGC	CAAATGCCTG	AAATCGCTGG	TGCGCTACCG	CAATAAGCAT
301	TATTTGGACG	ACGCGCTGGC	GGCGGGGGAA	AAAGTCATCA	TCCTGTACCC
351	GCACTTTACC	GCGTTCGAGA	TGGCGGTGTA	CGCGCTTAAT	CAGGATGTCC
401	CGCTGATCAG	TATGTATTCC	CACCAAAAAA	ACAAGATATT	GGACGAACAG
451	ATTTTGAAG	gccgcaACCG	CTATCACAAC	GTCTTCCTTA	TCGGGCGCAC
501	CGAagggctg	cgCGCCctcg	TCAAACAGTT	CCGCAAAAGC	AGTGCGCCGT
551	TCCTGTATCT	GCCCGATCAG	GATTTCGGAC	GCAACAATTC	GGTTTTTGTTG
601	GATTTTTTCG	GCATtcagaC	GGCAACGATT	ACCGGCTTGA	GCCGCATTGC
651	CGCGCTTGCA	AATGCAAAAG	TGATACCCGC	CATTCCTGTC	CGCGAGGCGG
701	ACAATACGGT	TACATTGCAA	TTCTATCCCG	CTTGGAATC	CTTTCCGAGT
751	GAAGACGCGC	AAGCCGACGC	GCAACGTATG	AACCGCTTTA	TCGAAGAACG
801	CGTGCGCGAA	CACCCGGAAC	AATATTTCTG	GCTGCACAAG	CGTTTCAAAA
851	CCCGTCCGGA	AGGCAGCCCC	GATTTTACT	GA	

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

g663.pep

1	MCTEMKFIFF	VLYVLQFLPF	ALLHKIAGLI	GSLAYLLVKP	RRRIGEINLA
51	KCFPEWDEEK	RKTVLKQHF	HMAKLMLEYG	LYWYASAKCL	KSLVRYRNKH
101	YLDDALAAGE	KVIILYPHFT	AFEMAVYALN	QDVPLISMYS	HQKNKILDEQ
151	ILKGRNRYHN	VFLIGRTEGL	RALVKQFRKS	SAPFLYLPDQ	DFGRNNSVFF
201	DDFGIQTATI	TGLSRIAALA	NAKVIPAIPV	READNTVTLO	FYPAWKSFPS
251	EDAQADAQRM	NRFIEERVRE	HPEQYFWLHK	RFKTRPEGSP	DFY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

m663.seq

1	ATGTGTATCG	AGATGAAATT	TATATTTTTT	GTACTGTATG	TTTTGCAGTT
51	TCTGCCGTTT	GCGCTGCTGC	ACAAGATTGC	CGACCTGACG	GGTTTGCTTG
101	CCTACCTTCT	GGTCAAACCG	CGCCGCCGTA	TCGGCGAAAT	CAATTTGGCA
151	AAATGTTTTT	CCGAATGGAG	TGAGGAAAAG	CGTAAAACCG	TGTTGAAACA

m663.pep

1	MCIEMKFIFF	VLYVLQFLPF	ALLHKIADLT	GLLAYLLVKP	RRRIGEINLA
51	KCFSEWSEEK	RKTVLKQHFK	HMAKLMLEYG	LYWYAPAGRL	KSLVRYRNKH
101	YLD DALAAE	KVII LYPHFT	AFEMAVYALN	QDIPLISMYS	HQKNKILDEQ
151	ILKGRNRYHN	VFLIGRTEGL	RALVKQFRKS	SAPFLYLDPQ	DFGRNDSV FV
201	DFFGIQTATI	TGLSRIAALA	NAKVIPAIPV	READNTVT LH	FYPAWKSFPG
251	EDAKADAQRM	NRFIEDRVRE	HPEQYFWLHK	RFKTRPEGSP	DFY*

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
g663	RKTVLQKHQFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
g663	AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
g663	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLLH					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
g663	FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

```
a663.seq
      1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
     51  TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
    101  CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
```

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTGGAGC ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTGTC
601 GATTCTCTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTCG
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCCTG CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTTA TCGAGGAACG
801 CGTGCAGCAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFPEWDGKK				
	10	20	30	40	50	60
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVILYPHFT				
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVILYPHFT				
	70	80	90	100	110	120
m663.pep	AFEMAVYALNQDIPLISMYS	HQNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS				
a663	AFEMAVYALNQDVPLISMYS	HQNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAIPV	READNTVTLH				
a663	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAIPV	READNTVTLH				
	190	200	210	220	230	240
m663.pep	FYPAWKSPFGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
a663	FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1  ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGAcgg gGCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT

```

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

```

g664.pep
  1 MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGGRACVFGE LVLAQQADV
  51 DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
 101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
 151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

```

m664.seq
  1 GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
  51 AGAAATTGTT CATCTCCTCA TAGCTGGCGG GCGCACCGG ATGGGCGGTC
 101 GGGCTGCGT CTTGCGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
 151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAT TCTTGGTCGC
 201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
 251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAT TACTCGTGTC CGACCACGGA
 301 TTCGATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
 351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCGCCCAT
 401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
 451 ACCGAAGCGC GTTTCGTCCC ATTTTCATCGC GTTTTTT.CAA CGATTCCACG
 501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAT ACTCGATTTT
 551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

```

m664.pep
  1 VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGGRACVFGE LVLAQQADV
  51 DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
 101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
 151 TEARFVPFHR VEXTIPRQSR PWACPLRWCK TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRACVFGEVLVAQQADVFDAAHGAAGAV					
	: : : : : : : : : : :					
g664	MIHPHHFRAFFINGHGVEIVHLLIADGAHRMGGRACVFGEVLVAQQADVLDAAHGAAGAV					
	10	20	30	40	50	60
m664.pep	AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG					
	: : : : : : : : :					
g664	AGKLLVAEHGQPFLQRKLEPVAAGYAVARPVVEIFVSDHGFNAFEIGIGGGAAVGEDELG					
	70	80	90	100	110	120
m664.pep	VKNVQTLVFHRAHIEIAHGDHENDHENIQVVFQTEARFVPFHRVEXTIPRQSRPWACPLRWCK					
	: : : : : : : : :					
g664	VKNVQTLVFHRAHIEIAYGDDHENIQVIFQPEARFVPLHRVFSTIPRQSRPWVCPPLRWCK					
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

```

a664.seq
  1 GTGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
  51 AGAAATTGTT CATCTCCTCA TATCGGCGG GCGCACCGG ATGTGCGGTC
 101 GGACCTGCGT CTTGCGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
 151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAT TCTTGGTCGC

```

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT .CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
  1 VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTC VFGE LVLAQQADV F
  51 DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
 101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
 151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep    VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRCVFGELVLAQQADVFDAAHGAAGAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTC VFGE LVLAQQADV DTAHGAAGAV
              10      20      30      40      50      60

              70      80      90     100     110     120
m664.pep    AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAGVGKDELG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90     100     110     120

              130     140     150     160     170     180
m664.pep    VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFX TIPQRSRPWACPLRWCK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         VKDVQTLVFHRTHEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPQRSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep    TRFX
              |||
a664         TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
  1 atgaagtGg acgaaacgcg cttcgGgttg GAAtatgact tggatatttt
  51 CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
 101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
 151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
 201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
 251 CGCTGAAGGA AGGGCTGACC GTGTCCGCG ACCAAGAGTT TTCCGGCGAC
 301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
 351 GAACCA GTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
 401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
 451 GGCGCGGAAG TGGTGC GGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
 501 CCAAAAAGGC ATGAAGCTAT ATTTcCaacg CCACGACGGA CAGGCAGTGA
 551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
 601 GACCAGTTCG CCTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
 651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
 701 TGCCGCCAC GCGGATATG GCGGACAAAC AGCCGATGAT GATTCCGTC
 751 AAAGTCGGGC TTCTGAACCG CAACGCGGAA GCGGTGGCAT TCGATTATCA
 801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
 851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCG TCGTTCCTC GCTGCTGCGC
 901 GGGTTCAGCG CGCCAGTGT TCTGAACTAT CCGTACAGCG ACGACGACCT
 951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```



```

1001 CCCAAACGCT CTACCGTCGC GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCGGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCaggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTtcgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTGCGGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTGCGC CTTATCGGCT CAAGcgcgcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCGCGTTGCG TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCAGCCGCA CCGCAAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTGCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAAatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```

g665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRRIE NIRLLRONQF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPTPTDM ADKQPMIPIV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLNY PYSDDDLLLL LAHDSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLNDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDRAQA KQENQSYEYS PETADWRTLRL
451 NVCRAFVLRA DPAHIETVAE KYGEMAQNMT HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHQAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

```

m665.seq
  1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
 51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGAG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCGC
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGGAAG TAGTGGCGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTC CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAACCG
701 TGCCGCCACG GCCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCCTC
751 AAGGTCGGGC TGCTGAACCG CAACGCGGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGCG TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTGCGCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTGCAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCACAAAA
1651 GCCCGTTTCG TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPTPDM TDKQPMPIPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQQA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFMVVAVGDFNMGMENKGLNIFNTKFVLADSRATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGMENKGLNIFNTKFVLADSRATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	70	80	90	100	110	120
	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
m665.pep	130	140	150	160	170	180
	PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQGMKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQGMKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	190	200	210	220	230	240
	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM					
	190	200	210	220	230	240
m665.pep	250	260	270	280	290	300
	TDKQPMPIPVKVGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMPIPVKVGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK					
	: : : : :					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
	: : : : :					
g665	LLAAVEKVISDDLLDNFAKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPAAAGWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMT					
	: : : : :					
g665	KWHELDNRQAAKQENQSYEYSPETADWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
	: : : : :					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	: : : : :					
g665	PKFSLENPNKARSLIGSFSRNVPHFAQDQSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
	: : : : :					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51  CATGGTCGTC GCCGTGGGCG ATTTCATAT GGGTGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGCGCAC
301 CGCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGTCCGAC CGCACATCCG GTGCGCCCCG
401 CCCGATATGA GGAGATGAAC AATTCTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGCGGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CTGCGGACGA TTCCGCGCGG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCT CCTTGTGGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTCTGA GTTAACCATC AAACAAACCG
701 TGCCGCCAC GCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCCTC
751 AAAATCGGGC TGCTGAACCTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGACAGA
851 CCTTCCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCTCT GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACCTA CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CACAAACGCT CTACGCCGT GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGCGCTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC TTTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCGG
1251 CTTTCTGCCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CCTGCGCGCC GATCCGCGC ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPTPDM ADKQPMPIPV
251 KIGLLNCNGE AVAFDYQGRK ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLL LAHSDAFTW EAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

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              10      20      30      40      50      60
m665.pep      MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATATD TDFEGIES
              |||
a665           MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATATD TDFEGIES
              10      20      30      40      50      60

              70      80      90      100     110     120
m665.pep      VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              |||
a665           VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              70      80      90      100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
              |||
a665           PEDAGPTAHPVRPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDM
              |||
a665           QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQRLKNNVFELTIKQTVPPTPDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMPIPVKVGLLNRNGEAVAFDYQGRATEAVLLLTEAEQTFLEGVTEAVVPSLLR
              :|||
a665           ADKQPMPIPVKIGLLNCNGEAVAFDYQGRATEAVLLLTEAEQTFQFESVTEAVVPSLLR
              250     260     270     280     290     300

              310     320     330     340     350     360
m665.pep      GFSAPVHLNYPYSDDDLLL LAHSDAFTWEAAQTLYRR AAVANLATLSDGVELPKHEK
              |||
a665           GFSAPVHLNYPYSDDDLLL LAHSDAFTWEAAQTLYRR AAVANLAALS DGVELPKHEK
              310     320     330     340     350     360

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1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIRAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQRIRAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCTTGAA ACCGAAGTGC ATTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAACAACAA
301 TCGCTGATGG GGCCTGTATG TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGCAACAA AATCGACGGC GGCAGATTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTAACGG AAGACCGTTT CACCACCATG
601 ACGCGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTGGGAA TATGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTAGCGGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCTTGC TGCGCCAGAA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAGGC GCGGAAGTGG
1151 TCGGGATGTA TCATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGCGC ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGCGGGG ACGCCCGTTT TGGAAGCCGA AGGCCGTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCGGGCTTC
1451 TGAACCGCAA CGCGAAGCG GTGGCATTCG ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGTGTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCTGCTC
1651 GCCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTGCGCCG GTCGCCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAATCT TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGGCGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACGCGCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCGCAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTGCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGACCGC CAAAACTTG GTGAAACAAG AATTGCAGT CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDBGHVV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRAVRRIEN IRLLRQNFPP
351 EDAGPTAHPV RPYSYEEMNN FYTMTVYEGK AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMPIPVK VGLLRNNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVID
601 DLLDNAFKAL LGGVPSEAEI WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLRN VCRAFLVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTALQHP KFSLENPNKA RSLIGSFSRN VPFHQAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQLQCIRA
851 QEGLSKDVGE IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGG GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACAACAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTTGTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCGAAGTT CACCACCACC ATCGTCGCGC ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGAGATTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCCG GGGCGATTTC GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGCG TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGCGGATT TCAATATGGG CCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTTC CCGACAGCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCT CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAC ATCCGCCTGC TGCGCCAGCA CCACTTCCCC
1051 GAAGACGCGC GCCCGACCGC CCATCCGGTG CGCCCGGCCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCGGGA AGGTCGCTCG
1351 AAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ACTATCAGGG CAAACGCGCG

```

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1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCCGCGCCA ACCTTGCCAC GCTTTCAGAC GGCCTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCACGAAT TGAACCGTCA GCGGCGGAAG CAGGAAAAAC AAAGCTACGA
2001 ATACAGCCCC GAAGCGCGCG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGTGTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGGCCCTC
2251 GTCGGCTCAA GCGCGCGCAG CGACACCTG CAACAGGTTC GAACCGCCTT
2301 GCAGCATCCG AAATTGAGCC TCGAAAAACC CAACAAAGCC CGTTGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCGCGATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCGCGCTTAG TGCAGGCGTT CAACCTCTGC AACAGGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFS DGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL YLDLIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDG AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMMPVK VGLLNRNGEA VAFDYQGKRA
501 TEAVLLLEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVISD
601 DLLDNFAFKL LLGVPSAEEL WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTLNR VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTN EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

```

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRILE	TDLHFDIAEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
	70	80	90	100	110	120
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFS DGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFS DGRHWV	KWEDPFAKPS
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
g665-1	YLFALVAGDL	AVTEDRFTT	MSGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGL
	250	260	270	280	290	300
m665-1.pep	YLDLIFMVVA	VGDFNMGAMEN	NKGLNIFNTK	FVLADSRAT	DTDFEGIESV	VGHEYFHNWT
g665-1	YLDLIFMVVA	VGDFNMGAMEN	NKGLNIFNTK	FVLADSRAT	DTDFEGIESV	VGHEYFHNWT

1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQFPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQFPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMMPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMADKQPMMPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLHDSDAFTRWEAAQTLYRRAVANLATLSGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLHDSDAFTCWEAAQTLYRRAVANLAALSDGIGLPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNRAAK					
g665-1	DLLDNAFKALLLGVPSEAEIWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDRAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPEAGWRTLNRVCRAFVLRADPAHIETVAEYKEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRVCRAFVLRADPAHIETVAEYKEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPHFHAEDGSGYRFIADKVIIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPHFHAQDGSYRFIADKVIIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRAQEGLSKDVGEIVGKILDX					
g665-1	VKQELQCIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GCGAGTATT CAGACGGCCG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTGCGG TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTGTCGCC
751 GTGGGCGATT TCAATATGGG TGCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TFCGTCTTGG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCG TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCCTGC TCGCGCAGCA CCAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCG GATATGAGGA
1101 GATGAACAAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TCGCGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTTACCT GCGACGATTT
1251 CCGCGCGCGG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTCGAGTT AACCATCAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAAGTCAA CGCGGAAGCG GTGGCATTG ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTGTCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGGTGCC GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGCTGTA
1851 AGCCGAGCTG TGGGACGCGG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCCG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCGCG
2151 GCTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTC
2251 GTCGGCTCAA GCCGCGCAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCC GCCCGCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

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This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKG LNIENFK FVLADSRTAT DTD FEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHVP RPARYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDFFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMIPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVLPKHEKL LAAVEKVISD
601 DLLDNFAFKAL LLGVPSEAE LWDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTL RN VCRAFVLRAD PAHIETVAEK
701 YAEMAQNMT H EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QVQ TALQHP KFSLENPNKA RSLIGSF SRN VPHFHAEDGS
801 GYRFIADKVI EIDREN PQVA ARLVQAFNLC NKLEPHRKNL VKQALQRI
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPV	LDGSAKLLSV
m665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPV	LDGSAKLLSV
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSERFTVEVETELPAENKSLMGLYASAGNLTQCEPEG					
m665-1	KINGAAADYVLEGETLTIAGVPSERFTVEVETELPAENKSLMGLYASAGNLTQCEPEG					
	70	80	90	100	110	120
a665-1.pep	130	140	150	160	170	180
m665-1	130	140	150	160	170	180
a665-1.pep	190	200	210	220	230	240
m665-1	190	200	210	220	230	240
a665-1.pep	250	260	270	280	290	300
m665-1	250	260	270	280	290	300
a665-1.pep	310	320	330	340	350	360
m665-1	310	320	330	340	350	360
a665-1.pep	370	380	390	400	410	420
m665-1	370	380	390	400	410	420
a665-1.pep	430	440	450	460	470	480
m665-1	430	440	450	460	470	480
a665-1.pep	490	500	510	520	530	540
m665-1	490	500	510	520	530	540
a665-1.pep	550	560	570	580	590	600
m665-1	550	560	570	580	590	600
a665-1.pep	610	620	630	640	650	660
m665-1	610	620	630	640	650	660
a665-1.pep	670	680	690	700	710	720
m665-1	670	680	690	700	710	720
a665-1.pep	730	740	750	760	770	780
m665-1	730	740	750	760	770	780
a665-1.pep	790	800	810	820	830	840
m665-1	790	800	810	820	830	840

1068

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRIRAEGLSKDVGEIVGKILD	X				
m665-1	VKQALQRIRAEGLSKDVGEIVGKILD	X				
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

g666.seq

1	ATGCTTTGTA	TGAATTATCA	ATCAAACCTCA	GGCGAAGGAG	TGCTTGTAGC
51	TAAAACATAT	TTATTGACTG	CATTGATAAT	GTCTATGGTA	ATCTCCGGAT
101	GTCAACTCAT	CCATGCCAAT	CAAGGTAAGG	TTAATACTAA	TTCTGCTGTC
151	ATCGCAGGTG	CAGACGCTCA	CACGCCTGAA	CATGTAACGG	GACTGACCGA
201	ACAAAAGCAG	GTGATTGCAA	GTGATTTTAT	AGTAGCGTCA	GCCAATCCAT
251	TAGCAACACA	AGCTGGCTAT	GATATCTTAA	AGCAAGGCGG	TAGCGCTGCA
301	GATGCGATGG	TGGCGGTGCA	GACGACACTA	AGCTTGGTAG	AGCCACAGTC
351	GTCAGGCTTG	GGCGGTGGTG	CATTTGTGTT	GTATTGGGAC	AATACCGCCA
401	AAACATTGAC	CACATTTGAT	GGGCGTGAGA	CGGCACCGAT	GCGTGCGACG
451	CCAGAATTAT	TTTTGGATAA	AGATGGTTAA	CCTTGAAAT	TTATGGAAGC
501	GGTGGTCGCT	CGGTAGGTAC	GCCTGCTATC	CCTAAACTGA	

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

g666.pep

1	MLCMNYQSNS	GEGVLVAKTY	<u>LLTALIMSMV</u>	ISGCQVIHAN	QGKVNTNSAV
51	IAGADAHTPE	HVTGLTEQKQ	VIASDFIVAS	ANPLATQAGY	DILKQGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLLDKDGX	PLKFMEAVVA	RXVRLLSLN*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

m666.seq	1	51	101	151	201	251	301	351	401	451	501
	ATGCCTTGTA	TGAATCATCA	ATCAAACCTCA	GGCGAAGGAG	TGCTTGTGGC						
	TAAAACATAT	TTATTGACTG	CATTGATAAT	GTCTATGACA	ATCTCTGGAT						
	GTCAAGTCAT	CCATGCCAAT	CAAGGTAAGG	TTAATACTCA	TTCTGCTGTC						
	ATCACAGGTG	CAGACGCTCA	CACGCGTGAA	CATGCAACGG	GACTGACCGA						
	ACAAAAGCAG	GTGATTGCAA	GTGATTTTAT	GGTAGCGTCA	GCCAATCCAT						
	TAGCAACACA	AGCTGGCTAT	GATATCTTAA	AGCAAGGCGG	TAGCGCTGCA						
	GATGCGATGG	TGGCGGTGCA	GACGACACTA	AGCTTGGTAG	AGCCACAGTC						
	GTCAGGCTTG	GGCGGTGGTG	CATTTGTGTT	GTATTGGGAT	AATACCGCCA						
	AAACATTGAC	CACATTTGAT	GGGCGTGAGA	CGGCACCGAT	GCGTGGCAGC						
	CCGGAATTAT	TTTTTGGATAA	AGATGGTCAA	CCATTGAAAT	TCTTGGGAAGC						
	GGTGGTCGTG	GTCGCTCGGT	GGGTACGCCT	GCTATCCCTA	AACTGA						

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```
m666.pep
1 MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHTSAV
51 ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGSAA
101 DAMVAQTTL SLVPEQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGO PLKFMEAVVU VARVRLLSL N*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/q666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNSSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHTSAVITGADAHTPE					
	: : : :					
g666	MLCMNYQSNSSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHTSAVIAGADAHTPE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPOSSGL					

1069

	: :
g666	HVTGLTEQKQVIA SDFIVASANPLATQAGYDILKQGGSAADAMVAVQTTL SLVEPQSSGL
	70 80 90 100 110 120
m666.pep	GGGAFVLYWDNTAKT LTTFDGRE TAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
g666	GGGAFVLYWDNTAKT LTTFDGRE TAPMRATPELFLDKDGXPLKFMEAVV--ARXVRLLSL
	130 140 150 160 170
m666.pep	NX
g666	NX
	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2175>:

```
a666.seq
1  ATGCCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTGGC
51  TAAACATAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101  GTCAAGCTAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151  ATCAACAGTG  CAGACGCTCA  CACGCTGAA  CATGCAACGG  GACTGACCGA
201  ACAAAGCAG  GTGATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251  TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGGCGG  TAGCGCTGCA
301  GATGCGATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351  GTCAGGCTTG  GGCGGTGGTG  CATTTGTGTT  GTATTGGGAT  AATACCGCCA
401  AAACATTGAC  CACATTTGAT  GGGCGTGAGA  CGGCACCGAT  GCGTGCGACG
451  CCGGAATTAT  TTTTGGATAA  AGATGGTCAA  CCATTGAAAT  TTATGGAAGC
501  GGTGGTCTGT  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

This corresponds to the amino acid sequence <SEQ ID 2176; ORF 666.a>:

a666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGCQVIHAN</u>	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	<u>VIASDFMVAS</u>	<u>ANPLATQAGY</u>	DILKQGGSA
101	DAMVAQVTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLDKDGG	PLKFMEAVVV	VARWVRLLSL	N*	

m666/a666 100.0% identity in 181 aa overlap

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTISGCQVI	HANQGKVNTHSA	VITGADAHTPE	
a666		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTISGCQVI	HANQGKVNTHSA	VITGADAHTPE	
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVI	ASDFMVASANPLAT	QAGYDILKQGGSA	ADAMVAVQTTL	SLVEPQSSGL	
a666		HATGLTEQKQVI	ASDFMVASANPLAT	QAGYDILKQGGSA	ADAMVAVQTTL	SLVEPQSSGL	
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNT	AKTLTTFDGR	ETAPMRATPEL	FLDKDGQPLKF	MEAVVVVARW	VRLLSL
a666		GGGAFVLYWDNT	AKTLTTFDGR	ETAPMRATPEL	FLDKDGQPLKF	MEAVVVVARW	VRLLSL
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
  1  atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
 51  tttccAtttg gtattcgtcc gcgctgaatc tgccgctgAc CAGAcagaaa
101  cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAttgCG
151  GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201  ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTcgCcat atcgtccagC
251  GGCACATTcg ccctcggtcG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301  GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCAActg AAATCGCGGC
351  tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GCGGTTGATG
401  CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451  GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501  TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551  TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601  ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651  GCTGCGCGAA CAGCACCCTG TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701  TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751  CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCGCCT
801  ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
  1  MRFVFCLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
 51  DFLQRARVER FPHEAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101  VALVITADV VPLEIAAAVE IAVARIPIAR GVDVYQGA V MQYGQVETAA
151  VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNVLVLP AHTAGNRHNL
201  MEVVLHKIAA GLCAAFLLRE QHHEFVIRQGR RQVIQRTDTL HIGYGFNIES
251  QNRIHGSTLH SKTDLRLLLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
  1  ATGCGGCTTT TCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
 51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101  CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151  GATTTCTTTC AGCCTGCCCC TATGGAATGC CTCCCAAACC TTGCTGCCGT
201  CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251  GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301  GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351  TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401  CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451  GTTCCAACCTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501  TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551  TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601  ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651  GCTGGGCAAT CAGCACCCTG TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
  1  MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFIIA
 51  DFLQPARMEC LPNLAADVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101  VALVITADV VPLEIAAAVE IAVAHIPIAR GVDVYQGA V MQYGQIETAA
151  VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHNL
201  MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep    MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFIIADFLQPARMEC
              ||:  | |:::  | ||:||||:| |||||:||||:| : | ||||| || | ||:|
```

g667	MRFVFLGGEIVSDPCDFHLVFRVESAADQTTETQIHQIRIHGIGFAIIADFLQRRARVER	10	20	30	40	50	60
m667.pep	LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE	70	80	90	100	110	120
g667	FPHFAAVHTQLARKAAQFRHIVQRHIRPRLVKREQIHQIAVALVITADVVPLEIAAAVE	70	80	90	100	110	120
m667.pep	IAVAHIPIARGVDVAVYQGAVMQYGGIETAAPVTDQLRRMFFNQFEKFSNDHFLAVIHLAD	130	140	150	160	170	180
g667	IAVARIPIARGVDVAVYQGAVMQYGVQVETAAPVADQLRRMFFNQFEKLGNDHFFAIVHLAD	130	140	150	160	170	180
m667.pep	GADMYFILPPTHAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL	190	200	210	220		
g667	GADMNLVLPPTAHTAGNRHNLMVVLHKIAAGLCAAFLLREQHHFVIRQGRRQVIQRTDTL	190	200	210	220	230	240
g667	HIGYGFNIESQNRIHGSTLHSKTDLRLCHX	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2181>:

```
a667.seq
1 ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51 TTTCCATTTT GTATTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACGCAC CTCGGTTTCG CATAATTGCG
151 GATTTCCTTC AGCATGCCCG CGTGGAACGC TCCCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCCGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGCCTTGATG
401 CCGTGTAGCA GCGAAGCGTA ATGCAGAACC GCGAGGTCGA ACCGCGCGCC
451 GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAAA CAGCACCAC T CATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT T TAAAA. CAG ACTTGCGCCT
801 ATTGTGTCAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2182; ORF 667.a>:

```
a667.pep
1  MRFVFLGGE  IVSDPLDFHF  VFVCVESAAD  QTETQIHQIG  IYRIGFAIIA
51  DFLQPARVER  LPHLAAVHTQ  LARKTAQFRH  IVQRHIRPRL  VKREQIHQIA
101  MTLVVAADV  VPLEIAVAE  IAVAHIPIAR  GVDVAV*QRTV  MQNRQVETAA
151  VPTDQLRRMF  FNQLEKFGDN  HFLAVIHLAD  CTDMDFILPP  THAARNRNLH
201  MKMMLHKIPT  RLSTAFLLGK  QHHFIVGQRG  RQVIQRDTL  HIGYGFNIES
251  QNRGHDSTLY  LKXDLRLLCH  *
```

m667/a667 79.0% identity in 224 aa overlap

	10	20	30	40	50	60
m667.pep	MRLFPGLCGQVIPHPFDHFHVFVRIQPAADQTETQVHQISVCRVGFAIIADFLQPAMEC					
a667	MRFVFCLGGEIVSDPLDFHFVFCVESAAADQTETQIHQIGIYRIGFAIIADFLQPARVER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m667.pep	LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE					
a667	LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLVVAADVVPLEIAAAVE					

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		70	80	90	100	110	120
m667.pep		130	140	150	160	170	180
		I A V A H I P I A R G V D A V Y Q G A V M Q Y G Q I E T A A V P T D Q L R R M F F N Q F E K F S N D H F L A V I H L A D					
a667							
		I A V A H I P I A R G V D A V X Q R T V M Q N R Q V E T A A V P T D Q L R R M F F N Q L E K F G D N H F L A V I H L A D					
		130	140	150	160	170	180
m667.pep		190	200	210	220		
		G A D M Y F I L P P T H A A R N R H N L M K M M L H K I A A R L S T A F V L G N Q H H L					
a667		:				:	:
		C T D M D F I L P P T H A A R N R H N L M K M M L H K I P T R L S T A F L L G K Q H H F I V G Q R G R Q V I Q R T D T L					
		190	200	210	220	230	240
a667		H I G Y G F N I E S Q N R G H D S T L Y L K X D L R L L C H X					
		250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```
g669.seq
1  ATGCGCCGCA TCGTTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A
```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

g669.pep
1 MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHG
51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQ TAL SRPAVFGYNA
101 DIKRIL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```
m669.seq
1  ATGCGCCGCA TCATTA AAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A
```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```
m669.pep
  1  MRRIKKHQF INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101  DIKRIL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIKKKHQPINAPHIVLEIRIMKLHRAVFVFLGRKRPHHHHSSLRQHGIEGMGDFDKQI					
	: :					
g669	MRRIVKKKHQPVNAPHIVLEIRIMKLHRAVFVFLGRKRPHHHHDSLRQHGIEGMGDFDKQI					
	10	20	30	40	50	60
	70	80	90	100		

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TACGCGCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIIKKHQP VNAPHIVLEI RIMKLHRAV FLGRKRPHH DRSLRRQHGI
51 EGMGDFKQI FRHVQSSNRQ NGRQPVCTK PNTASLTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIIKKHQPINAPHIVLEIRIMKLHRAVFLGRKRPHHDSLRQHGIEGMGDFKQI
             |||||:|||||
a669        MRRIIKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHDSLRQHGIEGMGDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCGGACCAT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNVTRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTGGTAAA
51 AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCGGACCAT TCGGGGTCGA GTGCGGAGGT CGGTTTCGTCA AACAAACATTA

```


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```

251 CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              |||||:|||||:|||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
              |||||:|||||
g670           SSIAFFSACSAFCPLTFIGARVMLSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGTTGTA
 51 AAACGCTTCC GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTTCGTA AACAACTTA
251 CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||:|||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

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	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACS AFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTCTGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAASLAK KKETHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGAGGCAAA
201 GGCGAGGTcG GCGAAGGAGG CGGCaaAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTCTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

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```

|||||
g671  RGWNEAKARSAKGAAKSLAKKETHATIEPASAITPRIVEMTMOAAMTAEARRSAMGRL
      70      80      90      100     110     120

      130      140      149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
|||||
g671  FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
      130      140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2199>:

```

a671.seq
1  ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAATG CCGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCCCCGG
101 TCAGCAGCGA GCGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGA ACGATGCAAA
201 GCGGATGTCG GCGAAGGGTG CCGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACGAGGA GGTCCGCAAC
351 GGGGAGGTTA TTCATTGCTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2200; ORF 671.a>:

```

a671.pep
1  MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

m671/a671 93.9% identity in 148 aa overlap

```

      10      20      30      40      50      60
m671.pep  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR
|||||
a671  MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDANANR
      10      20      30      40      50      60

      70      80      90      100     110     120
m671.pep  RGWNEAKARSAKEAAKSLAKKETHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL
|||||
a671  RGWNAKAMSAGAAKSLAKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
      70      80      90      100     110     120

      130      140      149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
|||||
a671  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
      130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2201>:

```

g672.seq
1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCGC GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTATC GACATCATTA AAGCACAAA AATCGCCGCC
151 GCACTGCCGC CGTTTGTGAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAT GCATTCTGCC GGCAGTTCGA CCGCCCCTAT
301 ATTAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC AACGCTCAGG CACTGCTGTT CGATGCCTAT CACCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGact GGacgctgtt ggcggaATAT
451 TCGGGCAAGC CGTGGGTGCT TGCCGGCGGG CTGACCCTTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAAGC GGTGACGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/q672 91.3% identity in 208 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAV DIIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAAFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAGADAVGL	VFFQGS	RAVDIARAK	KITAALPPFVS
			:	:	:	:
a672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYPQSPRAV	DIIKAQKITA	ALPPFVSVVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQN	IRRILAEVPI	HIIQFHGDE	DDAFCRQF	HRPYIKAIR	VQTASDIRNA
a672	LFVNESAQN	IRRILAEVPI	HIIQFHGDE	DDAFCRQF	HRPYIKAIR	VQTASDIRNA
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFD	AYHPSEYGG	TGNRFDW	TLLAEYS	SGKPWVL	AGGLTPEN
a672	DAQALLFD	AYHPSEYGG	TGNRFDW	TLLAEYS	SGKPWVL	AGGLTPEN
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASK	GKKDAAK	VAAFIAT	ANRLSRX		
a672	SGGVEASK	GKKDPAK	VAAFIAT	ANRLSRX		
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CCGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC CTTACCGATG CCGACCGCT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATTT

```

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAATAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTTRNVRTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF D NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
  1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
 51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTTRNVRTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF D TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNVRTGI
          |||||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNVRTGI
          10      20      30      40      50      60
          70      80      90     100     110     120
m673.pep YTDDTAQFVFVDTPGFQTDH RNALNDRLNQ NVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||||

```

1080

```

g673      YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGTGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGATAA GGACAAGCGC AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAGGTGC GCGCGGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCATTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF DT KVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	:					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCCGCCGCGG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCCAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1 ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
 101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
 201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
 301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
 351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCCGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV
 101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
 201 CTCTTCTGAA AAATTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
 301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
 351 CACGGAAAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV

1085

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCCGGCGT
 151 GTTCAAAACC ACTTCGTGCG CTTGCGGCGC TTTAATCAGG CAACGCGCCA
 201 ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
 301 GGTGCGGCCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTGCGTGGC
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GGCCTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
 1 MPQILVRIFL IRYSEFIWETV RLCRRFRHSR SVDFDVFDK DFNFLTAFR
 51 VQNHVFVAFR FNQATRQRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
 101 GRAEKYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT
 151 GTTCAAAACC ACTTCGTGCG CTTGCGGCGC TTTAATCAGG CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
 301 CGTCGCGCCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTGCGTGGC
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GGCCTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
 1 MPQILVRIFL IRYSEFIWETA RLCRRFRHSR SVDFDVFDK DFNFLTPFR

1086

51 VQNHVFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVDRKDFNFLT	PFRRVQNHVFAR				
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVDRKDFNFLT	AFRRVQNHVFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGR	FAQFGIDDDG				
g677	FNQATRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQT	DGRAEKYLVRGFAQFGIDDDG				
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAF	AVKIVAVFAAVACRPVDD	LDDFGAFFVD	QLIKLVFQCL		
g677	SLQTFGQETDAAVDFAHTAF	AVKIVAVFAAVACRPVDD	LDDFGAFFID	QLIKLVFQCL		
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAACC	ACTTCGTCGC	CTTCACGCGC	TTTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAAT	TTGTTTTGCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCGCGCGA	ACAGACCGAC
301	GGTCGCGCCG	AAAAACACTT	GGTCGGTCGC	TTCGCGCAAT	TCGGGATCAA
351	CGACGACGGC	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTCTG
401	ATTTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCGGTTG	CCTGCCGCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTAAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GCGTAATGT	AGTTTTTGGT	TTCGCTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVDRK	DFNFLT	PFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQT	D
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	<u>AVKVVAVFAA</u>	
151	<u>VAVACRPVDD</u>	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVDRKDFNFLT	PFRRVQNHVFAR				
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVDRKDFNFLT	PFRRVXNHVFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120

1087

```

m677.pep      FNQTTSQRRNPRNFVLRGIDFIDADDDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
|||||
a677          FNQTTSQRRNPRNFVLRGIDFIDADDDFDGLLAPVAAQQT DGRAEKHLVGRFAQFGINDDG
              70          80          90          100         110         120

              130          140          150          160          170          180
m677.pep      SLQTFGQETDAAVDFAHTAFAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
:|:|:|
a677          GFQTLGQETDAAVDFAHTAFAVKVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
              130          140          150          160          170          180

              190          199
m677.pep      PSGGRNVVFGFGTHIVCGX
|||||
a677          PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2231>:

g678.seq

1	ATGAATAGCC	TCCCCATTGC	CGACCTCCTC	GCCTccgCCG	TCATCGCCGC
51	CTGCATCGTC	ATTTCCACGA	TGCGCGGCGT	GATTGCGGAA	GCAggttcGA
101	TGGTgGCATG	ggtggTTTcc	tTCTTTTttg	ccAAACTCTt	tGCCGCACcc
151	ttcgccgACC	TCGCCTTTGc	ctCGTTCCAA	ccccgccTGT	TTGCAttggc
201	tCTGTcATTc	ATTTCCCTGT	TCGTcATTGC	CTGTCTGATC	CAGAAAATGC
251	TCCGTTTCGCT	GCTGACCGGT	GCAGTTTCGG	CGGTCGGTCT	GGGCTTTGCC
301	AACCGcATTt	TGGCGGGTGT	ATTCGGTGCA	TTGAAAGGCG	TTTTGATTGT
351	TACCCTGCTG	ATCATGCTTG	CTTCAAAAAC	CGACCTGCCC	GATACCGAAG
401	AATGGCAACA	GTCCTATACC	GTACCGTTTT	TCGTATCGCT	TTCGGAAGCG
451	GTGTTAAACC	atacggacAA	CGCacccgaa	tCCCTcgacg	acgactaa

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

g678.pep

1	<u>MNSLPIADLL</u>	<u>ASAVIAACIV</u>	<u>ISTMRGVIAE</u>	<u>AGSMVAWVVS</u>	<u>FFFAKLFAAP</u>
51	<u>FADLAFASFQ</u>	<u>PRLFALALSF</u>	<u>ISLFVIACLI</u>	<u>QKMLRSILTG</u>	<u>AVSAVGLGFA</u>
101	<u>NRILGKVFGA</u>	<u>LKGVLIIVTL</u>	<u>IMLASKTDLP</u>	<u>DTEEWQSYT</u>	<u>VPFFVSLSEA</u>
151	<u>VLNHTDNP</u>	<u>SLDDD*</u>			

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2233>:

m678.seq

1	ATGAATAGCC	TCCCCATTGC	CGACCTCCTC	GTCTCCGCCG	TCATCGCCGC
51	CTGCATCGTG	CTATCCGCGA	TGCGCGGCGT	GATTGCGGAG	GCAGGCTCAA
101	TGGCGGCATG	GGTGGTTTCC	TTCTTTTTCG	CCAAACTCTT	TGCCGCCTCC
151	TTCGCCGACC	TCGCCTTTGC	CTCGTTCCAA	CCCCGCCTGT	TTGCATTGGC
201	TCTGTCGTTT	ATTTCCCTGT	TCGTCAATTG	CTGTCTGATC	CAGAAAATGC
251	TCCGTTTCGT	GCTGACCAGT	GCAGTTTCGG	CGGTCGGTTT	GGGCTTTGCC
301	AACCGCATTT	TGGCGGCGCT	ATTCGGTGCA	TTGAAAGCGG	TTTTGATTAGT
351	TACCCTGCTG	GTCATGCTTG	CTTCAAAAAC	CGACCTGCCC	GATACCGAAG
401	AATGGCGGCA	ATCTTACACA	CTGCCGTTTT	TCGTATCGCT	TTCGGAAGCC
451	GTGTTGAACC	ATAGCGGCGG	CACGGCGGAA	ACTCCGGAAG	ACGATTGA

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

m678.pep

1	<u>MNSLPIADLL</u>	<u>VSAVIAACIV</u>	<u>LSAMRGVIAE</u>	<u>AGSMAAWVVS</u>	<u>FFFAKLFAAS</u>
51	<u>FADLAFASFQ</u>	<u>PRLFALALSF</u>	<u>ISLFVIACLI</u>	<u>QKMLRSL LTS</u>	<u>AVSAVGLGFA</u>
101	<u>NRILGGVFGA</u>	<u>LKGVLIIVTL</u>	<u>VMLASKTDLP</u>	<u>DTEEWRQSYT</u>	<u>LPFFVSLSEA</u>
151	<u>VLNHSGGTAE</u>	<u>TPEDD*</u>			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAVVVSFFFAKLFAASFADLAFASFQ					
	: : : :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAVVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFSISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIVTLL					
	: : :					
g678	PRLFALALSFSISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : : :					
g678	IMLASKTDLPDTEEWQSYTVPFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

a678.seq

1	ATGAATAACC	TCCCCGTTGC	CGACCTCCTC	GTCTCCGCCA	TCATCGCCGC
51	CTGCATCGTG	CTATCCGCGA	TGCGCGGCGT	GATTGCGGAG	GCTGGCTCAA
101	TGGCGGCATG	GGTGGTTGCC	TTTTTTTTCG	CCAAACTCTT	TGCCGCACCC
151	TTCGCCGACA	TCGCCTTTGC	ATCGTTCCAA	CCCCGCCTGT	TTGATTGGC
201	TCTGTCGTTT	ATTTCCCTAT	TCGTCAATTG	CTGTCTGATC	CAGAAAATAC
251	TCCGCTCGCT	GCTGACCGGG	GCAGTTTCGG	CGGTCGGTTT	GGGCTTTGCC
301	AACCGCATT	TGGGCGGCGT	ATTCGGTGCA	TTGAAAGGCA	TTTTGATTAT
351	TACCCTGCTG	GTCATGCTCG	CTTCAAAAAC	CGACTGCCCC	GATACCGAAG
401	AATGGCGGCA	ATCTTACACA	CTGCCGTTTT	TCGTATCGCT	TTCCGAAGCC
451	GTGTTGAACC	ATAGCGGCGG	CACGGCGGAA	ACTCCGGAAG	ACGATTGA

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

a678.pep

1	MNNLPVADLL	VSAIIAACIV	LSAMRGVIAE	AGSMAAWVVA	FFFAKLFAAP
51	FADIAFASFQ	PRLFALALSF	ISLFVIACLI	QKILRSLLTG	AVSAVGLGFA
101	NRLGGVFGEA	LKGILIITLL	VMLASKTDLP	DTEEWRSQYT	LPFFVSLSEA
151	VLNHSGGTAE	TPEDD*			

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	: : : : : :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIVTLL					
	: : : : : :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILIITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWRSYTLPPFVSLSEAVLNHSGGTAETPEDDX					
	: : : : :					
a678	VMLASKTDLPDTEEWRSYTLPPFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2237>:

g680.seq

1	ATGACGAAGG	GCAGTTCGGC	GATGTCCAGC	CCACGCGCGG	CGATATCGGT
51	GGCGACGAGG	ACGCGCAGGC	TGCCGTCTTT	GAAGGCGTTG	AGTGTTTCGA
101	GCCTGCTTTG	TTGGGAACGG	TCGCCGTGTA	TCGCTGTGTC	GGACAGGTTG

```

151  CGGCGCACCA GTTCGCGCGT TACGCGGTG ACGCTTTGTT TGGTtttgCA
201  AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251  GGTTGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301  GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451  TCGATAAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501  TTCGGCTTTG TTTAACTGA TGTTTTCTG TTTACATGG TCGAGCAGCC
551  GTCCGACGGT GCGCAGGACT ATTTGCGAGC CGGCACGCAG GTCGGCGGTT
601  TGTTTGTTCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651  GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

g680.pep

```

1  MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQKTI TWFCRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMEFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

m680.seq

```

1  ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51  GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CCGCGCACCA GTTCGCGCGT TACGCGGTG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTCGCG GCGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TCGACTTTG TTTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCAGC ATTTGCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

m680.pep

```

1  MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

                                10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
                                10      20      30      40      50      60

                                70      80      90     100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXVMSTAMMCCSTLALVVFAATSTVSGAFMKSC
          |||||:|:||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      TLCLVLQKTITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
                                70      80      90     100     110     120

                                130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```

1090

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```
a680.seq
  1  ATGACGAAGG  GCAGTTCGGC  AATATCCAGC  CCCCgcgcgg  CGATATCGGT
51  GGCgACGAGG  ACGCGcAGGT  TGCCGTCTTT  GAAGGCGGTT  AGTGTTTCGA
101 GCCGGCTTTG  TTGGGAACGG  TCGCCGTGTA  TCGCCTGTGC  GGACAGGTTG
151 CGGCGCACCA  GTTCGCGCGT  TACGCGGTGC  ACGCTTTGTT  TGGTTTTGCA
201 GAACACGATG  ACCTGGTTCA  TATGCAAATC  GACAATCAGC  CGTTCGAGCA
251 GGTTCGCGTT  CTGAATGGTA  TCGACGCGCA  TGATGTGCTG  CTCGACGTTG
301 GCGTTGGTGG  TGTCTTGCCG  GGCGACTTCG  ACGGTTTCGG  GCgCGTTcAT
351 GAAGTCTTGC  GCCAGTTTGC  GTATCGGGGC  GGAGAAGGTG  GCGGAAAAGA
401 GCAGGGTTTG  GCGTTGGCGG  GGCAGCATCT  GCATAGTTTt  GCGGATGTcG
451 TCGATAAAAC  CCATATCCAG  CATAcGGTcG  GCTTCGTCCA  AAACGACGAT
501 TTCGACTTTG  TTCAAATGGA  TGTTTTTCTG  TTTcACGTGG  TCGAGCAGCC
551 GTCCGACGGT  GGCgACGAGC  ATTTcGCAGC  CGGCAGcGAG  GTcGGCGGtC
601 TGTTTGTTCA  TATTcATACC  GCCGAACAAG  ACGGTGTGGC  GCAGCGGCAG
651 GTTTTTGATG  TAG
```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```
a680.ppe
1  MTKGSSAISS  PRAAISVATR  TRRLPSLKAL  SVSSRLCWER  SPCACADRL
51  RRTSSRVTRS  TLCLVLQNTM  TWFICKSTIS  RSSRLRF*MV  STAMMCSTL
101 ALVVSSCAATS TVSGAFMKSC  ASLRIGAEKV  AEKSRVVRWR  GSICMILRMS
151 SIKPISSAIRS ASSKTTITSL  FKWMFFCFTW  SSSRPTVATT  ISQPARRSAV
201 CLSIFIPPNK  TVWRSGRFLM  *
```

m680/a680 98.6% identity in 220 aa overlap

	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCIACADRLRRTSSRVTRS					
	: :					
a680	MTKGSSAIISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCIACADRLRRTSSRVTRS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m680.pep	TLCLVLQNTMTWFIKSTISRSSRLRFXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC					
a680	TLCLVLQNTMTWFIKSTISRSSRLRFXMVSTAMMCCSTLALVVSAAATSTVSGAFMKSC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m680.pep	ASLRIGAEKVAEKSrvvRWRGSIcMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					
a680	ASLRIGAEKVAEKSrvvRWRGSIcMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					
	130	140	150	160	170	180
	190	200	210	220		
m680.pep	SSSRPTVATTISQPARRSAVCLSI FIPPNKTVWRSGRFLMX					
a680	SSSRPTVATTISQPARRSAVCLSI FIPPNKTVWRSGRFLMX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2243>:

g681.seq
1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacgg


```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGcgt cgaggttgGG GCGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TCGGGTTGG GAAAGCAGTG CGGCGGTTT AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GGTCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTGTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCGCGCGT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

g681.pep

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGLECA AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VFVGFVAEE TPAAVVFKNG GFAVKEADGP VLFGDVGVDG AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

m681.seq

```

1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GATCGTCCGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAG
751 CGCATTCGGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

m681.pep

```

1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDLECA AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VFVGLVAEE TPAAVVFKNG GFAVEEADGP VLFGDVGVDG TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTT RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPI
          |||||
g681      MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSI
          10      20      30      40      50      60

```

1092

	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGDLGECVFGKLPCAA					
	: : : : :					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
	: : : : :					
g681	FGLGKQCGGFRVGFVDVGEADDAEVVGVVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
	: : : : :					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
	: : : : :					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTGCTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCTGTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAATGCG TTCATTGCGG GAATACGTT. GGGGAAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTT CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  IITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VEVGLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	: : : : : :					
a681	IITPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVGDLGECVFGKLPCAA					
	: : : : :					
a681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGGFGMPSEGSVLRLPVGDLGECVFCQFPRAA					
	70	80	90	100	110	120

1093

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYGN	TLGXKLTDFTTIR	ALSADGGGLVVQ	CAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCGN	TXGGKLADFTTIL	ALSADGGGLVVQ	CAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTTCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVS YGKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. EMAMPSEP DWIQTAFCA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

	10	20	30	40	50	60
m682.pep	MRDFTVWVS	YGKWRKNWD	IRYCLLHLI	LSSTRLRKC	GRILSGICE	PFCLITPDL
	:	:				
g682	MRDFAVWVP	YGERRKNWD	IRYCLPHLIR	LSPTLRKC	GRILSGICE	PFCLITPDL
	10	20	30	40	50	60

	70	80	90	100	110
m682.pep	PILILIDY----	EMAMPSEP	DWIQTAF	CMAYGFI	RFPTRQSG
		:			
g682	PILILIDYICV	NDEIKMP	SEPDIQT	AFCMAGF	IRFPTRQ
	70	80	90	100	110

	120	130
m682.pep	YPTRSLPKS	KKAYGX
g682	YPTRSLPKS	KKAYGX
	120	130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```
a682.seq
1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA
```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```
a682.pep
1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGR ILSGICEPFCL
51  ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
```

m682/a682 80.6% identity in 129 aa overlap

	10	20	30	40	50	60
m682.pep	MRDFTVWVS	YGKWRKNWD	IRYCLLHLI	LSSTRLRKC	GRILSGICE	PFCLITPDL
a682	MRDFTVWVS	YGKWRKNWD	IRYCLLHLI	LSSTRLRKC	GRILSGICE	PFCLITPDL
	10	20	30	40	50	60

	70	80	90	100	110	120
m682.pep	PILILIDYEM	AMPSEP	DWIQTAF	CMAYGFI	RFPTRQSG	VVRISPRTG
	:		:		:	
a682	PILILIEY--	-----	YIRFPTDR	PILTRPTG	VVRISPRTG	FRYPTR
			70	80	90	100

	130
m682.pep	LPKSKKAYGX
a682	LPKSKKAYGX
	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```
g683.seq
1  ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTACT
51  CCTATTTTGC ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151 GACAGTGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTTCGCTAC AGTTATTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGTLTEKQYETVCGKKLX					
g683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTCCNAG ATAAAAAAGT
201 TGTTACCAAT CTAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVNTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVNTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGCGGCGGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTTCT
301	GCCTCACGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLEPIAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGGE	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAAL	QGLKQAAQOM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGCGGCGGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLEPIAAAL	SLAACGTVQS	TQYFVLPDSR	YIRPATQGGE	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQQM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	:					
g684	MRLFPIAAALTLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS					
	:					
g684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTDKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX					
	:					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPIAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQQM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	:					
a684	MRLFPIAAALTLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS					
	:					
a684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
|||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTAT TGGGCAGCCT GCGCCGTCCT GCCGGCCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgtcg ccgtgtAcga CtgggCGGCG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTGC AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCAATTA CCGCGGGGCC GGGTGCAGAA GCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGA CAACGGCAAT ATCCGCACCA
551 CGCGCGAGAA GCAGATGGAG ACCCTGTCCG GGATTTTCGG TAAGGAAGCG
601 CGCTGGCGCG AATTGAATGC GCAGATTGAC GCGCTGTTCC CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCC GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GGCACATCGC GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CCGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1   LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAAEKT VSAASQAAST PVATLTVPTA RGDVAVPKNP ERVAVYDWAA
101 LDTLTEPGVN VGATTAPVRV DYLPAPFDKA ATVGTLEFPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNGN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAFG TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFYIYEKN PGWIFIIDRT AAIQOEGPAA
301 VEVLNLAALVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGCGGCG AACGGTGGGG ACGCTGTTCC
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCAATTACC
451 GCGGGGCCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCTGG TACGGGCAAC AAGGTGTCGG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCGCG GGCAGCTGTG
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCATCGGG CAGGAAGGCG CGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCGT GCCCGAACT ACATTGTCG GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTAAGGAGGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m685.pep		LFCRIGNFAFCGVVSAGCLLNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
g685		LFCRIGNFAFCGVVSAGCLLNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT					
		10	20	30	40	50	60
		70	80	90	100	110	
m685.pep		VSAASASA-----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTGLGVNVGATTAPVRV					
g685		VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTLEPGVNVGATTAPVRV					
		70	80	90	100	110	120
		120	130	140	150	160	170
m685.pep		DYLQPAFDKAAATVGTLFEPDYEALHRYNPQLVITGGPGAEEAYEQLAKNATTIDLTVDNGN					
g685		DYLQPAFDKAAATVGTLFEPDCESLHRHPQFVITGGPGAEEAYEQLAKNATTIDLTVDNGN					
		130	140	150	160	170	180
		180	190	200	210	220	230
m685.pep		IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAFG					
g685		IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKGRGLVLSVTGNKVSAFG					
		190	200	210	220	230	240
		240	250	260	270	280	290
m685.pep		TQSRSLASWIHGDIGLPPVDES LRNEGHGQPVSF EYI KEKNPDWIFIIDRTAAIGQEGPAA					
g685		TQSRSLASWIHGDIGLPPVDES LRNEGHGQPVSF EYI KEKNPGWIFIIDRTAAIGQEGPAA					
		250	260	270	280	290	300
		300	310	320	330	340	350
m685.pep		VEVL DNALVRGTNAWK RKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAA GKXX					
g685		VEVL DNALVCGTNAWK RKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX					
		310	320	330	340	350	

1	TTGTTTTGCC	GTATCGGGAA	TTTTGCGTTT	TGCGGCGTGG	TTTCTGCAGG
51	TTGTTTGCTT	AATAATAAAC	ATTCTTATTC	GTATGCAAAG	GAACCGCACA
101	CCGTGAAACC	GCGTTTTTAT	TGGCGAGCCT	GCGCCGTCCT	GCTGACCGCC
151	TGTTCCGCCG	AACCTCGCGC	CGAAAAAACT	GTATCCGCCG	CATCCGCATC
201	TGCCGCCACA	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC	TTGTGCGCGA
251	AGAATCCCGA	ACGCTGCGCC	GTGTACAGAT	GGGCGGCGTT	GGATACGCTG
301	ACCGAATTGG	GTGTGAATGT	GGGCGCAACC	ACCGCGCCGG	TGCGCGTTCG
351	TTATTTGCGA	CCTGCATTTG	ACAAGGCGGC	AACGGTGGGG	ACGCTGTTCG
401	AGCCCGATTA	CGAAGCCCTG	CACCGCTACA	ATCTCAGCT	TGTCATTACC
451	GGCGGGCCGG	CGCGGCGAAG	GTATGAACAC	TTGGCGAAAA	ACGCGACCAC
501	CATAGATCTG	ACCGGTGGACA	ACGGCAATAT	CCGCACCAAG	GGCGAAAAAG
551	AGATGGAGAC	CTTGCGCGGG	ATTTTTCGGCA	AGGAAGCGCG	CGCGCGGGAA
601	TTGAAGGCGC	AGATTGACGC	GCTGTTCCGC	CAAACGCGCG	AAGCGGCCAA
651	AGGCCAAAGGA	CGCGGCTGTG	TGCTGTCCGT	TACGGGCAAC	AAGGTGTCCG
701	CCTTCGGCAC	GCAGTGCCTG	TGGGCAAGTT	GGATACACGG	CGCATCTCGG
751	CTACCGCTGT	TAGACGAATC	TTTACGCAAC	GAGGGGCACG	GGCAGCTGTG
801	TTCCTTCGAA	TACATCAAAG	AGAAAAACCC	CGATTGGATT	TTCATCATCG

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPTYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSFPGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685    98.9% identity in 355 aa overlap

      10      20      30      40      50      60
m685.pep    LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
a685         LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
      10      20      30      40      50      60

      70      80      90     100     110     120
m685.pep    VSAASASAATLTVPARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
a685         VSAASASAATLTVPARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m685.pep    PAFDKAATVGTLFEPTYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGNIRTS
a685         PAFDKAATVGTLFEPTYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGNIRTS
      130     140     150     160     170     180

      190     200     210     220     230     240
m685.pep    GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSFPGTQSR
a685         GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSFPGTQSR
      190     200     210     220     230     240

      250     260     270     280     290     300
m685.pep    LASWIHGDIGLPPVDESLRNEGHPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
a685         LASWIHGDIGLPPVDESLRNEGHPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
      250     260     270     280     290     300

      310     320     330     340     350
m685.pep    DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX
a685         DNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLIQAAEQLKEAFKAEPVAAGKEX
      310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTTCCTT GCCGCGCGGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCGTCCGCGG GGTATGTTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCCT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686>:

```
g686.pep (partial)
  1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

```
m686.seq.
  1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGGC TCAGCATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCCG CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTCGTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTTCATCAGA ATCGGAATGT GA
```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

```
m686.pep
  1 MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGSEGGSGAXX	XXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

```
a686.seq (partial)
  1 ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
 51 TGAAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGGTCAGCA TACTACCGGT
151 ATTGTGGAAG CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CCGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

1102

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51  IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep    LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
a686                NFSCRADDVFDDICSAVESFGGIARSVQLG
                        10      20      30

              70      80      90      100     110     120
m686.pep    AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686                AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                        40      50      60      70      80      90

              130     140     150     160
m686.pep    GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
a686                GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
                        100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GGCCTTGCCG CCCTGTTCCG
51  CCTTGCCGCG TCGACAGCA AAGTCCAAAC CAGCGTCCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTTCG GCTATTTTGT TCCGCACTGC GCCCGCCTcg
251 AACCTGTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCACGCct
351 cGCCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAa ACcgctTTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTGCGC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687>:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWQKE MLPLARLAAA VDMAAAESKD VANSIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGGKVL AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAAACTAT
151 ACCGTCTTGT CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTGCAACCTG
251 TTTTAAAGCA ACACGCCAAG TCTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAACCGGCC TTTGACGGCA AAAAAGTCCT

```

m687.pwp

a687.seq

a687.pgp

```

1      MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51     TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101    EHVVVQKEML  TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLOEPEV
151    LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201    GKYKVEFADT  ESGMNTLIDL ADKVEEREQA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N. meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRHLALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSKHLALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAJSFKDDMYLRTEHVWQKEMLTARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAJSFKDDMYLRTEHVWQKEMLTARLAAAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQELTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX					
a687	KMQELTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTTGCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCCTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAAEAL	RAKQNADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTTGCACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCCTGCAGTG
101	CCGAACGCGT	TTCAGTGTTT	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*.

```
m688/g688      90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep      VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQNELEPRVAA
              |||  |||||  |||||  |||||  |||||  |||||
g688           VLHXTSRFAQKGSFVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQNELEPRVAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTVYFENGVLVRTEG
              |||||  |||||  |||||  |||||  |||||  |||||
g688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTVYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
              |:|||||:  :||:|
g688           DALQNAAEALRAKQNADKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACGCG AACCTCGCGC CGTCGCCTCC CTCCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLTVYF ENGVLVRTEG NALQNAAEAL RVKQNADKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688      93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep      VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQNELEPRVAA
              |||||  |||||  |||||  |||||  |||||  |||||
a688           VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQNELEPRAVAS
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTVYFENGVLVRTEG
              |||||  |||||  |||||  |||||  |||||  |||||
a688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKDRSNLTVYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
              ::|||||:  :||:|
a688           NALQNAAEALRVKQNADKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCAT CGATGCCTAC CTGCCCAGCA
101 TTCCCGAAAT GCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTc ggtgcgatgg tgcgcgattA TTATTCGGA CGAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
451 GCACCCATGG TCGGCGCATT GTTGCAAGGA TTGGGCGGAT GCGGGCGCAT
501 TTTCTGTTTC ttggcGgcgT ATTCGCCGGT GTCGCCGGT TTGGTACAGT
551 ATTTCTTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCA GGATGTGTTC
601 GGGCTGGTGG CGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTCAGG CATTAGCTT CGGTTTCATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCAGT TACGCCGAC
751 CGGTACGCAT GGGTGTTCG ACTCAACATC ATCAGATGA TGTTCCTCAG
801 CCGCGTTACC GCGTGGCGG TTAAGCCGTA CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTT TGCTGCGCG TCGCGTGCCT
951 GATGTTTTC GTCGGTACGC AGGCGCTGTT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCG
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGCG GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAA CCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

g689.pep (partial)

```

1  ..SPPLPPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYYSR RKAQMFAFI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPV LVQYFLNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLETSFV YRQLYHVTPH
251 RYAWVFALNI ITMFFFSRV AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301 AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CTTCTGCCC ATTATCCTGA AATGAGCGAA AAATGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCC
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCCTTCGGAC AGGTGGTCGG
351 CGGTTGCGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTGT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCTT GCCCAAGCCC GCCGTGCGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTAG CTTCGGTTTC ATGTTTCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGTTACGCCT
901 CATCAATACG CTTGGGCGGT TCGACTCAAC ATCATCACGA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGAT CCGCAAAGCA
1001 TCCTGTGTG GGGGATTGTC GTCCAGTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCGGTG TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTGCGTA CGCAGGGCTT GGTGCGTGCA AACACGCAAG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGCGAC GACGGTTCGG CAACCGTGAT GCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGGC TCTGCTCGCA TCGTGCCTGG

```


m689.pwp

ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

```

                                450      460
m689.pep    LWLCSHRAWKENGQSEYLYX
              |||||:|||| ::|
g689         LWLCSHKAWKENEKKRIL
              390      400

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

a689.seq

```

1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCGC GTTGTGCGG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCGGACG AGAATTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAAGTATGGG CGGTTTGTAT
201 GGCATGCTG GTTACGCTGA TCCGTTTTC CATCGATGCC TACCTGCCCC
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTGTGTTAT GTTCGGCAGC GCGTTTCGGAC AGGTGGTCGG
351 CGGTTCCGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGCCCGTCTA CTGCGTTGCC GTTGCCGCCA TCGTATTGCG TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGGT CCGGCATGAC
501 TGTGGTTCAT CCGGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCCAGAT GTTGGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTGCGT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCGTCGCGC GCAAAATCGG CAGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCGC
801 GATGGGTATC CTGTTTTCCT AGGCATTCAG CTTCGGTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTTACCA CGTTACGCCG
901 CACCAAGTAC CTTGGGCGTT TGCATCAAC ATCATCAGC TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGCTT GGTGCGTGCA AACACGCAGG
1151 CGTGTGTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGCGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGTCG TCTGCTCGCA TCGTGGCTGG
1351 AAAGAAAACG GCAAAGCGA ATACCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

a689.pep

```

1   LLIHYIVPVR PVLPGLLPVCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIIV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYHVTP
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLEFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTAATSCGIA LLWLCSHRAW
451 KENGQSEYL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHYIVPVRPVLPGLLPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHYIVPVRPVLPGLLPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS					
a689	SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIIVFLAAYSLVLLGLVQYFLPKP					
a689	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIIVFLAAYSLVLLGLVQYFLPKP					
	190	200	210	220	230	240
m689.pep						
a689						

1109

```

a689      |||||||
          GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||||
a689      AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          |||||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
          |||||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLWLCSHRAWKENGQSEY LX
          |||||||
a689      DGSATVMAATMTASTSCGIALLWLCSHRAWKENGQSEY LX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTGCAA
151 CCGCCGCGAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCCGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGC GgCAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATctgCctat
601 TTgaaccgGC ACAaCaacGG ACTTggcgGC AATTTC CAAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1  MKNKTSSLPL WLAAILLAAR SPSKEDKTK NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR QGGEPEPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq..

```

1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGCTTC GTCTCCGCG TCATCAGCTC CTTCCTCAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGCTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCAGCATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCCGC TATCTGAAAA TACACGGAGA AATGCTTGA AACAATCAC
701 TCTTCGGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQAIEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEETPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPKPFELD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

          10      20      30      40      50      60
m690.pep      MKNKTSSLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPSQTDLQPTASAPDNVK
g690           MKNKTSSLPWLAAIMLAARSPSKEDKTKENGASAASSASSASSQTDLQPAASAPDNVK
          10      20      30      40      50      60

          70      80      90     100     110     120
m690.pep      QAESAPPSNCTSLHPATGIDDLMQQAIEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
g690           QAESAPLNCTGLHPAAGIGDLIQQAIEHIDSDCLFALSHHELETRFGLPGGGYDNIQRL
          70      80      90     100     110     120

          130     140     150     160     170     180
m690.pep      LFPDIRPEDPDYHQIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
g690           LFPDIRPEDPDYHQIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
          130     140     150     160     170     180

          190     200     210     220     230     240
m690.pep      GQGEETPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
g690           GQGEETPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
          190     200     210     220     230     240

          250     260     270     279
m690.pep      ERNPKPFELDIHFDENGKITRIVVYEKNIYFNPNTGRIX
g690           ERNPKPFELDIHFDENGKITRIVVYEKNIY
          250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCCTC GTCCACGGCA TCCGCGCTT CGTCTCCGC GCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCCG TCAAATTGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAAGTGGG AACCCGTTTC GGCTTACCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCCA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGAATATG AAGACTTGCG TTACGGAAG
451 CGCAGCATCA GCGGCGAGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCAGCGGTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCGCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

1111

```

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
751 TTTTATAGACA TCCATTTTGA CGAAATGGC AAAATCACGC GTATTGTCGT
801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

```

1  MKNKTSSLLL WLAAMMLTAC SPSKEDKTKE NGASAASSTA SAASSAPQT
51  DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRQGGEPEK RTRYFEVSAT
201 PAYSSRHNNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50	
m690.pep	MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLOPTASAPD				
a690	MKNKTSSLLLWLAAMMLTACSPSKEDKTKENGASAASSTASAASSAPQ	TDLQPAASAPD				
	10	20	30	40	50	60
	60	70	80	90	100	110
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI					
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI					
	70	80	90	100	110	120
	120	130	140	150	160	170
m690.pep	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ					
a690	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m690.pep	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLLENQSLFRL					
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHGEMLLENQSLFRL					
	190	200	210	220	230	240
	240	250	260	270	279	
m690.pep	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX					
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRRX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

```

1  GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG
151 ACACAGGGTC AGCACAAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
201 GCGCGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

```

1  VLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQGQHNLRLK IRAAFKMGAD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
  1 GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTTT
  51 AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
 151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCAACG CCTTCAAAAT
 201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGGTCTGT CGTCGAAATC ATTTCTCTCG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTTGGCGT
 351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
  1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
  51 TQSQHNLRLK IRTAFKMAGD RARLKVMHSE HSRRRSVVEI ISSDVFNENE
 101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691    97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep    VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQSQHNLRLK
              |||||
g691         VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQGOHNLRLK
              |||||

      70      80      90     100     110     120
m691.pep    IRTAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNENEARDYVESRYLSGMDFAVDEL
              |||||
g691         IRAAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNENEARDYVESRYHSMDFAVDEL
              |||||

      70      80      90     100     110     120

      130     140
m691.pep    EIQRFFHILTPQQQMWLSSCLKX
              |||||
g691         EIQRFFHILTPQQQMWLSSCLKX
              |||||

      130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
  1 GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTTT
  51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
 151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GTCGGTCTGT CGTCGAAATC ATTTCTCTCG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTTGGCGT
 351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
  1 VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
  51 TQGOHNLRLK IRAAFKMAGD RARLKVMHSE HSRRRSVVEI ISSDVFNENE
 101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASF	LSMALLSCQLSHAAT	AYIPND	FQPNCDIRRLGLT	QSQHNELRK	
a691	VPLXAPCRFAKPAASF	LSMALLSCQLSHAAT	AYIPLND	FQPNCDIRRLGLT	QSQHNELRK	
	10	20	30	40	50	60
	70	80	90	100	110	120
m691.pep	IRTA	FKMAGDRARLK	VMHSEHSRRRS	VVEIISSD	VFN	RNEARDYVES
	:					
a691	IRAA	FKMAGDRARLK	VMHSEHSRRRS	VVEIISSD	VFN	RNEARDYVES
	70	80	90	100	110	120
	130	140				
m691.pep	EIQH	RRFFHILTP	QQQQMWLSS	CLKX		
a691	EIQH	RRFFHILTP	QQQQMWLSS	CLKX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2309>

```
g692.seq
1   GTATCGCACA CACGCTGTCTG CTGTTTCGGAA TCGAtacGCC GGATTtGGCG
51  GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTCTA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGCCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGCGGGT TTTgacGGCA GACCAGTTGA CATAGGCAA
301 GCTCGGCTCT TGGAAACAGG CTTCCGGTCAG CTTCAATGCC CTGCTTTATG
351 CGTAGTTGCC GTTGACGACG CTCGCGCGCG CGTCGCGCGC
401 AGTTGTGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCGC
451 GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCCGCTT TFGAGTTTGA
501 TCCAACCCAG TTCGTTTCAG ATCACCAAGG CGCGTCGCAA GTTGGAcggg
551 TcgtTGGGCG CGGATACGGT GTCGCGCTCT TTGACTTTCT CCAGCGATT
601 CAGTTTGCCC GGATACAGTC CCAAAGGCGC GGTCGGCAT TGAAGGCTT
651 CGGTGATGTC CAGGTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTTG
701 TGTGGGAAGA CGTTGATGTC CAACTCGCCC TCCGCTAATG CCAGATTTCG
751 GCGCACATAC TCggTAAATT cgacctATT gacgGTGTAg cCTTTTTTCT
801 CCAGCTCGGc tTGATTTTGT TCTTTGACCA TATcgcgaa gtcgccacg
851 gTCGTGCCGA agacgaTTT TTTTTTCGcC GcgcCGTTAT CGGCAGAAGG
901 GGCGCGGgca gagcgtgcGG GCGCGCTGTC TTTTtgaccg ccgCAGGCTG
951 CGAGGATgca GCGGAGtgcg gcggcggaaa ggGTTTTTGA GAAGGTTTTc
1001 atATTTTCTc ctga
```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

g692.pep

1	VSHTRCRCSE	SIRRIWRNGR	EWRIKGQKCR	LNTDAVQTAS	FYTTALFGCA
51	FIPCEGRVFEA	LEAFVRVGFE	RVGVGIGLYV	FKPLAVFVGG	FDGPRVPDIGN
101	ARLLEQGFQ	LHAAAYGVVA	VDDGKIHVGA	AAQLCGFKL	DDFDVQVQR
151	DVGFGCGQRI	DAVFEDPTQ	FVQHHQGACE	VGRVVGRRGY	GAVFDFQRF
201	QFARIQSQR	GRHLEFGDV	QVVFEEIVK	IGVLEDDVDV	QLALRQCQIR
251	AHIVKGFQDF	DGVAFFLQLG	LDLFFDHHIAE	VAHGRAEDDF	FFRRAVIGRR
301	GGRGCGKRA	FLTAAGCEDE	RECGGGKFE	EGHFIS*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```
m692.seq
1 GTGTTGCACA CGCTTTGTCG CTGTTCGGAA TCGATACGCC GGATTCTGGCG
51 GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGCTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCG
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTGCAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TCTCGGCGGT TTGACCGGA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGACAGGG CTTCGGTGAG CTTCATGCCG CTGCTTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGG
```

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGGCGAA GTTGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAAGACTT
651 CCGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTTT TTGACGCGCG CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTCCTATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1 VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVLG
151 DVRFGCGQRI DAVFEFDPQTQ FVEHHQDAGE VGRVVGGRYG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDFFDHIAE VADGRAEDDF FFRRRAVVG
301 RSGCGGRAVFLTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

```

m692/g692 91.1% identity in 338 aa overlap

      10      20      30      40      50      60
m692.pep VLHTLCRCSESIRRIIRNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
g692      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      10      20      30      40      50      60
      70      80      90     100     110     120
m692.pep LEAFVRVGFERVGVIGLGYVFKPLAVFVGFDGRPVDIGKARFLEQGFQ LHAAYGVVA
g692      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      70      80      90     100     110     120
      130     140     150     160     170     180
m692.pep VDDGKIHVGAATRQLRGFKLDDFDVQVLGDVRFVGGQRI DAVFEFDPQTQ FVEHHQDAGE
g692      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      130     140     150     160     170     180
      190     200     210     220     230     240
m692.pep VGRVVGGRYGAAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
g692      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      190     200     210     220     230     240
      250     260     270     280     290
m692.pep QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRRRAVVG--
g692      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      250     260     270     280     290     300
      300     310     320     330
m692.pep GGRSGCGGRAVFLTAAGGEDER ECGGKGFEF GFHIFSX
g692      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      310     320     330
g692      GGGRGCG-RAVFLTAAGCEDER ECGGKGFEF GFHIFSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1 GTGTTGCACA CGCTTTGTCTG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```



```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTTCGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCG GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGGTGAG CCTTTTTTCT
801 CCAGCTCGGG TTGATTTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGCGCA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1 VLHTLCRCSE SIRRI RRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGFV RVGVIGLVYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFQCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGGRYG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVGGG
301 RSCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSESIRRI RRNGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA			
a692	VLHTLCRCSESIRRI RRNGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGFERVGVIGLVYVFKPLAVFVGG	FDGRPVDIGKARFLEQGFQ	LHAAYGVVA			
a692	LEAFVRVGFERVGVIGLVYVFKPLAVFVGG	FDGRPVDIGKARFLEQGFQ	LHAAYGVVA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHVGAATRQLRGFKLDDFDV	FQVLGDVRFQCGQRI	DAVFEFDPTQ	FVEHHQDAGE		
a692	VDDGKIHVGAATRQLRGFKLDDFDV	FQVLGDVRFQCGQRI	DAVFEFDPTQ	FVEHHQDAGE		
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVGGRYGAAVDFDFQRFQLARVQS	QRRGRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
a692	VGRVVGGRYGAAVDFDFQRFQLARVQS	QRRGRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
	190	200	210	220	230	240
	250	260	270	280	290	300
m692.pep	QLALSQCQIRAYIVGKLDQFDGVAFFL	QLGLDLFFDHIAE	VADGRAEDDF	FFRAVVGGG		
a692	QLALSQCQIRAYIVGKLDQFDGVAFFL	QLGLDLFFDHIAE	VADGRAEDDF	FFRAVVGGG		
	250	260	270	280	290	300
	310	320	330			
m692.pep	RSGCGGRAVFLTAAGGEDERE	CGGKGFEFGFHIFS				
a692	RSGCGGRAVFLTAAGGEDERE	CGGKGFEFGFHIFS				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.seq
1   TCGGCATTG  TGTTGCCAA  ACATCCGATG  CCTGCGTTAA  CGCCTGCGTC
51  AACGTTTGA  CAAATCGGGT  TTGGTTTCGC  CCTCGCGGCG  CAGCTCCTTG
101 GGCAGGACGA  ACACGATGCT  TTCTTCCGCG  CCCCCCCTT  CGCGCACGGT
151 TTCATGCCCC  CATCCGCGTA  TGGTTGCCAA  TACTTCCCGC  ACCAACACTT
201 CGGGCGCGGA  CGCGCCTGCC  GTTACGCCGA  CTTTGCTTTT  GCCTTCAAAC
251 CACGTGCGTT  GCaggTAGGA  CGCGTTGTCC  ACCATATACG  CATCGATTCC
301 GCGCGATGCC  GCCACTTCGC  GCAGGCGGTT  GCTGTTGGAC  GAATTGGGCG
351 AACCAGCAC  AATCACGATG  TCGCACTGTT  CCGCCAGCTC  TTGACGGCG
401 GTTTGCCGGT  TGGTCGTCCG  ATAGCAGATG  TCTTCCTTGT  GCGGATTGCG
451 GATATTGGGG  AAACGCGCGT  TCAGCGCGGC  GATGATGTCT  TTGGTTTCAT
501 CGACCGAGAG  CGTGGTTTGG  CTGACATAGG  CGAGTTTGTC  GGGGTTTCTG
551 ACTTCGAGTT  TTGCCACATC  TCCGACCGTT  TCGACCAAAA  GCATTTTGCC
601 CCGGTGTCGG  TGCCCATCG  TGCCTTCGAC  CTCGGCGTGC  CCCTTATGCC
651 CGATCATGAT  GATTTACAG  TCTTGGGCAT  CCAGTCGGGC  GACTTCCTTA
701 TGCACCTTCG  TCACCGAGCG  GCAAGTCGCA  TCAAATACCC  GGAAACCGCG
751 CTCCGCCGCT  TCCTGCTGCA  CCGCCTTCGA  TACGCCGTGT  GCCGAATAAA
801 CCAGTGTCCG  CGCGGCGGC  ACTTCCGCCA  AGTCTTCGAT  AAACACCGCG
851 CCTTTTTCGC  GCAGGTTGTC  CACGACGAAT  TTGTTGTGGA  CGACTTCGTG
901 GCGACATAA  ACCGGCGCGC  CGAATTCTTC  CAAAGCACGT  TCGACAATAC
951 TGATTGCCCG  ATCCACACCG  GCGCAGAAAG  CGCGCGGATT  GGCAAGGATG
1001 ATGGTTTTTC  CGTTCATAAG  TTTTGCATTC  CGTGTTTACA  CGGCATTAC
1051 GTTTTTTTGC  TNNATCTTTG  CGATGGACGA  TATTGTCAAG  CACCGCCAAC
1101 ACCGCACCGA  CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694 >:

```
g694.pep (partial)
1   SAEVLPHKPM  PALTPASTFA  QIGFGFALAA  QLLGQDEHDA  FFRAPPFHAG
51  FMPPSAYGCO  YFPQHFGRG  RACRYADFAF  AFKPRALQVG  RVVHHIRIDS
101 ARCRHFAQAV  AVGRIGRTDH  NHDVALFRQL  FDGGLPVGRR  IADVLVRIA
151 DIGETRVQRG  DDVFGFIDRE  RGLADIGEFV  GVSDFEFCHI  SDRFDQKHFA
201 RCKLPHRAFD  LGVPLMPDHD  DFTVLGIQSG  DFLMHFRHQR  ASRIKYPETA
251 LRRFLHLRLR  YAVCRINQCR  ARRHFRQVFD  KHRAFFAQVV  HDEFVDDFV
301 AHINRRAEFF  QSTFDNTDCP  IHTGAEAARI  GKDDGFSVHK  FCIPCSGDIH
351 VFLLXLCDGR  YQAPPTPHR  RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.seq
1   TTGGTTTCCG  CATCCGGCAC  ACGGCAAAAA  TGCCGTCTGA  AGCCTGTTCA
51  GACGGCATTT  GTGTTGCCCA  AACATTCAAC  GCCTGCGTCA  ACGTTTGCAC
101 AAATCGGGTT  TGGTTTCGCC  CTCGCGGCGC  AACTCTTTGG  GCAGGACGAA
151 CACAATGCTT  TCTTCCGCAC  CCTCGCCTTC  GCGTACGGTT  TCGTGCCCCC
201 ATCCGCGTAT  GGTGTCAGT  ACTTCCCGCA  CCAACACTTC  GGGCGCGGAC
251 GCGCCTGCCG  TTACGCCGAC  TTTGTTTTTG  CCCTCAAACC  ATGCGCGTTG
301 CAGGTAGCCT  GCATTATCCA  CCATATACGC  ATCGATTCCG  CGCGATGCCG
351 CCAGTTCGCG  CAAGCGGTTG  CTGTTGGACG  AATTGGGCGA  ACCGACCACA
401 ATCACGATGT  CGCACTGTTC  TGCCAACTCT  TTGACGGCGG  TTTGCCGGTT
451 GGTCGTGCGA  TAGCAGATAT  CTTCTTGTG  CGGATTGCGG  ATATTGGGGA
501 AACGCGCGTT  CAGCGCGGCG  ATGATGTCTT  TGGTTTCATC  GACCGAGAGC
551 GTGGTTTGGC  TGACATAGGC  GAGTTTGTCT  GGGTTTCTGA  CTTCGAGTTT
601 TGCCACATCT  CCGACCGTTT  CGACCAAAAG  CATTTTGCCC  GGCACAAGCT
651 GCCCCATCGT  TCCTTCGACC  TCGACGTGCC  CTTATGCCC  GATCATGATG
701 ATTCACAGT  CTTGGGCATC  CAGTCGGGCG  ACTTCCTTAT  GCACTTTCTG
751 CACCAGCGGG  CAAGTCGCAT  CAAACACGCG  GAAACCGCG  TCCGCCGCTT
801 CTTGCCGCGC  CGCCTTCGAT  ACGCCGTGTG  CCGAATAAAC  CAGTGTGCGC
851 CCCGGCGGCA  CTTCCGCCAA  GTCTTCAATA  AACACCGCAC  CTTTTTCACG
901 CAGGTGTGCC  ACGACGAATT  TGTGTGAAC  GACTTCGTGG  CGCACATAAA
951 TCGGCGCGCC  GAACCTTTCC  AAAGCACGTT  CGACAATACT  GATTGCCCGA
1001 TCCACACCAG  CGCAGAAGCC  GCGCGGATTG  GCAAGGATGA  TGGTTTTCTC
1051 GTTCATAAGC  CCGGTATTTT  GTTTTCAGAC  GGCATCAATA  TTTTCTTCT
1101 TGGGTTTAC  GGTGGACGAT  GTTGTCCAAC  ACCGCCAACA  CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1   LVSASGTROK  CRLKPVQTAF  VLPKHSTPAS  TFAQIGFGFA  LAAQLFGQDE
51  HNAFFRTLAF  AYGFVPPSAY  GCQYFPHQHF  GRGRACRYAD  FVFALKPCAL
101 QVACIIHHIR  IDSARCRHFA  QAVAVGRIGR  TDHNDHVALF  CQLFDGGLPV
```

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

	10	20	30	40	50
m694.pep	LVSASGTRQK	CRLKPVQTAFVLPKHS----	TPASTFAQIGFGFALAAQLFGQDEHNAFFR		
		:		:	
g694		SAFVLPKHMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR			
		10	20	30	40
	60	70	80	90	100
m694.pep	TLAFAYGVFP	PSAYGCGYFPHQHFG	RGRACRYADVFAL	KPCALQVACII	HHIRIDSARC
	:	:			: :
g694	APPF	AHGFMP	PSAYGCGYFPHQHFG	RGRACRYADFAFA	KPRALQVGRVVHHIRIDSARC
	50	60	70	80	90
					100
	120	130	140	150	160
m694.pep	RHFAQAVAVGR	IGRTDHNHDVALFC	QLFDGGLPVGRRI	ADIFLVRIADIG	ETRVQRGDDV
				:	
g694	RHFAQAVAVGR	IGRTDHNHDVALFR	QLFDGGLPVGRRI	ADVFLVRIADIG	ETRVQRGDDV
	110	120	130	140	150
					160
	180	190	200	210	220
m694.pep	FGFIDRERGLA	DIGEFVGVSDFE	FCHISRDFDQKH	FARRKLPHRS	FDLDVPLMPDHDDFT
g694	FGFIDRERGLA	DIGEFVGVSDFE	FCHISRDFDQKH	FARCKLPHRA	FDLGVPLMPDHDDFT
	170	180	190	200	210
					220
	240	250	260	270	280
m694.pep	VLGIQSGDFLM	HFRHQRASRIKHA	ETALRRFLPHRL	RYAVCRINQCR	RARRHFRQVFNKHR
					:
g694	VLGIQSGDFLM	HFRHQRASRIKYP	ETALRRFLHLRL	RYAVCRINQCR	RARRHFRQVFDKHR
	230	240	250	260	270
					280
	300	310	320	330	340
m694.pep	TFFTQVVHDE	FVVNDFVAHINRA	ELFQSTFDNTDC	PIHTSAEAA	RIGKDDGFLVHKPGI
	: :				
g694	AFFAQVVHDE	FVVDDFVAHINRA	EELFQSTFDNTDC	PIHTGAEAA	RIGKDDGFSVHKFCI
	290	300	310	320	330
					340
	360	370	380		
m694.pep	SFSDGINIFLL	GFYGGRC	PTPPTPHRRRX		
	:				
g694	PCSDGIHVFL	XXLCDGRY	CQAPPTPHRRRX		
	350	360	370		

a694.seq

1	TTGGTTTCGG	CATCCGGCAC	ACGGCAAAAA	TGCCGTCTGA	AGCCTGTTCA
51	GACGGCATT	GTGTTGCCCA	AACATTCAAC	GCCTGCGTGA	ACGTTTGAC
101	AAATCGGGT	TGGTTTCGCC	CTCGCGGCG	AACTCTTTGG	CGAGGACGAA
151	CACAATGCTT	CTTCCGCAC	CCTCGCGTTC	CGGTACGGT	TGTCGCCCC
201	ATCCCGGTAT	GGTTGCCGAT	ACTTCCCGCA	CCAACACTTC	GGGCGCGGAC
251	CGCGCTGCCG	TTACGCCGAC	TTGTTTTTGG	CCCTCAAACC	ATGCGCGGTG
301	CAGGTAGCCT	GCATTATCCA	CCATATACGC	ATGCATTCCG	CGCGATGCCG
351	CCACTTTCGG	CAAGCGGTTG	CTGTTGGACG	AATTGGGCGA	ACCGACCACA
401	ATACCATGAT	CGCACTGTTC	TGCCAACTCT	TTGACGGCGG	TTTGCCGGTT
451	GGTCGTCGCA	TAGCAGATAT	TTCCCTTGTG	CGGATTCCGG	ATATTGGGGA
501	AACGCGCGTT	CAGCGCGGCG	ATGATGTCTT	TGTTTTCATC	GACCGAGAGC
551	TGGTTTTCGC	TGACATAGGC	GAGTTTGTGC	GGGTTTCTGA	CTTCGAGTTT
601	GTGCCACATC	CCGACCGTTT	CGACCAAAAG	CAGTTTGCCC	GGCGCAAGCT
651	GCCCCATCGT	TCCTTCGACC	TCGACGTGCC	CCTTATGCCC	GATCATGATG

1118

```

701 ATTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTC AACCGCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRIADI FLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVVD FVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

	10	20	30	40	50	60
m694.pep	LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
a694	LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m694.pep	AYGFVPPSAYGCQYFPHQHFGRGRACRYADVFALKPCALQVACIIHHIRIDSARCRHFA					
a694	AYGFVPPSAYGCQYFPHQHFGRGRACRYADVFALKPCALQVACIIHHIRIDSARCRHFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m694.pep	QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRIADIFLVRIADIGETRVQRGDDVFGFI					
a694	QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRIADIFLVRIADIGETRVQRGDDVFGFI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m694.pep	DRERGLADIGEFVGVSDFEFCHISDRFDQKHFARRKLPHRSFDLDVPLMPDHDDFTVLGI					
a694	DRERGLADIGEFVGVSDFEFCHISDRFDQKHFARRKLPHRSFDLDVPLMPDHDDFTVLGI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m694.pep	QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT					
a694	QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m694.pep	QVVHDEFVVD FVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD					
a694	QVVHDEFVVD FVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD					
	310	320	330	340	350	360
	370	380				
m694.pep	GINIFLLGFYGGRCCTPPTPHRRRX					
a694	GINIFLLGFYGGRCCTPPTPHRRRX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACCGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATT CAATCAAAAC CTGCCGAACG ATACGCCGAT
151 TGTCCCATC ACCCTGCCCG TCGGCGACGG TTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTTC CCGTTCCGG AGGGCAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGACTATC TGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCCCTCCG GCAGGACATA CGTCCAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTAATACCG AAGGCGGCAG CGCATCCGCA CATAACGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGTTTTCTG CCGCAGCCGC CTGTGTAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCCA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1  LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCQNSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVPEGSRTTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTRYGK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACCG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCCGCATCC TCAAAGATT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTTC CCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGACTATC TGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCCTCCG GCAGGGCATA CGTCCAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CCGTTGAAA GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCCA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVELNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

1120

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRHQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
g695	LPQTRPARRHHRHQYFVERKGDARSGFXCAAQCONSQRQFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m695.pep	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIYPVPVPTLQDR					
g695	FDPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTemptQENASDGIYPVPVPTLQDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDGRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDGRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m695.pep	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGIAQRSMYLLQSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAASLLKGADGGDGGGIAQRSMYLLQSRARMGNCS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA					
	250	260	270	280	290	300
m695.pep	AVRKRX					
g695	AVRKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCCTCAAG	CTGTGCCGCG	AAGGCGGCAT	CATTGCCATC	GACAATATTT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCCGATGC	GCCGCCCAGC
101	GTCGGCATCC	TCAAAGATTT	TAATCAAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCTTG	CTTCTGAAAA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTGGCTG	TCCGTATCCG
251	CCGCCTGTT	TCCCCCTGTT	TCCCGCAATA	TTCAGGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCGGACGCT	ATTCCCTATC	CCGTTCCAC
351	TCTGCAAGAC	CGTTTGATT	ATCTGGAAGG	CACACTCGTC	CGCCTGTCGA
401	ACGAAGTGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCTT	CCAGCAGGGC	ATACGTCCAA	AAACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAAGGCGG	CAGCGCATCC	GCACATACCG
551	TCGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCCTGTTG	AAAGGCGCGG	ACGGAGGCGA
651	CGGCGGCAGC	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTATCG	AAATCGGAGG	GCGTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAATCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGCC
851	GCAGCCTGAT	ACAGACCTAT	CCCGGCAGCC	CGGCGGCAAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRQYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIWL	SVSAACSSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGTLV	RLSNEVETLN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQQKDIAR	ATWRSLIQTY	PGSPAARKRAA
301	AAVRKR*				

Computer analysis of this amino acid sequence gave the following results:

1121

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAPHRPHHPARRRR					
a695	LPQACPARRHCHHRQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	
m695.pep	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT---EMSTRENASDGIPYPVPTL					
a695	FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIPYPVPTL					
	70	80	90	100	110	
	120	130	140	150	160	170
m695.pep	QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDDRKLKEHYLNTEGGS					
a695	QDRLDYLEGTLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDDRKLKEHYLNTEGGS					
	120	130	140	150	160	170
	180	190	200	210	220	230
m695.pep	ASAHTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSAQRSMYLLQSRARMGN					
a695	ASAHTVETAQNLYNQALKHYKSGRFSAAASLLKGADGGDGGGSAQRSMYLLQSRARMGN					
	180	190	200	210	220	230
	240	250	260	270	280	290
m695.pep	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAR					
a695	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAR					
	240	250	260	270	280	290
	300					
m695.pep	AAAAVRKRXX					
a695	AAAAVRKRXX					
	300					

The following partial DNA sequence was identified in *N. gonorrhoeae*

g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:

g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

m696.seq

1	TTGGGTTGCC	GGCAGGCGGC	ATCCCATCAT	TTTGGCCAAG	GCAACAAATT
51	ATTTGGCGGC	ATCTTTTCATT	TTGTCTGCCG	CTTCTGAGT	CGCGTCGGCA
101	GCTTTGTTCA	AAGTATCTTT	AGCTGCTTCA	GTTACAGCTT	CTTTGGCTTC
151	AGTTACAGCT	TCCTCGGCAC	TTGCCTTTGC	ATCAGCCGCA	GCATCTTTGA
201	CTTGGTCTTT	CGCTTCTTCG	ACGGCAGAAG	CGGCAGACTC	GGCGGCAGAA
251	GCCGCACTGT	CTTAAACATC	GGACTCAACG	GCTTGAACCG	CTTCCTTAAC
301	CTCCTGTTTG	GCTTCTTGCG	AACAAGCTGC	CAAGGCAGCC	GCCATCATTG
351	CGGCAATCAA	TAA			

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

m696.pep

1	LGCRQAASHH	FCQGNKLFGG	IFHFVCRFLS	RVGSFVQSIF	SCFSYSFFGF
51	SYSFLGTCLC	ISRSIFDLVF	RFFDGRSGRL	GGRSRSVFNI	GLNGLNRFLN
101	LLFGFLRTSC	QGSRRHHCNQ	*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

a696.seq

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```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTTCATT TTGTCTGCCG CTTCCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

          10      20      30      40      50      60
m696.pep    LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGF
a696         LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGF
          10      20      30      40      50      60

          70      80      90     100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRSVFNI GLNGLNRFLNLLFGFLRTSCQGS
a696         ISRSIFDLVFRFFDGRSGRLGGRSRSVFNI GLNGLNRFLNLLFGFLRTSCQGS
          70      80      90     100     110     120

m696.pep    X
            |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTGC
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTC CTTAACCAGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTAATGACCG AGGCTTACCG
651 GCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC GGATGCGGCG
751 GTGGGGTTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGCGGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSLMTLFSV LVPMFAGFEI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKKGKVS
101 VGVSGSVRQL GCVLLGEVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```


m700.seq

1	ATGGACAGCC	TGATGACGTT	GCTTTCGGTA	TTGATACCGA	TGTTTGCCGG
51	ATTTTTTATC	CGTGTGCCCA	AGCCTTACCT	GCCCCGCTTG	GATAAAGGTGC
101	TATCGGTCTT	GGTGTATGCT	GTGCTGCTGC	TGATCGGCGT	CTCGTTGTCTG
151	CGCGTGGAGG	ATTTGGGTTC	GCGGTTGGAC	GATATGGCGT	TGACGGTTCT
201	TGGGCTGTTT	GTTTGACGG	TCGGGGCGAA	CCTGCTTGCT	TTGCGAGTGT
251	TGGGAAAGTT	ATTCCCGTGG	CGGATAAAGG	GGAAGGGGAA	GGGCGCTTTCG
301	GTCGGCGTGT	CGGGCAGTGT	GGGGCAGCTC	GGATGCGTGC	TGCTCGGATT
351	TGCATTCCGC	AACTGATGC	GCGATATTTG	GATGCCGTCT	GAAAGCGCGG
401	GCATGTATTG	TCTGATGCTG	CTGGTGTTC	TCATCGGCGT	ACAGCTCAAA
451	AGCAGCGGCG	TATCGTTGCG	GCAGGTTTTG	GTCAACCGCA	GGGGTATTTCG
501	GTTGTCGGTC	TGGTTTATGC	TTTCATCTCT	TTCGGGCGGG	CTGCTGTTTG
551	CCGCATCGAC	AGACGTTGTG	TCGTGGACGA	AAGGTTTGCG	GATGGCTTCC
601	GGCTTCGGTT	GGTATTCCCT	CTCGGGTTTG	TCATGACCG	AGGCTTACGG
651	CGCGGTATGG	GGCAGCATCA	TGCTGCTGAA	GCATTTGGCA	CGAGAGCTGT
701	TTGCACTGGC	ATTTATCCCG	CTGCTGATGA	AGCGTTTTTC	AGATGCGGCG
751	GTGGGGGTTG	GCGGTGCGAC	CAGTATGGAT	TTTACATTGC	CCGTGATTCA
801	GGGTGCGGGC	GGTTTGAAG	TCGTGCCGGT	AGCGGTCAGC	TTCGGCGTGG
851	TGGTCAATAT	CGCCGCCCCG	TTTCTGATGG	TGGTGTTTTC	CGCTTTGGGT
901	TGA				

m700.pap

```

1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKGKGV
101 VGVSGSVGQL GCVLGFAFG KLMRDIWMP ESAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSLSGG LLFAASTDGV SWTKGLAMAS
201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSM FTLPVIQGAG GLEVPVAVS FGVVNIAAP FLMVVFSALG
301 *

```

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	: : :					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFLVCTVGANLLALAVLGKLFPPWRIKGKGKGVSVGVSGSVGQLGCVLLGFAFG					
g700	DMALTVLWLFLVCTVGANLLALAVLGKLSFWRIGGKGKGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSRLRQVLNRRGIRLSVWFMLSSLSGG					
			:			
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSRLRQVLLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
		:				
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
151 CGCGTGGAGG ATTTGGGTTT CCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAAGTATGTC GCGATATTG GATGCCGCTT GAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTCTG
501 GTTGTGCGTC TGGTTTATGC TTTTCTCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTGATGACCG AGGCTTACCG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTGGCA CGAGAGCTGT
701 TCGCGTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGTTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCTG
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTC TCCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSLV
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPP RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYLSGL VMTEAYGAVW GSIALNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKGKGVSVGVSGSVGQLGCVLLGFAG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSG	LVMTEAYGAVWGSIMLLNDLARELFALAFIP				
	: :					
a700	LLFAASADGVSWVKGLAMASGFGWYSLSG	LVMTEAYGAVWGSIALLLNDLARELFALAFIP				
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTL	LPVIQAGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG				
a700	LLMKRFPDAAVGVGGATSMDFTL	VIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG				
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACCG CTTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAACTTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCAACTC TTTCGCCGGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTTCG GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCTGTC GCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51  FKRFSSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GSTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACCG CTTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTTCG GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VVWAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSG SSTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVVWAPNSFASFKRFSSISQT					
	:					
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVVWAPNSFAGFKRFSSISHT					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
	:					
g701	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSISQST MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQST					
	: : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPPEAGLMVWVAPNSFASFKRFSISQST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
a701	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtg g cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TCGGCGCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAA t cgCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTCC cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVPPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACATG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALAR DSCSPGLMAKTAPASSTALSCSGLVTVPPAP					
	:					
g702	MPCSKASWISPGVATPGIRGMPLLRLPALAR DSCKPGLMAKTAPASSTALSCSGLVTVPPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS					
	:					
g702	MMALGISLAI RRMASPTGVRKVISRVGMPPSTRARDKST AVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVL RVEWGILLRW DRLX					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACATG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10 20 30 40 50 60

1128

```

m702.pep      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTPAP
|||||
a702          MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTPAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m702.pep      TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
|||||
a702          TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
              70      80      90      100     110     120

              130     140
m702.pep      RGVSLDISVLRVEWGILLRWDR LX
|||||
a702          RGVSLDISVLRVEWGILLRWDR LX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTTGGA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCCT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTctgTGc gcTGTgagg aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTVV AQEVKRLKD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTTGGA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYV VYYVNSREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703						
	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	:					
	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLDRSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	:					
	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYV					
g703	:					
	190	200	210	220	230	240
	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYV					
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703						
	250	260	270	280		
	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAGAACG AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
 351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
 551 TCTTGAAACA ATATTCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTC CGCCGCTTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGCGCA ATTTACGGCA ACGCCGTGA

1130

701 AAAACGGCGA TTTCTACGGC GTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

	10	20	30	40	50	60
m703.pep	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m703.pep	LENEVNTTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVNTTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m703.pep	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m703.pep	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
	250	260	270	280	289	
m703.pep	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
a703	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
 1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
 151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
 251 TGGAAACCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
 301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCC
 401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAATCAGG
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
 501 CAACCAAAAA GAACGCAAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
 551 TGGGGATGAT GCAGACGATG ATGTTGCGCG TGCCGACCTA CCTTACGGC
 601 GGCACATCG AACCAGATT CCGCAAATC CTCCATTGGG GCGGCTTTTT
 651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA


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801  TGC GGGG CAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851  TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901  GCCGCCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCC ATCATATGCC
951  CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTCGCACAT CGTCCGCCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCAATTAC
1401 CTGCCCCCTG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCTCG CCCAAACCAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCCTG CCGCGGCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GGCGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAAA CAGAAGGCGG
1851 CGGCAGCGCG GTTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCGC CCGCAGCGGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

a704.pep

```

1  MKKTCFHCGL DVPENLHLTV RYENEDRETCCAGCQAVAS IIDAGLGSYY
51  KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVMLGGI
101 TCAACVWLE QLLRTDGIV RIDLNYSTHR CRVWDDGKI RLSDDLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFYCAVPF YQGALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAELAEQYAS SFIFGELLTA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEAQRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLIMIGDI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep  MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90      100     110     120
m704.pep  ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVMLGGITCAACVWLEQQLLRTDGIV
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVMLGGITCAACVWLEQQLLRTDGIV

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1132

	70	80	90	100	110	120
	130	140	150	160	170	180
m704.pep	RIDLNYSTHRCRVVDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKERKQYIVRLA			
a704	RIDLNYSTHRCRVVDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKERKQYIVRLA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m704.pep	VAGLGMMQTMFALPTYLYGGDIE	PDFLQILHWGGFLMVL	PPVVFYCAVPFYQGALRDLKN			
a704	VAGLGMMQTMFALPTYLYGGDIE	PDFLQILHWGGFLMVL	PPVVFYCAVPFYQGALRDLKN			
	190	200	210	220	230	240
	250	260	270	280	290	300
m704.pep	RRVGMDTPITVAIIMTFIAGV	SLATNAGQGMFESIAML	LFLLGGRFMEHIARRKAGD			
a704	RRVGMDTPITVAIIMTFIAGV	SLATNAGQGMFESIAML	LFLLGGRFMEHIARRKAGD			
	250	260	270	280	290	300
	310	320	330	340	350	360
m704.pep	AAERLVKLIPAFCHHMPDYP	DTQETCEAAVVKLAGD	IVLVKPGETIPVDGTVLEGSSAV			
a704	AAERLVKLIPAFCHHMPDYP	DTQETCEAAVVKLAGD	IVLVKPGETIPVDGTVLEGSSAV			
	310	320	330	340	350	360
	370	380	390	400	410	420
m704.pep	NESMLTGESLPVAKMPSEK	VTAGTLNTQSPLIIRT	DRTGGGTRL	SHIVRL	LDRALAQKPR	
a704	NESMLTGESLPVAKMPSEK	VTAGTLNTQSPLIIRT	DRTGGGTRL	SHIVRL	LDRALAQKPR	
	370	380	390	400	410	420
	430	440	450	460	470	480
m704.pep	TAEALAEQYASSFIFGELL	LAVPVFIGWTL	YADAHTALWITVALL	VITCPCALSLATPTAL		
a704	TAEALAEQYASSFIFGELL	LAVPVFIGWTL	YADAHTALWITVALL	VITCPCALSLATPTAL		
	430	440	450	460	470	480
	490	500	510	520	530	540
m704.pep	AASTGTLAREGILIGGKQ	AIETLAQTTDII	FDKTGTLTQGKPAVRR	ISLLRGTD	EAFFVLA	
a704	AASTGTLAREGILIGGKQ	AIETLAQTTDII	FDKTGTLTQGKPAVRR	ISLLRGTD	EAFFVLA	
	490	500	510	520	530	540
	550	560	570	580	590	600
m704.pep	VAQALEQQSEHPLARAIL	NCRISDGSVPDIAIK	QRLNRIGEGVGAQLTVN	GETQVWALGR		
a704	VAQALEQQSEHPLARAIL	NCRISDGSVPDIAIK	QRLNRIGEGVGAQLTVN	GETQVWALGR		
	550	560	570	580	590	600
	610	620	630	640	650	660
m704.pep	ASYVAEISGKEPQTEGG	SAVYLGSGFQAVFY	LDPLKDSAAEAVRQ	LAGKNLTLHIL		
a704	ASYVAEISGKEPQTEGG	SAVYLGSGFQAVFY	LDPLKDSAAEAVRQ	LAGKNLTLHIL		
	610	620	630	640	650	660
	670	680	690	700	710	720
m704.pep	SGDRETAVAETARALG	VAHYRAQAMPEDK	LEYVKALQEGKKV	LMI	GDGINDAPVLAQAD	
a704	SGDRETAVAETARALG	VAHYRAQAMPEDK	LEYVKALQEGKKV	LMI	GDGINDAPVLAQAD	
	670	680	690	700	710	720
	730	740	750	760	770	780
m704.pep	VSAAAAGGTDIARDG	ADIVLLNEDLRTVA	HLLDQARRRHI	IRQNLIWAGAYNII	AVPLA	
a704	VSAAAAGGTDIARDG	ADIVLLNEDLRTVA	HLLDQARRRHI	IRQNLIWAGAYNII	AVPLA	
	730	740	750	760	770	780
	790	800	810	820		
m704.pep	VLGYVQPWIAALGMS	FSSSLAVLGNALRL	HKRGKMQSEKMPSEQX			
a704	VLGYVQPWIAALGMS	FSSSLAVLGNALRL	HKRGKMQSEKMPSEQX			
	790	800	810	820		


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g705      SGGIFQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||||
g705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           |||||
g705      AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGCTTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCG GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATGTGTGTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
651 TTGTAAAGTG CTGTTCTCTG TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLQV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep      10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||
m705          10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP

           70      80      90      100     110     120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
           |||||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
a705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||||
m705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
a705.pep  AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           |||||
m705      AAVVTVTELFRAVQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

```
g706.seq
1  ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51  CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GgAtgaCCGT CTTCGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cggTgGAacg taTGctcggt acggtcatcg
251 ggctgGGCGC GGGTTTGGgc gTTTTATGGC TGAACCAGCA TTAtttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccttatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCGCG
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGCAACCTT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCTT CATCAACGGC
901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

```
g706.pep
1  MNSSQRKRLS GRWLSYERY RHRRLIHAVR LGGTVLfATA LARLLHLQHG
51  EWIGMTVFVV LGMLQFQGAi YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVpML AGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLIg AAIaIAAAKL LPLKSTLMWR FMLADNLADc SKMIAEISNG
201 RRMTRERLEq NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

```
m706.seq
1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAAcG TATGCTCGCG ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGCAACCTT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGAG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

```
m706.pep
1  MNTSQRNRLV SRWLSYERY RYRRLIHAVR LGGAVLfATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGAi YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVpML AGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLIg AAIaIAAAKL LPLKSTLMWR FMLADNLADc SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING
```

1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQNRNRLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQRKRLSGRWLSYERYRHRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
m706.pep	70	80	90	100	110	120
g706	LGMLQFQGAIIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVTGTASALAGWAA					
	70	80	90	100	110	120
m706.pep	130	140	150	160	170	180
g706	VGKNGYVPMLAGLTMCMILIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
	130	140	150	160	170	180
m706.pep	190	200	210	220	230	240
g706	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
m706.pep	250	260	270	280	290	300
g706	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
	250	260	270	280	290	300
m706.pep	310	320	330	340	350	360
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
m706.pep	370					
g706	RQHLRQSLLE TREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CGGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTATATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
  1 MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFDSG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSCLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNQSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
m706	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG					
	10	20	30	40	50	60
a706.pep	70	80	90	100	110	120
	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHNLLFYLTVG					
m706	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHNLLFYLTVG					
	70	80	90	100	110	120
a706.pep	130	140	150	160	170	180
	VGKNGYVPM LAGLTMCLIGDNGSEWFDSGLMRAMNVLIGAAIAIAAAL					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAL					
	130	140	150	160	170	180
a706.pep	190	200	210	220	230	240
	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSCLA					
m706	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSCLA					
	190	200	210	220	230	240
a706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNQSEIRLLDRHFTLLQTD					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNQSEIRLLDRHFTLLQTD					
	250	260	270	280	290	300
a706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQR					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQR					
	310	320	330	340	350	360
a706.pep	370					
	RQHLRQSLLE TREHSX					
m706	RQHLRQSLLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1  ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGC GTGCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCCGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
551 CAGATATTC AATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGG AAAACGACCG GCAAATATCA AGGAAATGTC GCTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTTTGCGCG ACAAACGGA CTTGACTGAT GCCACGGTA CGGAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCAATTA TTCGGTGCCC GTAAAAAAT
851 ATCGGTTTTC TTTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCGGAG CGCATGCTTT GCGGTAAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCGG CTCTGCAGGC TGGGAAGCCG AATGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AACGGCGGC
1201 GATATCTCTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCCGCC CCATTATTTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGTACAC CGTTCGCGGA TTTGATGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGCG CAGTGGTCGG
1551 CTTAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1  MEIINDAELI RSMQRQOHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSSQ IIQPNMDSG ILKLRVSAGE IGDRIYEERK DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRLRP SVKTDIQUIP SEEEGKSDLQ
201 IKWQNKPIR FSIGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAAE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQFF YATAIQAWN KTPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1  NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAGAAC TCGCTCGTTT GCCGAGTGT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TNGTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```



```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATT CAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFTKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEEKRD KSAEGSISAF NNKXPLYRNK ILNLRDVEQG
101 LENLRLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ YQSSLAERM
251 LWXXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHRAYLX
301 RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10          20          30
                                XKETAFTKTMCLGSNNLSRLQKAAQQILIVR
                                |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
          50          60          70          80          90         100

          40          50          60          70          80          90
a707.pep  GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDKSAEGSISAFNNKXPLYRNKI
          |||
m707      GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKFPLYRNKI
          110         120         130         140         150         160

          100         110         120         130         140         150
a707.pep  LNLRDVEQGLENLRLRLPSVKTDIQUIPSEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
          |||
m707      LNLRDVEQGLENLRLRLPSVKTDIQUIPSEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
          170         180         190         200         210         220

          160         170         180         190         200         210
a707.pep  GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
          |||
m707      GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK
          230         240         250         260         270         280

          220         230         240         250         260         270
a707.pep  WLFSFNHNGHRYHEATEGYSVNYDYNKGQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
          |||
m707      WLFSFNHNGHRYHEATEGYSVNYDYNKGQYQSSLAERMLWRNRLHKTSVGMKLWTRQTY
          290         300         310         320         330         340

          280         290         300         310         320         330
a707.pep  KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTGMRQSMPEPEENGGGTI
          |||
m707      KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTGMRQSMPEPEENGGDIL
          350         360         370         380         390         400

```

	340	350	360	370	380	390
a707.pep	PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
m707	PGTSMRKIIITASLDAAAPFILGKQQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
a707.pep	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
m707	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
	470	480	490	500	510	520
a707.pep	VGGMFAYDLFAGKPLHKPKGFQTNTN TVYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTNTN TVYGFNLNYSFX					
	530	540	550	560		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

g708.seq

```
1 ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51 GGGCGCGCTG AGCACTTCTT ACCGCCCTCG GCGGGCAGAA AAGCGCAATC
101 AGGTTTCCAA TCATGAAACC CAGTTGGCGA TGGAAATATAT GCGCGGCTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCTGTGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCAGAACTCA AACAAACTAC GGCTGGTTCC GTGTCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGCTTG
501 CCTCGCGCGC CAGCCGCGAGT TCCCACCCGC ATTTAAAGAA CTGGCGGCAG
551 CCAAAATGCT GGCCGGCGAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CTTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCCTCTC
751 ACCGGTCAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```
g708.pap
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVR AEIY QYLVNDKAQ ESFRQALS I K
101 PDSA EINNYY GWFLCGR LNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQS RVEVLQA DDLLLGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```
m708.seq
1  ATGCCCTTTTA  AGCCATCCAA  ACGAATCTCT  TTATTACTCG  TTCTTGCCCTT
51  GGGCGCGTGC  AGCACTTCTT  ACCGCCCTC  GCGGGCAGAA  AAAGCCAACT
101 AGGTTTCCAA  ATATCAAAAC  CAGTTGCGAA  TGGAAATAT  GCGCGGTFCAG
151 GACTACCGTC  AGGCGACGGC  AAGTATTGAA  GACGCCCTGA  AATCGGACCC
201 TAAAAACGAG  CTTGCCTGGC  TGGTCCGTGC  CGAAATCTAT  CAATACCTGA
251 AAGTTAACGA  CAAGGCGCAG  GAAAGTTTCC  GGCAAGCCCT  CTCCATCAAA
301 CCCGACAGTG  CCGAAATCAA  GCAAACTAC  GGTGTGTTCC  TATGCGGCGAG
351 GCTCAACCGC  CCTGCCGAAT  CTATGGCATA  TTTCGACAAA  GCTCTGGCCG
401 ACCCCACCTA  CCCGACCCCT  TATATTGCCA  ACCTGAATAA  AGGCATATGC
451 AGCGCAAAAC  AGGGGCAATT  CGGATTGGCG  GAAGCCTATT  TGAACCGTTC
501 CCTCGCCGCC  CAGCCGCGAT  TCCCACCCGC  ATTTAAAGAA  CTGGCGGCA
551 CCAAAATGCT  GGCCGGGCGAG  TTGGGCGATG  CCGATTACTA  CTTTAAAAAC
601 TACCAAAGCA  GGGTAGAAGT  CCTTCAGGCC  GATGATTTGC  TGCTAGGCTG
651 GAAAATTGCC  AAAGCCCTCG  GCAACGCACA  GGCGGCATAC  GAATATGAG
701 CACAATTGCA  GGCGAATTC  CCTCTCTCGG  AAGAATTGCA  AACCCTCCTC
751 CACGGTCAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.ppt

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIE
101 PDSAEINNYY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||||||
g708           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIEKPDSEINNYYGWFLCGRLNR
              |||||:|||||
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIEKPDSEINNYYGWFLCGRLNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
              |||||||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYFFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
              |||||||
g708           LARTKMLAGQLGDADYFFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||||||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTGCTGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACT NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCGAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNYY XWFLCGRLNR PAESMAYFDK ALADPTYXP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRLNR					
m708	DALKSDPKNELAWLVRAEIIQYLKVNDKAQESFRQALSIPDSAEINNXYWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1 ATGTTTGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCAATTG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGGT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCGGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGcggg cgcgattgTT tccggTGTGT TTTTCGGCGA
501 TAAATGTCC CCGCTTCCG ACACCACGGG CATTTCGCG TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 GCGTGCGTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGCACT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGCGA AGCGTTTAAA
901 GACATTGCCA AACTGATTTT CCGCGGCGGC TTGGAGAGTA TGTCTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGC GC
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCCG TCCGTACCTT CTGACGAAT
1051 GCCGGACGCG CGACGTTTCCG CGTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCGATTGGA GAGCAATATT TGAGCATCCT GCTTCGGGA GAAACGTTCA
1151 AACCCTTTA CGACAACTC GGCCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGGACGGT GATTAAACCG CTCGTGCCGT GGAGCGGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGCGGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1 MFAFKSLDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQAGMIGAL NQGMGAVYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGLSIPT YFYSAFALC SVIGVSIGSS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFH IKNMMYTTP
201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAV AVLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAVRTFLTN

```

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCATTGG
 101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
 151 TACGCGTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGCGATGAT
 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCCTCCTT
 351 CGCGCTGTGT TCCGTCATCG GCGTGTCAT CGGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
 451 GATATGGCGA TGACGCGCGG CGCGATTGTT TCGGGCGCAT TTTTGGCGA
 501 CAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCGCGC TCCATCGTCG
 551 TGCGCTGATT TCGGTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG
 651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA
 701 CCGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCCT GTTGGTCATT
 751 TCGGTGTGTA TGCGCATCAA CGCGTCGTC GCCATGCTCT TTACCGTCAT
 801 GGTTGCCGTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGCGCA AGCGTTTAAA
 901 GATGTTGTCA AACTGATTTT GCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
 951 GCAAACCATC GTGATCTCTG GGATGAGTTT GGGCGGACTG TTGTTTGCCT
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTGACGAAT
 1051 GCCGACGCG CGACGTTTCA GGTGCCATG ACTTCGGTCG GGGTTAATTT
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTGTGCGGT GAAACGTTCA
 1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTCGCGGACG
 1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
 1251 CGGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCTT GTTATTCGGT
 1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAFKSLDLM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 YYGFLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA
 151 DMAMTAGAIV SGAFFGDKMS PLSDDTGISA SIVGIDLFEB IKNMYYTIP
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRFTLTN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQGMGAIYLFFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLFFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQGMGAIYLFFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLFFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFEBIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEBIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFEBIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEBIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFVTVMVAVVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVVMAMLFVIAAVAVVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQIVILGMSLGGLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
g709	DIAKLISRGGLESMTFTQIVILGMSLGGLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLTEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCG GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTATT TTTCCGCCCT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TNTTNGGCGN
501 CAAAATGTCN CCGCTTTCGG ATACGNCGGG CATNTCCGCG TCCATTGTCT
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCGCT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTC TCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCNGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCANCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCTT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGGLISPT YFYFSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFEH IKNMYYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV VAMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQTI VILGMSLGGL LFALGAIPSL LDAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIXLEWLPHMSIIAAIVVLILYGLARGLKYN					
m709						
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMAIYLFFFIFGLMVSALMMSGAIPITLMYYGFGFLISPTYFYFSAFALC					
m709						
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVGVAXMGXXXAFXAXMXXXXXIVXXAXXGXKMSPLSDTXGXSA					
m709						
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNMMYTTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709						
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMRVNAVAMLEFVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX					
m709						
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGAIPSLDAVRSFLTNAGRXTFSVAM					
m709						
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709						
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
m709						
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCCGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCGCGTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAT	CGGCGGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

m710.pep

1	METHEKIRLM	RELNKWSQED	MAEKLAMSAG	GYAKIERGET	QLNIPRLEQL
51	AQIFKIDMWD	LLKSGGGGMV	FQINEGDSGG	DIALYASGDV	SMKIEFLKME
101	LKHCKEMLEQ	KDKEIELLRK	LTETV*		

```
a710.seq
1  ATGGAACCC  ACGAAAAAT  CCGCCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGGCAGGC  GGGTATGCCA
101 AAATCGAACG  AGGCGAAACG  CAGTTGAATA  TCCCgcGTTT  GGAGCAGTTG
151 GCGCAGATTT  TCAAAATTGA  TATGTGGGAC  TTGCTCAAAT  CGGGCGGGCG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATG
301 GAATTAATAAC  ACTGTAAAGA  AATGTTGGAA  CACAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A
```

```
a710.pep
1  METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
51  AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
101 ELKHCKEMLE HKDKEIELR KLTETV*
```

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710						
	10	20	30	40	50	60
	70	80	90	100	110	120
a710.pep	LLKSGGGGMVLQINDVDTSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR					
m710						
	70	80	90	100	110	

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```


1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

m711.seq

```

1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCC CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATGTGTTGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCCTATAAA GGCTCGGCAT TGTGGGCAGT TTAAATATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

m711.pep

```

1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMDYAVGD
151 SRTRPAHSAI DGLVRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

a711.seq

```

1  ATGCCCCGCGC CTGATTGTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCC CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATGTGTCGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG

```

1148

```

901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIKTS
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIKTS
	10 20 30 40 50 60
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN
	70 80 90 100 110 120
a711.pep	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG
	130 140 150 160 170 180
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD
	190 200 210 220 230 240
a711.pep	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEKQRLDIDGK
m711	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEKQRLDIDGK
	250 260 270 280 290 300
a711.pep	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD
	310 320 330 340 350 360
a711.pep	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI
	370 380 390 400 410 420

1149

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
  1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
 51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101  AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151  CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201  TTTGTTGCGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
251  CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301  GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351  GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401  TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451  ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501  TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551  CCGTGAGCAC CGGCAATACC GGCTAACTT ATCAAGCCAA TGCCTTTACC
601  GCGGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTCCA AAGTGGCGGG
651  CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701  AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751  GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801  CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851  GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGGTGTG
901  GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951  GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTA CTGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTTGA
1401 TTTGATTTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
  1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPQKVL MVAPMLTAGI
 51  QPALEPVQLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101  AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151  ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201  GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251  GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301  AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351  QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401  SDRLLPKVKS EILDVLIKLD QAEIIEAE A NKGKLVVARA QNDPNRVNAI
451  IPADVNVNLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1   ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAGAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1   MQNNSYGYAV SVRVGKKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VQALTHIAN SVGLHPWLEP DGLTVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
251 VVVSADNLNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLQPGLR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAEAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1   ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```

1152

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```

1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDCLKWVYKD PTMTLHRPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMSLRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*

```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKWVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKWVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVVSADADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWLWQPGQR					
m713	PTMTLHRPKTVVVSADADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWLWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFLMGRRFMSLRMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	VHVIDDEHGIDAVFFLMGRRFMSLRMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGKKGKKQAETAVFEX					
m713	KGVSHKGKKGKKQAETAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
 51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101  TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151  CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201  CGGTACGGGC AAAAACCGCC AGCACCGTGT GTTGGCCGTC ATGGCCAAGC
251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTGTGCG TTTGGCCGAG
301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351  TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401  GGCACGTTAA PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFR
451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551  CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
 51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFR
151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
  1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
 51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101  TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151  AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201  CCGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGGCCGTC ATGGCCAAGC
251  TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTGTGCG TTTGGCCGAG
301  GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351  TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401  GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCGCGGCC
451  GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501  CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551  CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
  1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
 51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101  AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFR
151  GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEI MWVWHVNVRG GNNRITRFRAGISAAGDRLTDYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNVRRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGCTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGCTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GGCCGCGCGG GCCGTGCGG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
  1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
  1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQGSAGSGASKSAEGSCGASKSAEG					
	10	20	30	40	50	60

m716.pep	AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	:					
g716	SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
  1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
  1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60

a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
  1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGCGCGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCCTGA  CGCCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCCG
601  CGCGCGCCGT  TTTGCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGCGCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCTCCC  TCCTGCTGCC
951  GGAAACTTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgcTGTTTT  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCTTG  TGCCGCCTCA  TTCTGGTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTC  TGCTTgCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgtAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTTGCAC  AAAGTGTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCCATAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYYAAAD  KDTLFKTLFL  PPLLFSAAlA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLE  LSFLPIRFL  LVLRMGRAL  AFSSAQLVPR
151  LAILLLLPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAPFSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKKY  AGLEQLGVYS
251  MGISFGGAAL  LLQSIYSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGIISP  LASLLLPENY  AAVRFTVVSC  MLPPFLYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALAAANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTPANYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGCGCGCGGG  GCTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCG  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCCTGA  CGCCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCCG
601  CACGCACCGT  TTTGCCCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGCGCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGCTGCC
951  GGAAACTTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTGTTG  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCTTG  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTC  TGCTTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTTGCAC  AAAGTGTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCCATAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLRLMEGRAL AFSSAQLVPK
151 LAIIIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSIYSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPFLCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF					
g717	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF					
	70	80	90	100	110	120
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRLMEGRALAFSSAQLVPKLAILLLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRLMEGRALAFSSAQLVPKLAILLLPLTVGLLHFPANTSVLTAVALA					
	130	140	150	160	170	180
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSIYSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSIYSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
	250	260	270	280	290	300
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPFLCTLAISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPFLCTLAISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
m717.pep	370	380	390	400	410	420
	LGALANLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILHRKDLHKLHLYLKKQGFPLX					
g717	CLASSAAYTCFGTPANYPLFAGVWAAAYLAGCILHRKDLHKLHLYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTCAAAAC CCTGTTCTTG CCGCCGCTGC

```

1158

```

251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTCGCT CGACGATGCC GCCGCCGCA TCGGGCTGGT
351 GCTGTTTGA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GCGGAACACC GCCGCTCTGA CCGCGTTTA CCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCGTCCG
601 CCGCACCGT TTTTCATCCG CGTCTGCAT CCGCGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTGTTTCCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTTC
801 AACGGTCTGG ACACCGTATA TTTCCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTGCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTCC GGTTCATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CCGCGGCGCG CGCGGCGCGG
1151 CGGTTGCCTG TGCCGCCTCA TTTGGCTGT TTTTGTTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCGC TTTATATGCA
1251 CACATTGTTC TGCCTGGCCT CCTCGCGCGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGAA AGATTGCAC AAAGTGTTC ATTATTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLRMEGRAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLLKY AGLEQLGVYS
251 MGISFGGAAL LFQSIFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCRLWQPLK RPLMYHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
a717.pep	YVREYYAAADKDTLFKTLFLPPLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF
m717	YVREYYATADKDTLFKTLFLPPLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
a717.pep	NLAAAFLLFQNRCRLKAVRRAPFSSAVLHRLRYGIPIALSSIAYWGLASADRLFLLKY
m717	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGIPIALSSIAYWGLASADRLFLLKY
a717.pep	AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

1159

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|||||
m717  AGLEQLGVYSMGISFGG AALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
      250      260      270      280      290      300

      310      320      330      340      350      360
a717.pep ALCLTGIFSP LASLLLPENYA AAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
|||||
m717  ALCLTGIFSP LASLLLPENYA AAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
      310      320      330      340      350      360

      370      380      390      400      410      420
a717.pep LGALAANLLLGLAVPSGGARGA AAVACAASEFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717  LGALAANLLLGLAVPSGGARGA AAVACAASEFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
      370      380      390      400      410      420

      430      440      450      460      470
a717.pep CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
||:|||||
m717  CLTSSAAYTCFGTPANYPLFAGVWAA YLAGCILRHRKDLHKL FHYLKKQGFPLX
      430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCGGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTC AAT TCTCAGCTCA ACCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRTL SWLYM FKHYAVH DFA EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLOMADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLV DVG VQ
251 IPESWVRDKL VIPDVQEGEA VLV RQVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCTGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCTGCCTT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAATGGGGA
501 CAAAGACAAC GGGCTGCTGC TGGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTGTGGCC GCTGGGCTGG GTCTTCATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGCAAAA TACGCGCGGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGAAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAATCG
901 GCCGCGCGG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTG GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTGCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAAGCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTACGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHSELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLMD DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWKDKN GLLLR TRENP EGEALWPLGW VVHTQKSR SV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMP IRIK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMA DWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTRPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPNVRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDENSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

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a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS					
m718	SDGLYVPRNFIHRPQSWFKWKDKNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAAANGMTSAGNPFLLQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAAANGTATSNPFLQMA DW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	340	350	360	370	380	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGGCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC CCGTGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCG TTCGAGCGGT GCGGAAATC GGTCAACACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTGC GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG CCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAAACGCG AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHLEFADI EERDS DIAAN MGRKRALLT LNWVRVAPPRN
101 ATPPEEKLSL QAYEMMDSL P TLEDLIMDLM DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLLR TRENP EGEALWPLVG VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATS NPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
 51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
 101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
 151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
 201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
 251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
 301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
 351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
 401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGCGCTT
 451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
 501 CAAAGACCAAC GAGCTGCTGC TCGGTACCCG CGAAAAATCCG GAAGGCGAAG
 551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAAATC GCGCAGCGTC
 601 CAGCAGGCGC GCAACGGGCT TTTCGCGACG CTTTCCTGGC TGTATATGTT
 651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTTGGAG CTGTACGGCA
 701 TGCCCATCCG TATCGGCCAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
 751 AACACCCTGC TTCGAGCGGT GCGGAAATC GGTCACAACG CGGCAGGCAT
 801 CATGCCAGAA GGTATGGAAA TCAGCTGCA CAACGCGGCA AACGCGATGA
 851 CTTCGCGCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
 901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
 951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
 1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
 1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
 1101 GCGGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
 1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
 1201 TGGGTGCGCG ACAAACCTGG CATTCCAGAT GTGCGAGGAG GTGAGGCTGT
 1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
 1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGACG GCATCAGGAA
 1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTTC
 1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
 1451 ACAGCTACGA GGAGGCGAGT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
 1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
 1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
 51 LFEDAESGDI RAQHELFAEI EERDSIAAN MGTRKRALLT LNWRVAPPRN
 101 ATPEEELSD QAYEMMDSLP TLEDLIMDLMD DAVGHGFSAL EVEWVFSDDL
 151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKSRSV
 201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPDIRIK YGATATKEEK
 251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
 301 AARLILQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
 351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRA					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRA					
	10	20	30	40	50	60
a718.pep	RAQHELFAEIERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
m718-1	RAQHELFAEIERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	RAQHELFAEIERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
m718-1	RAQHELFAEIERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRNP					
	130	140	150	160	170	180

1163

	190	200	210	220	230	240
a718.pep	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQADWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQADWCEKS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAAA GCCATACTTA TCGGTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TCGGTTTAA CTTTGGCGC GCAGCGGCAA GGCATCACA AATGATTGG
251 CACGGGCGGC GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CCGTGACGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTGAGAAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACTT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAAGTATGTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGCTT TGCAATCGGG TTAGACGGC ACTTTCGAGG TGCGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTGCG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCCTGC CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAACT CTGTCGCCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTTGTGCAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTCAGGCGCA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGCCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTTGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTCCTAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GGCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pep

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGSPAEEA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAQQEQEQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKAGGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPE GLRGTKTTFE
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSINI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GGCGGCGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTGTA TGCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTTG GAGTGCGGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTGGA ACAAATTGCA CTTTCCCGAT
601 CCGGGCGGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTATGGA TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGGTT GGTGCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTGTC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGG TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GCGGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

m720.pep

```

1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AEAQEIVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIIPDNLLTG RFSDGLQNRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAATAE
351 SGGLTANAVY TEAYQTAE SL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPPIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

a720.seq (partial)

```

1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GCGGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGCGGCA
301 GGCCGCTGA ATGCGTTGGT TCGGCGGCTC ATCAACCAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCAA TCGACGGTAC GATACCAA ATCGCCCACG
401 AGTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

a720.pep (partial)

```

1 GLQNRLNRLT AKQVQVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESLRAAA
101 GRNLALVA AV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HIHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

                250      260      270      280      290      300
m720.pep      SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQVQAQAVRLLSTSSLL
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a720          GLQNRLNRLTAKQVQVQAQAVRLLSTSSLL
                10      20      30

                310      320      330      340      350      360
m720.pep      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAASGGLTANAVYTEAY
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a720          SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAASGGLTANAVYTEAY
                40      50      60      70      80      90

                370      380      390      400      410      420
m720.pep      QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAAAELVRLNP
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a720          QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAAAELVRLNP
                100      110      120      130      140      150

                430      440
m720.pep      HIHHPAFIKRGTLVNSYAKX

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1166

a720
|||||
HIHHPAFIKRGTLVNSYAKX
160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCCG CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGCGGCGAT TGTCCGCGCT CGTGAAGGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG
1001 CAAAATATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHIVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAGWM RWLEFTPKGM
101 FAEVETDKA AAAIAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLPKOP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCCG CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTT CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGCGGCGAT TGTCCGCGCT CGTGAAGGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTGTAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG
1001 CAAAATATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
  51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
 151 MDEVLAASA QILKPETEQN PMKELLQQLF GLPDAGEEEL KAALSALVEA
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
 251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
 301 ENAQPVAAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
 351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
a721.pep	70	80	90	100	110	120
	SSRNQLVVDYEHXTLYKEKNQGPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLYKEKNQGPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEQNPMKELLQQLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEQNPMKELLQQLF					
	130	140	150	160	170	180
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPPGGLAFLTGFI					
	250	260	270	280	290	300
a721.pep	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAMMLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAMMLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
  51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
 101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
 151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
 201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCCGC AATCCTACCA
 251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
 301 GACGACCTGC AAGTGCATAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
 351 CGCCGTTATC GGCAGCGGCG GCACGCGGGA AATACCGGCA ATCGCCGACG

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401 AGCCGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCAGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCAGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
  1 ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
 51 AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGCGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTTCGGTA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTA CTGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGCGCG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTT CCAAGGCTGT GGTTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCTGGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
  1 MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAIIHAQLH
 51 FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RCVCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
  ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
  1 -----+-----+-----+-----+-----+-----+ 60
    TACTCAAACCTCATTTAACCGCTTTTTTTGCCGTGTTTGACGATTTTATAGCCGCTTTGG
a    M S L S K L A K K T A Q T A K N I G E T -
    CTGCGCGCGGCCTTTTCGGGAAAAATCACGCTGGTGGTGTCTCCGAGCCGATACAGCGC
 61 -----+-----+-----+-----+-----+-----+ 120
    GACGCGCGCCGAAAGCCCCTTTTGTAGTGCACACCACAGCAGGCTCGGCTATGTCGCG
a    L R A A F R G K I T L V V S S E P I Q R -
    GTGCAGTTGAGCGGCTTGCGCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+-----+ 180
    CACGTCAAACCTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a    V Q L S G L A D E T L Q D L E H L Q E Y -
    GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+-----+ 240
    CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCCGTTA
a    G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241 -----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301 -----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCCACGTTTTTAGCACTAATTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAAAACAATACGAGGTTAATGCG
361 -----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAGTGTGACGGCGCAA
421 -----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGAGCCACCTTTAGC
481 -----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATTCG
a      G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541 -----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCCGTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGCGGAA
601 -----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCTGGGCGTATGGCTGTCGTAGCCGCGTTTTGGAATGGCCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661 ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

```

m724.pep
  1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
 51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101  PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAPL
151  VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201  ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

```

a724.seq
  1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
 51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAATCACG CTGGTGGTGT
101  CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151  CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201  CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251  GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301  CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351  GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAACTGCA
401  AACAATACGA GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451  GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```


1171

```

501  CGGCATGGCC  GTCGAGGGCG  GCGACGGAGC  CACCTTTAGC  GGCGATGTTA
551  ACCAAACGGG  CGGCAGCTTT  AACACCGACG  GCGACGTGGT  GGCCGGCAAT
601  ATATCGTTGC  GCCAGCACCC  GCATACCGAC  AGCATCGGCG  GCAAAACCTT
651  ACCGGCGGAA  CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
  1  MSLSKLAKKT  AQTAKNIGET  LRAAFRGKIT  LVVSSEPIQR  VQLSGLADET
 51  LQDLEHLQEY  GFASHPPDGS  EAVVIPLGGN  TSHGVIVCSQ  HGSYRIKNLK
101  PGETAIFNHE  GAKIVIKQ GK  IIEADCDVYR  VNCKQYEVNA  ATDAKFNA PL
151  VETSAVLTAQ  GQINGNGGMA  VEGGDGATFS  GDVNQTGGSF  NTDGDVVAGN
201  ISLRQHPHTD  SIGGKTLPAE  PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK					
m724	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNA PLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNA PLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
  1  ATGGTGCGCA  CGGTTAAAAG  CTACAACGGC  GAGGCCGACG  ATTTGGCGGG
 51  GCAAATCCAT  ACGCTGCCTG  CGGTTTGGGT  AACGTATGGC  GGCAGCAAAG
101  TTGAGCCTGC  CAGCACCGGC  GCGGTATGCG  GACGTTATCA  GGATACCGCC
151  GAATTTGTGG  TGATGGTGGC  GGCCCGCAAT  CTGCGCAACG  AGCAGGCGCA
201  GCGGCAAGGC  GGCATCGACA  GCCGCGAAAT  CGGCAGCAAC  GATTTAATCC
251  GCGCTGTTTC  CCGCTGCTT  GACGGCCAGC  GGCTCGGTTT  TGCCGATAGC
301  CGCGGCTTGG  TGCCCAAAGC  GGTGCGCGCG  ATTGCCAATC  ATGTGCTGCT
351  GCAAAACGCC  GCAGTAAGCA  TATATGCGGT  TGAGTATGCC  ATCCGCTTTA
401  ACACCTGCGG  GTTGGAAAAT  GACCGCTACC  CCGAACGCAC  CGACAATCCC
451  GACGACCCCA  ACCATATCTT  TACCAAGTAT  CAGGGTACAT  TGAGCGAGCC
501  GTGGCCTGAT  TTCGAGGGGT  TGGACGGCAA  AATTTACGAC  CCGCAATCCG
551  CCGATGAAAT  ACCTGTAAAC  CTAACCCTTA  AGGATAAGCA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
  1  MVRTVKSYNG  EADDLAQI H  TLPVAVVTY G  GSKVEPASTG  GVCGRYQDTA
 51  EFVVMVAARN  LRNEQAQRQ G  GIDSREIGSN  DLIRAVRRL L  DGQRLGFADS
101  RGLVPKAVRA  IANHVLVQNA  AVSIYAVEYA  IRFNTCGLEN  DRYPERTDNP
151  DDPNHIFTKY  QGTLSEP WPD  FEGLDGKIYD  PQSADEIPVN  LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

q726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

m726.seq

1	ATGACCATCT	ATTTCAAAAA	CGGCTTTTAC	GACGACACAT	TGGGCGGCAT
51	CCCCGAAGGC	GCGGTTGCCG	TCCGCGCCGA	AGAATACGCC	GCCCTTTTGG
101	CAGGACAGGC	GCAGGGCGGG	CAGATTGCCG	CAGATTCCGA	CGGCCGCCCC
151	GTTTTAACCC	CGCCGCGCCC	GTCCGATTAC	CACGAATGGG	ACGGCAAAAA
201	ATGGAAAACT	AGCAAAAGCC	CCGCGCCGCG	CGGTTTCGCC	AAACAAAAAA
251	CCGCGTTTGGC	ATTCCGCGTC	CGGGA AAAAG	CGGACGA ACT	CAAAACAGC
301	CTCTTGCGCG	GCTATCCCCA	AGTGGAATC	GACAGCTTTT	ACAGCGAGGA
351	AAAAGAAGCC	CTCGCGCGGC	AGGCGGACAA	CAACGCCCCG	ACCCCGATGC
401	TGGCGCAAAT	CGCCGCGCA	AGGGGCGTGG	AATTGGACGT	TTTGATTGAA
451	AAAGTTATCG	AAAAATCCGC	CCGCTTGGCT	GTTGCCGCCG	GCGCGATTAT
501	CGGAAGCGT	CAGCAGCTCG	AAGACAAATT	GAACACCATC	GAACCCGCGC
551	CCGATTGGA	CGCGCTGGAA	AAGGAAATCG	AAGAATGGAC	GCTAAACATC
601	GGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

m726.pcp

1	MTIYFKNGFY	DDTLGGIPEG	AVAVRAEYYA	ALLAGQAQGG	QIAADSDGRP
51	VLTPPRESDY	HEWDGKKWKI	SKAAAAARFA	KQKTALAFRL	AEKADELKNS
101	LLAGYPQVEI	DSFYRQEKEA	LARQADNNAP	TPMLAQIAAA	RGVELDVLIE
151	KVIEKSARLA	VAAGAIIGKR	QQLEDKLNTI	ETAPGLDALE	KEIEEWTLNI
201	G*				

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2451>:

a726.seq

1	ATGACCATCT	ATTTCAAAAA	CGGCTTTTAC	GACGACACCT	TGGGCAGCAT
51	CCCCGAAGGC	GCGGTTGCCG	TCCGCGCCGA	AGAATACGCC	GCCCTTTTGG
101	CAGGACAGGC	GCAGGGCGGG	CAGATTGCCG	CAGATTCCGA	CGGCGCCCC
151	GTTTTAACCC	CGCCGCGCCC	GTCCGAATAC	CACGAATGGG	ACGCAAGAA
201	ATGGGAATTC	GGCGAAGCCG	CTGCCCGCCG	CCGTTTCGCC	GAACAAAAAA
251	CCGCGACGGC	ATTCCGCGCT	GCGGCAAAAG	CGGACGAACT	CAAAAACAGC
301	CTCTTGGCGG	GCTATCCCCA	AGTGGAATAT	GACAGCTTTT	ACAAAGCAGG
351	AAAAGAAGCC	CTCGCGCGGC	AGGCGGACAA	CAACGCCCCG	ACCCCGATGC
401	TGGCGCAAAT	CGCCGCGCGA	AGGGCGGTGG	AATTGGACGT	TTTGATTGAA
451	AAAGTTGTCT	AAAAATCCGC	CCGCTGGCC	GTTGCCGCCG	GC GCGATTAT
501	CGGAAAGCGG	CAGCAGCTCG	AAGACAAATT	GAACACCATC	GAAACCGCGC
551	CAGGATTGGA	CGCGCTGGAA	AAGGAAATCG	AAGAATGGAC	GCTAAACATC
601	GGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

a726.pep

1	MTIYFKNGFY	DDTLGSIPEG	AVAVRAEYYA	ALLAGQAQGG	QIAADSDGRP
51	VLTPRPPESEY	HEWDGKKWEI	GEAAAAARFA	EQKTATAFRL	AAKADELKNS
101	LLAGYPQVEI	DSFYRQEKEA	LARQADNNAP	TPMLAQIAAA	RGVELDVLIE
151	KVVEKSARLA	VAAGAIIGKR	QQLEDKLNTI	ETAPGLDALE	KEIEEWTLNI
201	G*				

a726/m726 95.5% identity in 201 aa overlap

```

          10          20          30          40          50          60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEYYAALLAGQAQGGQIAADSDGRPVLTPPRPSEY
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726      MTIYFKNGFYDDTLGGIPEGAVAVRAEYYAALLAGQAQGGQIAADSDGRPVLTPPRPSDY
          10          20          30          40          50          60

```

1173

```

              70      80      90      100      110      120
a726.pep    HEWDGKKWEIGEAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
            |||||:::|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep    LARQADNNAPTPMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQQLEDKLNIT
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        LARQADNNAPTPMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep    ETAPGLDALEKEIEEWTNLNIGX
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        ETAPGLDALEKEIEEWTNLNIGX
              190      200

g727.seq    not found yet

g727.pep    not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPPD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep    MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQQYKSAFAKQQAVIDKMERDKAQALLLSAQN
              10      20      30      40      50      60
              70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDSRNPNTGF
              70      80      90      100     110
              120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX
m727      RLFSPQIPPNTQIPPX
              120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

g728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGCGCAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGACAAAT CTTTCACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGATG GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

g728.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFAV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRKGIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVDW FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

m728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAATG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

m728.pgp

1	MFKKFKPVL	SFFALVFAFW	LGTGIAYEIN	PRWFLSDTAT	EVPKNPNAFV
51	AKLARLFRNA	DRAVVIVKES	IRTEENLAGT	VDDGPLQSEK	DYLALAIRLS
101	RLKEKAKWFH	VTEQEHGKEV	WLDYHIGEGG	LVAVSLSQRS	PEAFVNAEYL
151	YRNDRPFSVN	VYGGTVHGEN	YETTGEYRVV	WQPDGSVFDA	AGRGKIGEDV
201	YEHCLGCYQM	AQVYLAKYRD	VANDEQKVWD	FRKESNRIAS	DSRNSVIFYQN
251	MREMLPRGMK	ANSLVGYDA	DGLPQKVYVS	FDNGKKRQSF	EYYLKNGNLNF
301	IAQSSTVALK	ADGVTADMGT	YHAQQTSHYLD	GGRIVREEKQ	GDRLPDFPLN
351	LENLEKEVRR	YAEAAARSG	GRDDLHW*		

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / q728

	10	20	30	40	50	60
m728.pep	<u>MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNFAVAKLARLFRNA</u>					
	: : : : :					
g728	<u>MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFRNA</u>					
	: : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHEGKEV					
	: : : : : :					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHEGEEV					
	: : : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVIYGGTVHGENYETTGEYRVV					
	: : : : : :					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVIYGGTAHGENYETTGEYRVV					
	: : : : : :					
	130	140	150	160	170	180
	190	200	210	220	230	240
m728.pep	WQPDGGSVFDAAGRKGIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKSERNIAS					
	: : : : : :					
g728	WQPDGGSVFDAAGRKGIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	: : : : : :					
	190	200	210	220	230	240
	250	260	270	280	290	300
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	: : : : : :					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	: : : : : :					
	250	260	270	280	290	300
	310	320	330	340	350	360
m728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	: : : : : :					

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```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360

           370
m728.pep  YAEAAAARRSGRRDLSHX
           |||||
g728      YAEAAAARRSGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGTTTCA CGTAACGGAG CAGGAACATG GGGAAAGAGGT
351 TTGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTTC GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTGGAAGAT
1051 TTGAAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLERNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

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	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	: : : : : :					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVIFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	: : : : : :					
m728	DSRNSVIFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDEKEVSR					
	: : : : : :					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDL SHX					
	: :					
m728	YAEAAARRSGGRRDL SHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATGTGCTGCC TGCAACATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCgg
351 caaTGTCAGC AGCAGCTACA ATGTCGGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TCGGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGCGAACA GCGCGCAAT GCCTTGCCAA CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTGTGA
801 AAAACTGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGc CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GGCGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TACTTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGATTGTC TCGATGCGGA ACGCATCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

```

1178

```

201  ELRYKAGVIS  AVALRQOEAL  IESAKADYAH  AARSREQARN  ALATLINRPI
251  PEDLPAGLPL  DKQFFVEKLP  AGLSSEVLLD  RPDIRAAEHA  LKQANANIGA
301  ARAAFFPSIR  LTGTVGTGSA  ELGGLFKSGT  GVWAFAPSIT  LPIFTWGTNK
351  ANLDVAKLRQ  QAQIVAYESA  VQSAFQDVAN  ALAAREQLDK  AYDALSKQSR
401  ASKEALRLVG  LRYKHGVSGA  LDLLDAERIS  YSAEGAALSA  QLTRAENLAD
451  LYKALDGGGLK  RDTQTGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2465>:

m729.seq

```

1   ATGGATACTA  CATTGAAAAC  CACCTTGACT  TCTGTTGCAG  CAGCCTTTGC
51  ATTGTCTGCC  TGCACCATGA  TTCCCCAATA  CGAGCAGCCC  AAAGTCGAAG
101 TTGCCGAAAC  GTTCAAAAAC  GATACCGCCG  ACAGCGGCAT  CCGCGCCGTC
151 GATTTAGGTT  GGCACTGACT  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201 CGACATCGCA  CTCGAGCGCA  ATACCAGTTT  GCGTACCGCC  GTATTGAACA
251 GCGAAATCTA  CCGCAAACAA  TACATGATTG  AGCGCAACAA  CCTCTGCCC
301 ACGCTTGCCG  CCAATGCGAA  CGACTCGCGC  CAAGGCAGCT  TGAGCGGCGG
351 CAATGTAAGC  AGCAGCTACA  AAGTCGGACT  GGGTGCGGCA  TCTTACGAAC
401 TCGATCTGTT  CGGGCGTGTA  CGCAGCAGCA  GCGAGGCGGC  ACTGCAAGGC
451 TATTTGCGCA  GCACCGCCAA  CCGCGATGCG  GCACATTTGA  GCCTGATTGC
501 CACCGTTGCC  AAAGCCTATT  TCAACGAACG  TTACGCCGAA  GAAGCGATGT
551 CTTTGGCGCA  ACGTGTTTTG  AAAACGCGCG  AGGAAACCTA  CAAGCTGTCC
601 GAATTACGTT  ACAAGGCAGG  CGTGATTTCG  GCCGTCGCCC  TACGTCAGCA
651 GGAAGCCCTG  ATCGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCA
701 GCCGCGAACA  GGCGCGCAAT  GCCTTGGCAG  CCTTGATTAA  CCAACCGATA
751 CCCGAAGACC  TGCTGCGCGG  TTTGCCGCTG  GACAAGCAGT  TTTTGTGTTA
801 AAAACTGCCG  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCGATA
851 TCCGTGCTGC  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901 GCACGCGCGC  CCTTTTCCC  ATCCATCCGC  CTGACCGGAA  CCGTCGGTAC
951 GGGTTCTGCC  GAATTGGGTG  GGTGTTCAA  AAGCGGCACG  GGCGTTTGGT
1001 CGTTCGCGCC  GTCTATTACC  CTGCCGATTT  TTACCTGGGG  TACGAACAAG
1051 GCGAACCTTG  ATGTAGCCAA  GTGCGCCAA  CAGGTACAAA  TCGTTGCCTA
1101 TGAATCCGCC  GTCCAATCCG  CATTTCAGA  CGTGGCAAAC  GCATTGGCGG
1151 CGCGCGAGCA  GCTGGATAAA  GCCTATGACG  CTTTAAGCAA  ACAAAGCCGC
1201 GCCTCTAAAG  AAGCGTTGCG  CTTGGTCGGC  CTGCGTTACA  AGCACGGCGT
1251 ATCCGGCGCG  CTCGACTTGC  TCGATGCGGA  ACGCAGCAGC  TATGCGGCGG
1301 AGGGTGCGGC  TTTGTGCGCA  CAACTGACCC  GCGCCGAAAA  CCTTGCCGAT
1351 TTGTACAAGG  CACTCGGCGG  CGGATTGAAA  CGGGATACCC  AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

m729.pep

```

1   MDTTLKTTLT  SVAAAFALSA  CTMIPQYEQP  KVEVAETFKN  DTADSGIRAV
51  DLGWHDYFAD  PRLQKLIDIA  LERNTSLRTA  VLNSEIYRKQ  YMIERNLLP
101 TLAANANDSR  QGSLSGGNVS  SSYKVLGAA  SYELDLFGRV  RSSSEALQG
151 YFASTANRDA  AHLSLIATVA  KAYFNERYAE  EAMSLAQRVL  KTREETYKLS
201 ELRYKAGVIS  AVALRQOEAL  IESAKADYAH  AARSREQARN  ALATLINQPI
251 PEDLPAGLPL  DKQFFVEKLP  AGLSSEVLLD  RPDIRAAEHA  LKQANANIGA
301 ARAAFFPSIR  LTGTVGTGSA  ELGGLFKSGT  GVWSFAPSIT  LPIFTWGTNK
351 ANLDVAKLRQ  QVQIVAYESA  VQSAFQDVAN  ALAAREQLDK  AYDALSKQSR
401 ASKEALRLVG  LRYKHGVSGA  LDLLDAERSS  YAAEGAALSA  QLTRAENLAD
451 LYKALGGGLK  RDTQTDK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```

m729.pep      10      20      30      40      50      60
               MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
g729          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
               MNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD
               10      20      30      40      50      60

```


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	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNV					
g729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
	:		:	:		
g729	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
	:					
g729	KAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	:					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWFSAPSITLPIFTWGTNKANLDVAKLRQ					
	:		:	:		
g729	ARAAFFPSIRLTGSGTGSVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	:					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA  CATTGAAAAC  CACCTTGACT  TCTGTTGCAG  CAGCCTTCGC
51  ATTATCCGCC  TGCACCATGA  TTCCCAATA  CGAGCAGCCC  AAAGTCGAAG
101  TTGCCGAAAC  GTTCAAAAAC  GATACCGCCG  ACAGCGGCAT  CCGTGCGGTC
151  GATTGTGGTT  GGCATGACTA  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201  CGACATCGCA  CTCGAGCGCA  ATACCAAGTT  GCGTACCGCC  GTATTGAACA
251  GCGAAATCTA  CCGCAAACAA  TACATGATTG  AGCGCAACAA  CCTCCTGCCC
301  ACGCTTGCCG  CCAATGCGAA  CGACTCGCGC  CAAGGCAGCT  TGAGCGGCGG
351  CAATGTAAGC  AGCAGCTACA  AAGTCGGACT  GGGTGCAGCA  TCTTACGAAC
401  TCGATCTGTT  CGGGCGTGTA  CGCAGCAGCA  GCGAGGCGGC  ACTGCAAGGC
451  TATTTGCGCA  GCACCGCCAA  CCGCGATGCG  GCACATTTGA  GCCTGATTGC
501  CACCGTTGCC  AAAGCCTATT  TCAACGAACG  TTATGCCGAA  GAAGCGATGT
551  CTTTGGCGCA  ACGTGTTTGG  AAAACGCGCG  AGGAAACCTA  CAAGCTGTCC
601  GAATTACGTT  ACAAGGCAGG  CGTGATTTC  GCCGTCGCC  TACGTCAGCA
651  GGAAGCCCTA  ATCGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCA
701  GCCGCGAACA  GGCAGCGAAT  GCCTTGGCAA  CCCTGATTAA  CCAACCGATA
751  CCCGACGACC  TGCCCGCCGG  TTTGCCGTTG  GACAAGCAGT  TTTTGTGTTGA
801  GAAGCTGCCG  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCGATA
851  TCCGTGCTGC  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901  GCACGCGCCG  CCTTTTCCC  ATCCATCCGC  CTGACCGGAA  GCGTCGATAC
951  GCATTCTGCC  GAATTGGGCG  GGCTGTTCAA  AAGCGGCACC  GCGGTTGGT
1001  TGTTCGCACC  TTCCATTACC  CTGCCGATTT  TTACCTGGGG  TACGAACAAG

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1180

```

1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```

1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSYKVLGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRLV KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

	10	20	30	40	50	60
a729.pep	MDTTLKTTLT SVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDFAD					
m729	MDTTLKTTLT SVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDFAD					
	10	20	30	40	50	60
a729.pep	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
a729.pep	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
a729.pep	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
m729	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
	130	140	150	160	170	180
a729.pep	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
m729	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
	130	140	150	160	170	180
a729.pep	EAMSLAQRLVKTREETYKLSELRYKAGVIS AVALRQOEALIESAKADYAH AARSREQARN					
m729	EAMSLAQRLVKTREETYKLSELRYKAGVIS AVALRQOEALIESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	EAMSLAQRLVKTREETYKLSELRYKAGVIS AVALRQOEALIESAKADYAH AARSREQARN					
m729	EAMSLAQRLVKTREETYKLSELRYKAGVIS AVALRQOEALIESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420

1181

	430	440	450	460
a729.pep	LDLLDAERSSSYSAEGAALSAQLTRAENLADLYKALGGGLKRDTQTDKX			
m729	LDLLDAERSSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDTQTDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1  GTGAAACCGC  TGCGCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GGCGGTCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CGGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGGAGC  GTTTCGACC  GCACCGGCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCA  GATGGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTGGTT  ACACCGTCCG  CTTTTCGGGA
301 CACGGACACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCC GCCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGCAATTT  ACCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 GCGCAACGCG  ACAGCCCGCA  GTATCAAAC  CAATCCGACC  GACACCGCA
551 GCATCCGGCA  ACGCATATTC  GACAACTACA  ACAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCACGGC  GTCGCCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGCG  AAGCCTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TGCGCAACAT
801 CGCCCCCTTA  CCCGCCGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCTT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAACCGGT  TACCGCCGCA  TACGGCAATC  CGTATCAAGA  AACCCTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCTGA  TTTCCAACCG
1251 CATCCACCCG  TTTTATTTCG  ACGGCAAATG  GATTAAGGCG  GAAGATTAA
1301 AAGCGGGAAG  CCGGCTGTTA  TCCGAAAGCG  GCAAACCCA  AACCCTCCGC
1351 AACATCGTTG  TCAAACCAAA  ACCGCTCAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGGTAA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTTCGCG  AAGGAAAGCA  ATATTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1  VKPLRRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQQAIIQG  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEHGHE  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADENRKA  MFEHNAKLDR  WGNMSEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPI  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTADGY  KAIAHIQAGD  RVLSKDEASG  ETGYPVTAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYSDGKWIKA  EDLKAGSRLL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNQAE  TEGVWVHND  PPKPKPTNHA
501 QQRKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1  GTGAAACCGC  TGCGCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GGCGGCCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC

```

1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGC AAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTGAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEHGEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADENRKM FEHNAKLDR WGNMSMEFNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

	10	20	30	40	50	60
g730.pep	VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
g730.pep	VSDRTGKINVIQDYTHQMGNLLIQQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
g730.pep	VSDRTGKINVIQDYTHQMGNLLIQQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
g730.pep	KGNVDDGFTVYRLNWEHGEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEHGEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
g730.pep	KGNVDDGFTVYRLNWEHGEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEHGEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
g730.pep	DTRSIRQRIFDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSMEFNGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
g730.pep	DTRSIRQRIFDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSMEFNGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSMEFINGVAAGALNPFI					
	190	200	210	220	230	240

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730						
	250	260	270	280	290	300
	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYTCSEFHGSTLVKTADGY					
m730						
	310	320	330	340	350	360
	QENPNAAETVEAVFNVAATAAKVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVRTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGCAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GGC GGCCGCA  CTCATACAGC  CCGCCCTCGC  GGC GGACTTG  GCGCAAGACC
101 CGTT CATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACC ACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACG GATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GGC GGCAATT  ACCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TCGCGAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAAC TAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAAC TG
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGNSF
201 SDRADEANRK  MFEHNAKLDR  WGNSEFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFP GK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

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1184

a730 / m730 88.6% identity in 376 aa overlap

a730.pep	10	20	30	40	50	60
	VKPLRRLIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	10	20	30	40	50	60
	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
a730.pep	70	80	90	100	110	120
	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	70	80	90	100	110	120
	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
a730.pep	130	140	150	160	170	180
	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	130	140	150	160	170	180
	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
a730.pep	190	200	210	220	230	240
	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFII					
m730	190	200	210	220	230	240
	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFII					
a730.pep	250	260	270	280	290	300
	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	250	260	270	280	290	300
	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
a730.pep	310	320	330	340	350	360
	QENPNAAETVEALVNVLPFAKVKNLTAKAPGKAAVSGDFSAAYNTRTRTKVTTETEGLN					
m730	310	320	330	340	350	
	QENPNAAETVEAVFNVAATAKAKAPGKAAVSGDFADSY-----KKKLALSDSAR					
a730.pep	370	380	390	400	410	420
	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGGHLFPKGPKGTTTFPQHW					
m730	360	370	380	390	400	410
	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNF					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

g731.seq

```

1  gatttttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGCGAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTTCGGA ACGGAACCGA GTGGCACCAG AAAGCGGGCG AAGCCTTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

g731.pep

```

1  DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

m731.seq

```

1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCTCTC TTCCGACGTT GCCGCATCCG

```

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACTTCTTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep

1	<u>MNIRFFALT</u> V	<u>PVLSLAACA</u> V	PEAYDDGGRG	HMPPVQNQAG	TDDFRAFSCE
51	NGLSVRVRHL	DSGKVALRLD	GRRAVLSSDV	AASGERYTAE	HGLFGNATEW
101	HQKGGEAFFG	FTDAYGNSVE	TSCRAR*		

g731/m731 95.2% identity in 84 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

```
a731.seq
1  ATGAATATCA GGTTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
201 GCGGTTGGAC GGCAGGCGTG CCGTCTCTC TTCGACGTT GCCGCATCCG
251 GCGAACGCTA TACCGCCGAA CACGTTTGT TCGGAAACGG AACCGAGTGG
301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep

1	<u>MNIRFFALT</u>	<u>PVLSLAACAV</u>	PEAYDDGGRG	HMPPVQNQAG	TADFRAFSCE
51	<u>NGLSVHVRRL</u>	<u>DGGRIALRLD</u>	GRRAVLSSDV	AASGERYTAE	HGLFGNGTEW
101	HQKGGEAFFG	FTDAYGNSVE	TSCRAR*		

a731/m731 94.4% identity in 126 aa overlap

		10	20	30	40	50	60
a731.pep		MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTAD	FRAFSCENGLSVHVRRL				
m731		MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDD	FRAFSCENGLSVRVRHL				
		10	20	30	40	50	60
		70	80	90	100	110	120
a731.pep		DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQK	GEAFFGFTDAYGNSVE				
m731		DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQK	GEAFFGFTDAYGNSVE				
		70	80	90	100	110	120
a731.pep	TSCRARX						
m731	TSCRARX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq

1	ATGTCGAAAC	CTGTTTTTAA	GAAATCGCA	CTTTATACTT	TGGGTGCAAT
51	CAGCGGCGTG	GCCGTAAGTC	TGGCGGTGCA	GGGTTTGTCC	GCCGagaagg
101	ACGGgcgGGA	TAACGAagtC	CTGCCGGTGC	AATCCATCCG	TACGATGGCG

1186

```

151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCGGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTTCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTGCGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCTGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTGCGCG AGTTGAAAAC GATTCCGATG ACGGtaATTG TcaaTTCCGG
951 TTCggttCC GCGTCGGAGA TTGtcgCCGG CGCATTCGAG GACCACAAAC
1001 GCGCGGTCTAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTTCAGG ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GGCGGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CcttgccGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAGG ACGATCAGTT GCGTAAGGCT TTGGATTGTT TCAAGTCGCC
1401 CGAGCAGTTG CAGAAGTCTT TGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVFEKKIA LYTLGAISGV AVSLAVQGFA AEKDGDRNEV LPVQSIRTMA
51 EVYQGQIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEFGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TSLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDG MVLKAVPEDYV YMGGDPLAG
301 IPAECLKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFQKGSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAK PVSNDKKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCGGA TTGAGGACAC GCCTGCCGAA CGGGCGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGG
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTTCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCATTCTCTG AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCTGCGCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCTAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1187

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAAGAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GAT'TCCCAAC
1351 CCTGCCAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFVKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEGGLGME IGQEDGFVKV VSPIDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAEKLTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFVKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFVKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGFEGGLGMEIGQEDGFVKV					
	:					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGFEGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIDTPAERA EVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSA A FL PSEAVVSTKGRDGKDRMV LKAIPEDYV YGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSA A FL PSEAVVSTKGRDGKGMVLKAVPEDYV YGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
g732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
	310	320	330	340	350	360

	370	380	390	400	410	420
m732.pep	KLTTALYYT	PNDRS	IQAQGIV	PDVEVK	DKERIF	ESREADLVGHIGNPLGGEDVNGETLAV
g732	KLTTALYYT	PNDRS	IQAQGIV	PDVEVK	DKERTF	ESREADLVGHIGNPLGGEDVNSETLAV
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEK	GKKKKDE	DLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK			
g732	PLEKDADKPAAKEK	GKKKKDE	DLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK			
	430	440	450	460	470	480
	490					
m732.pep	PVSNKDKKDKKDKX					
g732	PVSNKDKKDKKDKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```
a732.seq
1 ATGTGCAAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGGTGGGA TAACGAAGTC TGCCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACT TATCAGGCA AATCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGCG
451 ATGACGGTCA CGCAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCTG GCAAAAATGC CGACAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAGGAA AATAAGGAA
701 AACCCTCAA GGGGCTGGTG TTGGATTTGC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCCGGCT GTCCGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTGCTCAGC ACCAAGGGAT GCGACGGCAA AGATCCGATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTGCCG AGTTGAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCATCTGA
1101 TTATACGCCG AAGCACCCTT CTATTACGG CAGGGGATG GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GGCAGGATTG
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CTTTGCCGTG CCGCTTGAAA AAGATCGGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAGGGAC GAGGATTTGT CTTCAGGCG GATTCCCAAC
1351 CCTGCCAAG ACGACCAGTT GCGGAAAGCT TTGGATTTAG TCAAGTCGCC
1401 CGAGCATGGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```
a732.pep
1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYQGIKANY YQDKPADLF EGAMKGMVAG LDPHSEYMDK KGAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAII KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YMGGDSLAG
301 IPAELKTSIP TVLVNSSGSAS ASEIVAGALQ DHKRAVIGT QSFGKGSVQT
351 LIPLSNGTAV KLTTALYTP NDRSIQAQGI VPDVEVKKDE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDAKPA VKEGKKKKDE EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEOW QKSLGLAAKK PVSNKDKKKDK KDKK*
```

1189

a732/m732 99.6% identity in 494 aa overlap

a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
a732.pep	LDLRDDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSL
m732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAI PEDYVYGMGGDSL
a732.pep	IPAE LKTI PMTVLVN SSGSASASEIVAGALQD HKRAVIVGTQSFGKGSVQTLIPLSNGSAV
m732	IPAE LKTI PMTVLVN SSGSASASEIVAGALQD HKRAVIVGTQSFGKGSVQTLIPLSNGSAV
a732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
m732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
a732.pep	PLEKDADKPAVKEKGKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
m732	PLEKDADKPAVKEKGKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
a732.pep	PVSNKDKKDKKDKKX
m732	PVSNKDKKDKKDKKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGTTT TGA AAAACG cGACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGCGCA CGCCATTG GACTGCTGC

```

1190

```

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
351 CGGtaaAGGA GGCAAGCGAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

```

1  MNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
51  LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

```

1  ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
201 CAAAAAATG AATGCCGCCC CGGGTGC GCGCCATCTG GGACTGCTGC
251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
351 CGGTAAAGGA GGCAAGCGAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

```

1  MNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNP	KTLSRL	SLCAAVLALT	ACGGNGQKSL	YYYGGYPDTV	YEGLKNDDTSLGKQTEKMEK
g733	MMNP	KTLSRL	SLCAAVLALT	ACAGGGHKNL	YYYGGYPDTV	YEGLKNDDTSLGKQTEKMEK
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKM	NAAPGAHAHL	GLLLSRSGDK	EGAFRQFEE	EKRLFPESGVF	MDFLMKTGKG
g733	YFAEAANKM	NAAPGAHAHL	GLLLSRSGDK	EGAFRQFEE	EKRLFPESGVF	MDFLMKTGKG
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

```

1  ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
201 CAAAAAATG AATGCCGCCC CGGGTGC GCGCCATCTG GGACTGCTGC
251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
351 CGGTAAAGGA GGCAAGCGAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

1 MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

a733/m733 100.0% identity in 123 aa overlap

	10	20	30	40	50	60
a733.pep	MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
m733	MMNPKTL SRL SLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	GKRX					
m733	GKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

g734.seq
 1 ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
 51 GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
 101 AGGATGCAAA CGATGTTTGG CAGGTAAAA CCACAAAAGA AGATTCGGCG
 151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTTGCAAAG GTCAGGACAC
 201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCTGT
 251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
 301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
 351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
 401 AATGCGGCTT GGAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
 451 GCTGTTCGCT CCTTAATCCA ACACCTGAAA TAA

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

g734.pep
 1 MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
 51 KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
 101 MRVENAVVIT SPRFTSVHQV ALNQCIKKYQ AQGQCGLQTV YCTSSSYGG
 151 AVRSLIQHLK *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

m734.seq (partial)
 1 TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCCG TCGTGTCTGCT
 51 GAACAATACC TGTGTCGCGC TGGCATAACC GAAAGCCTTG GGCGCGCTGC
 101 GTGTGACAAA CGCCGTCGTG ATTACTTCTC CGCGTTTTAC GAGCGTTCAT
 151 CAGGTGCGAC TCAACCAAGT CATCAAAAAA TACGGCGTAC AGGGACAATG
 201 CGGCTTGGA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAAGT
 251 TCGGCTCTTT GATTCAAAAT CTCAATAA

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

m734.pep (partial)
 1 SGIAEDEPTG CRSVSVSLNNT CVALAYPKAL GALRVDNAV VITS PRFTSVH
 51 QVALNQCIKK YGVQGCGLQ TVYCTSSSY GGTVRSLIQN LK*

m734/g734 92.4% identity in 92 aa overlap

	10	20	30
m734.pep	SGIAEDEPTGCRSVSVSLNNTCVALAYPKAL		
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVSVSLNNTCVSLAYPKAL		

1192

	40	50	60	70	80	90
m734.pep	GALRVDNAVVISPRFTSVHQVALNQCIKKYGVQGCGLQETVYCTSSSYGGTVRSLIQN					
g734	GAMRVENAVVISPRFTSVHQVALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQH					
	100	110	120	130	140	150
m734.pep	LKK					
g734	LKK					
	160					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2497>:

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCT TTCTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:

```
a734.pep
1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV ALAYPKALGA
101 MRVENAVVIT SPRFTSVYQV ALNQCIKKYQ AQGCGLQETV YCTSSSYGG
151 TVRSLIQNLK *
```

a734/g734 95.6% identity in 160 aa overlap

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
a734.pep	ALNQCIKKYGAQGCGLQETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGCGLQETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

g735.seq not found yet

g735.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2499>:

```
m735.seq
1  ATGAATCTCG TGAAACTGCT GGC GAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTGCGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAAGCGG
```

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351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GCGCAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTGCGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
	:					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN KKEIENVLTQ DRKNAGGGCI					
	:					
m735	YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN KKEIENVLTQ DRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
	:					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT

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601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSEFS ITLFLNLA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVI
 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGT TTTTGCCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTTG GCGGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTTCG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAA ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVI
 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA	KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS				
g736	MNFIRSVGAKTLGLIQSEFSITLFLNLA	KSGTAFARPRLSVRQVYFAGVLSVLIVAVS				
	10	20	30	40	50	60
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
g736	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
g736	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPMQNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTCCGT	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA
101	CGGCTTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTCCG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTG	TCGGCATGGT
201	CTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAAATTCAAA	TCCGCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTAAACCC	CGTCGCCCCA	GTGGTTGCGC	CGCGCTTTTG	GGCGGGCGTG
451	TTTTCCATGC	CGCTTTTGGC	TTGATTTTC	AACGTGGCGG	GTATTTTCGG
501	CGCGTATTTG	GTCGGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT
551	GGTCGCAAAT	GCAGAACAA	ATCACGATAC	ATTACGATGT	AATCAACGGT
601	CTGATCAAAT	CCGCCGCGTT	CGGCGTGGCG	GTAACGCTGA	TTGCCGTGCA
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTTGGCGGT	CGATTTTATA
751	TTGACCGCGT	GGATGTTTAC	AGATTGA		

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NMAVNPVAR	VVAPRFWAGV
151	FSMPLLASIF	NVAGIFGAYL	VGVTWLGLDS	GIFWSQMNN	ITIHYDVING
201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGIL	RASTRTVVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
m736	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

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```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep   ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCGCGC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq..

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCGCGC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAQAEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737        MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAQAEKAAWAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737        VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

a737.seq
 1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
 51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep
 1 MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
 101 VISSRRDD*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEKAALAR
m737	MNFKRLLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq
 1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCG CCAAACCTGCC
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGGCC
 151 GCGGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
 201 TGATGTCAAA ATCCCGGCCA TCAGCTTCCT CTGTTTGCA ATGGCGGCAT
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
 301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
 451 CAGTTTGCCG GCTGGGAAAA CACCCCTCTG CTTCAAAACA TCATCGTTCA
 501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCTCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCAAAGC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
 951 CCGCTGGAAC AGTTTGTGCC AACAAACCTT CCTGATCAAT GCCGAACAGC
 1001 ACACCATAA CGACAACTTC CTCAGCACCT TGTTCACCCA TTCCACAAC
 1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
 1151 CCCCCGCATC ACTTTTCTCT CTGTGCGCGC TTGCCGTGAG TATGTGCCAC
 1201 AGTAGGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCCTTCGG
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
 1401 CCCC GCCGCT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAAC
 1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTAC TCCGCCACCT

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHTIHDNF LSTLFTSHSN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTF RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKALKYRKY SATYRIALYL MRQGVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1 ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACGCGC
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCCGCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCGCCA CTAGCTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCTG
351 CCGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCTCGG CGTAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTACCGCGC TGTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCTTGC CGCCTCCAG TCCGCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTCACCCA TCCCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCGG
1251 ACTGATGCTC TCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCG CATATTGCA
1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCGTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGAAACA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLLEA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAAFQ SAPIFGHGWN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLVLAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGL IAFKKAANLG ILTASAAIFA
451 GLLHLWDWYT RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1 ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACGACC
51 GATTTACATC CTGCCCCGCT TCCTTTGGAT AGGCATCGTC CCCTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCCGCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAA ATCCCGCCA TCAGCTCCT TCTGTTGCA ATGGCGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTT
401 CCTGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTCAAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTACCGCGC TGTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTACCCA TTTCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGTCGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTTCGG
1251 ACTGATCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCA
1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
1451 TCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCTATTAC CCGTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

51	<u>AAGLIVLLFL</u>	<u>TAGKKLFDVK</u>	<u>IPAISFLFA</u>	<u>MAEFWYLQAR</u>	<u>LMNLIYPGMN</u>
101	<u>DIVSWIFILL</u>	<u>AVSAWACRSL</u>	<u>VAHFGQERIV</u>	<u>TLFAWSLLIG</u>	<u>SLQOSCIIVI</u>
151	<u>QFAGWEDTPL</u>	<u>FQNIIVYSGQ</u>	<u>GVIGHTGORN</u>	<u>NLGHYLMWGI</u>	<u>LAAAYLNGQR</u>
201	<u>KIPAA LGVIC</u>	<u>LIMQTAVLGL</u>	<u>VNSRTILTYI</u>	<u>AAIALILPFW</u>	<u>YFRSDKSNRR</u>
251	<u>TMLGIAAAVF</u>	<u>LTALFQFSMN</u>	<u>TILETFTGIR</u>	<u>YE TAVERVAN</u>	<u>GGFDLPRQI</u>
301	<u>EWNKALAAFO</u>	<u>SAPIFGHAWN</u>	<u>SFAQQTFLIN</u>	<u>AEQHNIYDNL</u>	<u>LSNLFTHSHN</u>
351	<u>IVLQLLAEMG</u>	<u>ISGTL LVAAT</u>	<u>LLTGIAGLLK</u>	<u>RPLTPASLFL</u>	<u>ICTLAVSMCH</u>
401	<u>SMLEYPLWYV</u>	<u>YFLIPEGLML</u>	<u>FLSPAEASDG</u>	<u>IAFKKAANLG</u>	<u>ILTASAAIFA</u>
451	<u>GLLHLDWYTY</u>	<u>RLVNAFSPAT</u>	<u>DDSAKTLNRK</u>	<u>INELRYISAN</u>	<u>SPMLSFYADF</u>
501	<u>SLVNFA LPEY</u>	<u>PETQTWAEAE</u>	<u>TLKSLKYRPH</u>	<u>SATYRIALYL</u>	<u>MRQ GKVAEAK</u>
551	<u>QWMRATQSY Y</u>	<u>PYLMPRYADE</u>	<u>IRKLPVWAPL</u>	<u>LPELLKDCKA</u>	<u>FAAAPGHPEA</u>
601	KPCK*				

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/q738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLPYIYLPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	: : :					
g738	MSAETTVSGARPAAKLPYIYLPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m738.pep	TAGKKLFVDVKIPAISFLLFMAAAFYWQLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	: : : :					
g738	TAGKKLFVDVKIPAISFLLFMAAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGIGHIGQRN					
	: : : :					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m738.pep	NLGHYLMWGILAAAYLNGQRKIPAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	: :					
g738	NLGHYLMWGILASAYLNGQRKIPAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
m738.pep	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNITILETFTGIRYETAVERVANNGGFTDLPRQI					
	: :					
g738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANNGGFTDLPRQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m738.pep	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIYDNLNLSNFLTHSHNIVLQLLAEMG					
	: : : :					
g738	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHTIHDFNSTLFTSHSHNII LQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m738.pep	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	: : : :					
g738	ISGTLLVAATLLTGIAGLLKRSLTPASLFLLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
m738.pep	FLSPA EASDGIAFKKAANLGILTASAAIFAGLLHLDWTYTRLVN AFS PATDDSAKT LN RK					
	: : : :					
g738	FLSPA EASDGIAFKKAANLGILTASAAIFAGLLHLDWTYTRLVNS FSPAADDS AK T LN RK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKALKYRPHSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

a738.seq

```

1  ATGCCCCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CAAACTGCC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTCGCTCAG GCTGCAACCG TCGCCGACT TTTACCACGA TGCCCGCGC
151 GCAGCCGCC TGATTGTCCT GTGTTCCTC ACGGCAGGAA AAAAGCTGT
201 TGATGTCAA ATCCACCTA TCAGCTTCCT TCTGTTTGA ATGGCGCGT
251 TTTGGTATC TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACT GCCGTCAGCG CGTGGGCCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTT
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCG CCTACCTCA CGGACAACGA
601 AAAATCCCG CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTT GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACGCGC TGTTCGAAT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTACCCA TTCCCAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTCG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGAAGT GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAACCCCT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

a738.pep

```

1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAD
51  AAGLIVLLFL TAGKKLFDVK IPPISFLLEA MAAFWYLQAR LMNLIYPGMN
101 DIVSWFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

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1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAFQ SAPIFGHGWN SFAQOTFLIN AEQHNHNDL LSNLFTHSHN
 351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAH	PAAKLP	PIYILPCFL	WIGIVPFT	FALRLQPS	PDFYHDA
m738	MPAETTVSGAH	PAAKLP	PIYILPCFL	WIGIVPFT	FALKLKPS	PDFYHDA
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVK	KIPPISFLL	FAMAAFWYL	QARLMNLI	YPGMNDIV	SWIFILLAV
m738	TAGKKLFDVK	KIPISFLL	FAMAAFWYL	QARLMNLI	YPGMNDIV	SWIFILLAV
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQERIV	TLFAWSLL	IGSLLQSC	IVVIQFAG	WEDTPLFQ	NIIVYSGQ
	:					
m738	VAHFGQERIV	TLFAWSLL	IGSLLQSC	IVVIQFAG	WEDTPLFQ	NIIVYSGQ
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWG	ILAAAYLN	GQRKIPPA	LGAICLIM	QTAVLGLV	NSRTILTY
m738	NLGHYLMWG	ILAAAYLN	GQRKIPPA	LGVICLIM	QTAVLGLV	NSRTILTY
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRR	TILGIAAA	VFLTALFQ	FSMNTILE	TFTGIRY	ETAVERVAN
m738	YFRSDKSNRR	TLGIAAA	VFLTALFQ	FSMNTILE	TFTGIRY	ETAVERVAN
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAFQ	SAPIFGHG	WNSFAQOT	FLINAEQ	HNIHDNLL	SNLFTHSH
m738	EWNKALAAFQ	SAPIFGHG	WNSFAQOT	FLINAEQ	HNIYDNLL	SNLFTHSH
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLVAAT	LLTGIAGL	LKRPLTPA	SFLICTLA	VSMCHSM	LEYPLWYV
m738	ISGTLLVAAT	LLTGIAGL	LKRPLTPA	SFLICTLA	VSMCHSM	LEYPLWYV
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAEASDG	IAFKKAAN	LGILTASAA	IFAGLLH	LWDWYTRM	VNAFSPAT
m738	FLSPAEASDG	IAFKKAAN	LGILTASAA	IFAGLLH	LWDWYTRL	VNAFSPAT
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISAN	SPMLSFYA	DFSLVNF	ALPEYPET	QTWAEATL	KSLKYRPH
m738	INELRYISAN	SPMLSFYA	DFSLVNF	ALPEYPET	QTWAEATL	KSLKYRPH
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLKDKCAFAAA	PGHPEA			
m738	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLKDKCAFAAA	PGHPEA			
	550	560	570	580	590	600

a738.pep	KPCKX
m738	KPCKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA ADSTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAA PKETPKEKET PKENHTKPD TPKNTPAKPHK EILDNLFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCTT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRQPDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAA PKETPKENHT KPDTPKNTPP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

```

      10      20      30      40      50      60
m739.pep  MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE PQHTDSPRET
          10      20      30      40      50      60

      70      80      90      100     110     120
m739.pep  EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA
          70      80      90      100     110     120

      130     140     150     160           170
m739.pep  DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD
          :  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD
          130     140     150     160     170     180

      180     190
m739.pep  PKNTPPKPHKEILDKLF
          ||||| |||||:||
g739      PKNTPAKPHKEILDNLFX
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KQPADTAQT DRQPDDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLFX*

```

a739/m739 93.9% identity in 197 aa overlap

```

      10      20      30      40      50      60
a739.pep  MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTE PQHTDSPRET
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET
          10      20      30      40      50      60

      70      80      90      100     110     120
a739.pep  EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          70      80      90      100     110     120

      130     140     150     160     170     180
a739.pep  DRQPDDAGAQ AENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD
          130     140     150     160     170

```

1204

```

                190
a739.pep      PKNTPPKPHKEILDNLFX
              |||||
m739          PKNTPPKPHKEILDKLF
                180      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gccCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gTTTGATT
201 GAAACgtcaa ACCATGTTC TGTTTATTCC GATTGTTTG CTGGTTGTGT
251 ATTTGTTCCA CTATTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFTIKHH LKQGFDLKRQ TMLFPIIVL LVVLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AACTCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVLPHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KQHLINGII LACEATFLFK FVLFDTIKHH
              |||||
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KQHLINGII LACEATFLFK FVLFTIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIIL LIVLPHYFG AFX
              ||| |||||
g740          LKQGFDLKRQ TMLFPIIVL LVVLFHYFG AFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVLPHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLIVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||:|||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
          |||||
m740      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTCT
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TCAAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACATGCCGA CGGAAACTG ACCTATACCA TAGATTTTCG CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPONGTLL SAQGAETFK AGGKDNSLNT GKLKNDKISR
101 PDFVQKIEVD QGTITLASGE FQIYQDHSV VVALRIEKN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT
201 GCGGACACAA GGTGCGGAAA AACTTATGG AACCGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCA AGCAGGGAAA CGGCAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGCGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDQSVR KNEKLKLAQ GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSK KMVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQGNKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---	ALILTACSSGGGGVAAD	IGAGLADALTAPLDH	KDKGLQSLTL	DQ
	: :	:		:	:
g741	VNRTTFCCLSL	TAGPDSRLQRRGGGGVAAD	IGTGLADALTAPLDH	KDKGLKSLT	LEA
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLA	AQGAEKTY---	GNGDSLNTGKLKND	KVSRFD	FIRQIEVDGQLIT
	:	: :	:	:	:
g741	SIPQNGTLT	LSAQGAEKTFKAGG	KDNSLNTGKLKND	KISRFD	FVQKIEVDGQTIT
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHS	ALTAFQTEQIQD	SEHSGKMVAKRQ	FRIGDIA	GEHTSF
	:	:	:	:	:
g741	FQIYKQDHS	AVVALRIE	KINNPDKIDSL	INQRSFLV	SDLGGEHTAF
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGG	KLTYTIDFAAKQ	GNGKIEHLK	SPELNVDL	AAADIKPD
	:	:	:	:	:
g741	AFSSDDADG	KLTYTIDFAAKQ	GHGKIEHLK	TPEQNVEL	ASAEKKADEK
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSL	GIFGGKAQ	EVAGSAEVK	TVNGIRHIGL	AAKQX
	:	:	:	:	:
g741	GEEKGT	YRLALFGDRAQ	EIAGSATV	KIGEKV	HEIGIADKQX
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCCGAC ATCGGCGCGG
 101 TGCTTGCCGA TGACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
 201 GCGGCACAA GGTGCGGAAA AACTTATGG AAACGGCGAC AGCCTCAATA
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAG
 301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGCGGAG AGTCCAAGT
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
 401 AAGATTCGGA GCATTGAGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
 451 GGCGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
 501 CAGGGCGACA TATCGCGGGA CGGCATTCCG TTCAGACGAT GCCAGTGGAA
 551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGACA CGGCAAAATC
 601 GAACATTTGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
 651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCCTTACA
 701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep
 1 VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHKDKSL
 51 QSLTLDQSVR KNEKLKLAQ GAETYGNGD SLNTGKLKND KVSFRDFIRQ
 101 IEVDGQLITL ESGEFQVYKQ SHSALTALQT EQVQDSEHSG KMAVAKRQFRI
 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYTID FAAKQGHGKI
 201 EHLKSPELNV DLAAADIKPD KKRHAVISGS VLYNQAEKGS YSLGIFGGQA
 251 QEVAGSAEVE TANGIRHIGL AAKQ*

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
	: : : : :					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
	: : : : :					
m741	KNEKLKLAQAQGAEKTYNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
	: : : : :					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQGHGKIEHLKSPELNVDLAASDIKPKDKRHAIVISGSVLYNQAEKGS					
	: : : : : :					
m741	AGGKLTYYTIDFAAQGNKGKIEHLKSPELNVDLAAADIKPDGKRHAIVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
	: : : :					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TAAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCGGTAGG	CTTTTGTACT	GAAAAAACG
401	AAGTCATCCC	GTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTGATAATA	CTGCTTTTCA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTCCA	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC	CAATGGGGAA	TTAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTTCGGCG	GGAGCATGAT	TTCTTTGTCT	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGACCGG	CGATTTGTCT	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCGAC	GGCACGCCTG	CCTTACCCTG	TTTTCCTGGT	ACGGTGCCGG
1301	TTTGGAAGAC	CGTCAAAGTG	GCAGACGACC	ATGTTCCCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTCGCTGA	CTGCCAGCAC
1401	GCCTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

1208

```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTCCGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

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This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

m742.pep

```

1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N Q K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E Y A A G L S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D K C M S D P F A
201 L D F I C Q G S W G D P G V D A D K A E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D R Q W G I K L D L T G T Y G L F G R E H D F F V G Y A Y G D E
301 K I R S E Y L E I Y E R R Y R V R P N T G A T H G V Y A G S C Q E E P D G D L S S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A S T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I R A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N S S A D P Y N F S N F T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

a742.seq

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1  A T G G T T T A C G G C A T T G C C G A A G C C G A T G C G G G C A C A G C A G T G T G C T T A C
51  T T T G G G C G G C A T G T A T C A G A A G A T A G G G A G G T T C C T G A T T T T C G G G C A
101 T T A T T T T G T C T G T G A A A A T C A G A A A A C T G C C C G T T C A G T T C A A C G C C T
151 G C C T G C A A C C G G C T T T G C A A C T G C C G C G C A A C A C T T A T T T G G G G A G A G A
201 T T G G T C G C G G T T G A G T G C T G A C A A A T A C A A C C T T T T C T C A G G T T C A A A C
251 A T G T G T T G A C A A C G G T T G G C A G C T A A T G C C G A A G T G T C T T A T A C C A A G
301 A A T G A A T C C G A T G C G A A G G T G G G G C A G T T T T T C T G A A A A A C G A A C A T G C
351 G G C G G G T T T G T C A G A T G A G G A T G C G G T A G G C T T T T T G A C C G A A A A A A C G
401 A A G T C A T C C C G T T C G A G C C G A A A G A T A A G G C A T T G G A G A A A C T G A A A G C A
451 T A T C G T G A C G A A A C C G C C A A G G A A T A C C G T G A G C G C A A A G A C G A T T T T G T
501 T A A A A A C C G T T T C G A T A A T A C T G C T T T C G A G C A G T A C C G C A G C C C G T G
551 C C G C A G A A C G C A A A G C C G G T T T G A C G A G T G T A T G A G T G C C C T T T T G C G
601 C T G G A C T T T A T C T G T C A A G G T T C T T G G G G G A T C C G G G T G T T G A T G C C G A
651 C A A G T C G G A A T T T G T C G A T A A G C C C T T G C G A A G G A A G G C A T C T T T A A T A
701 A T G C G G C A C A C G T T T T C C A A A C A G C C T G T A T G A C T C T T C C T T A A T C G G
751 A A G G C T A C C G C C A A C C G A C G A T A C A G T T A T A T G C C G T T G C G G C A T A C C A A
801 A G A C G A C C G C C A A T G G G G A A T T A A A C T T G A C C T G A C C G G C A C A T A T G G G C
851 T G T T C G G G C G G G A G C A T G A T T T C T T G T C G C T A T G C C T A C G G C A T G A A
901 A A G A T A C G T T C C G A A T A T C T G G A A T C T A C G A A C C C G C C A C A G A G T A C G
951 T C C G A A T A C A G G G G C A A C G C A C G C G C G T G T A T G C G G G A A G T G T C A G G G G G
1001 A G C C G G A C G G T G A T T T G T C T T C T C T T T G G T C A G G G G G C A T A A G A A C C C
1051 G A T T G G C A G G C G T A C G A T G A A A A G G C A A C C G T A C C G T T T A T G C C G A A G A
1101 A T G C A G G A A T G C C A A G A A A A T A A A A C C G A G C C C A A G C T C G A T G C C G A A G
1151 G C A A G C A G G T G T A T T A C T A T G A C G A A T A C A G C G C A G C C G A C G C C A G T A

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1209

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGGT ACGGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG CTTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTTCGCTG CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTTCAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCGCCGAAG TCAACGCCGA
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGC CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGTAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

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This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
  1 MVGIAEADA GDSSVLTGG MYQKSREVPD FSGIILSCEN QKTAPFSSTP
 51 ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDECM SAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVGYAYGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGE PDGDL S PLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYN DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVMV ADDHVPALYN
451 YAKYLNNTKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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a742/m742 98.5% identity in 783 aa overlap

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              10      20      30      40      50      60
a742.pep      MVGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR
              |||
m742           MVGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR
              10      20      30      40      50      60

              70      80      90      100     110     120
a742.pep      NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL
              |||
m742           NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL
              70      80      90      100     110     120

              130     140     150     160     170     180
a742.pep      SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR
              |
m742           SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR
              130     140     150     160     170     180

              190     200     210     220     230     240
a742.pep      SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAAQRFP

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1210

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|||||:|||||:|||||:|||||:|||||:|||||:
m742      SRRAAERKAGFDKCMSDFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
          190      200      210      220      230      240

          250      260      270      280      290      300
a742.pep   NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          250      260      270      280      290      300

          310      320      330      340      350      360
a742.pep   KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      KIRSEYLEIYERRVRPNTGATHGVYAGSCQEEP DGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360

          370      380      390      400      410      420
a742.pep   RTVYAEECRNAAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      RTVYAEECRNAAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD
          370      380      390      400      410      420

          430      440      450      460      470      480
a742.pep   GTPAFTGFSGTVPVWKT VKVADHDVPALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGG
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      GTPAFTGFSGTVPVWKT VKVADHDVPALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGG
          430      440      450      460      470      480

          490      500      510      520      530      540
a742.pep   LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
          490      500      510      520      530      540

          550      560      570      580      590      600
a742.pep   QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAF LQGRLNASFALFYLEQKNR
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAF LQGRLNASFALFYLEQKNR
          550      560      570      580      590      600

          610      620      630      640      650      660
a742.pep   TVVDFGYVPGAGGKQGSFQTVAKPIGKVVS RGAEFELSGELNEDWKVFAGYTYNKSRYKN
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVVS RGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660

          670      680      690      700      710      720
a742.pep   AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720

          730      740      750      760      770      780
a742.pep   RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780

a742.pep   WQFX
          |||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein (*Pseudomonas putida*) Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNTNKTHSLTAGTRFNVTLRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFNLTDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQFASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDSAKTVLPLVGTNYEVGWKGAFLOQRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTCAGGCG CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSRLD DKAHVHLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCTG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

1212

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATTATGAC CATATGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSCLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRSTATGM RIAGKDT PQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPPG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

	10	20	30	40	50	60
a743.pep	MNQNHFSCLKILTVM LLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT					
m743	MNQNHFSCLKILTVM LLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a743.pep	IDRMSTATGMRIAGKDT PQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
m743	IDRMSTATGMRIAGKDT PQSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a743.pep	SRGFYIDQIGEDGITVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPPG					
m743	SRGFYIDQIGEDGMTVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPPG					
	130	140	150	160	170	180
a743.pep	TVNLIRKR					
m743	TVNLIRKX					

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAAC TG GAAAGACAGC ATATGCTGTT TATTTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGATCC GGAAATTGTA
451 CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTAA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTATTATGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
1051 AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTTCTCG AAATTTTTTG AATTTTTAAA CGGGAAGAT AGATTAAAT

```

1213

```

1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGA AAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAAC TGA AACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAGGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKTLFEG FVDAANYRRR ENKDLFNRI F VKGEYLDL ELPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQ IITTESKFQA NLGFIERKEK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNQN TKLQDNSVEL DWRTDYKSYR
301 SSKIFGVFDH LLRTQEQEKD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKKSKEY VVAEDFDNTS FOREYSIYLL
401 GEIKDHLLEY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLOFLF DLNVIAAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTTA TGCCTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTGTG ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKT SKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCCTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCTCAGTT CCGATCTGCG CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACCGGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCCGAAAAC GGGGAAACCG
251 CGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 CACAGCGAAA TCAGCGAGCC TGAACGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCAGAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAC TGCTGCCGAA AAAACCAAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

751	GCGCAAAAAA	CGGACAAAGC	GGACAAAACC	AAAACCGCGG	AGAAGGAAAA
801	ATCCGGCAGG	CGGGGCAAAA	AAGCGGCCAT	TCAGGCAGGT	TATGCCGAAA
851	AACGAGCGCG	CTTAGGCTTC	CAGCGCAAAA	TGAAGGCGCG	GGGTATCGAT
901	TCGACCATCA	CGGAAATCAT	GACCCGACAC	GGCAAAAGTT	ATCGCGTCAA
951	ATCAAGCAAC	TATAAAAACG	CAAGGGATGC	CGAATCGCAT	TTGAACAAAC
1001	TGCGCGTGCA	CGGCATCGCC	GGCCAGGTAA	CGGATGAATA	G

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

g746.pep

1	MSENKQNEVL	TGYEQLKRRN	RRRLVTASSL	VAASCILLAA	ALSSDPADSN
51	PAPQAGETGA	TESQTANTAQ	TPALKSAAEN	GETAADKPQD	LAGEDKPSAA
101	DSEISEPENV	GAPLVLINDR	LEDSNIKGLE	ESEKLQQAET	AKTEPKQAKQ
151	RAAEKVSATA	DSTDTVAVEK	PKRTAEPKPK	KAERTAEAKP	KAKETKTAEK
201	VADPKPTAAE	KTKPDATAKS	SAVKEAKKAD	KAEGKKATAEK	DRSDGKKHET
251	AQKTDKADKT	KTAPEKESGK	AGKKAAIQAG	YAEGERALSL	QRKMGAAGID
301	STITEIMTDN	GKVVYRVKSSN	YKNARDAERD	LNKLRVHGIA	GQVTNE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

```
m746.seq
1 ATGTCGCGAAA ACAAAACAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAA CGGC AAGTTGCGCT GTTGCCGCCT
101 CCTGCACTCT GCTGGCAGCC GCCCTCAGTT CCGCGCCTGC GTGCACAGAT
151 GCCGCGCGAAA CAAGCGGCGT AGAAAAACAA CGCGCAGGTG CGGCACAAAC
201 CCCTGCCTTG TAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCCAAG
251 ACAAGCCTTG GGCGCCGCAG AGCGAAATCA GCGAGCTGA AACCTAGGC
301 GCGCCGCTTG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAAG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GTCGCCGAAA AAGTGCCGCG AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGA AAAACCGC AAACCGACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAA CCGAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAA AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCCGACG
701 GCAAAAAACA CGAAACGGCA CAAAAAACCG ACAAGCGGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCTTCCA GCGCAAAATG AAGCGGCGG
851 GTATCGATTG GACCATCACC GAAACTTATGA CCGCAACAGG CAAAGCTTAC
901 CGCGTCAATC CAAGCAACTA TAAAAACGCA AGGGATGCCG AACCGGATT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

```
m746.pap
  1 MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51 AGETSGVNEK AGAAQPTAL KSAADKPDQL AGEDKPSAAD SEISEPENVG
101 APLVLLNERL EDSNIGLEA SEKLQQAETA KTAPKQAKQR AAEKVPTAD
151 STDTVAVEKP KRTAETKPKQ AERTAKAKPK AKETKTAEKV ADPKPTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKTTAEKD RSDGKKHETA QKTDKADTK
251 TAEKEKSGDK AAIQAGYAEK ERALSQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGTAQGT NE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

m746/g746 89.9% identity in 346 aa overlap

	10	20	30	40	50	
m746.pep	MSENKQNEVLSGYEQLKRNRNRRRLVTASCLVAASCILLAAALSSGPAEQT---	AGETSG				
	: :	:	:	:	: :	
g746	MSENKQNEVLTGYEQLKRNRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA					
	10	20	30	40	50	60
	60	70	80	90	100	109
m746.pep	VENKAAGAAQTPAKSAA-----DKPQDLAGEDKPASAADSEISEFENVGAPLVLINER					
	: : : :					
g746	TESQTANTAQTTPALKSAAENGETAADKPQDLAGEDKPASAADSEISEFENVGAPLVLINDR					
	70	80	90	100	110	120

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```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
g746      LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ
              130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
              190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALSQRKMKAAAGID
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALSQRKMKAAAGID
              250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
              310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA  ACAAACAAA  CGAAGTCCTG  AGCGGTACG  AACAACTCAA
51  ACGGCGCAAC  CGCCGCCGCC  TCGTAACGGC  AAGTTGCCTG  GTTGCCGCCT
101 CCTGCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151 GCCGGCGAAA  CAAGCGGCGT  AGAAAACAAA  GCGGCAGGTG  CGGCACAAAC
201 CCCTGCCTTG  AAATCCGCCG  CCGACAAACC  GCAGGACTTG  GCAGGCGAAG
251 ACAAGCCTTC  TGCCGCCGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301 GCGCCGCTGG  TGCTGATTAA  CGACCGCCTC  GAAGACAGCA  ACATCAAAGG
351 TTTGGAAGCA  TCCGAGAAAC  TGCAACAGGC  AGAAACCGCC  AAAACCGCAC
401 CGAAGCAGGC  AAAACAACGC  GCTGCCGAAA  AAGTGCCGGC  AACTGCCGAC
451 AGTACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACTG  CCGAAACAAA
501 ACCGCAAAAA  GCGGAACGCA  CTGCCAAAGC  CAAGCCCAAA  GCCAAAGAAA
551 CCAAAACCGC  CGAAAAAGTT  GCCGACAAAC  CGAAACTGC  CGCCGAAAAA
601 ACCAAACCGG  ATACGGCAAA  ATCCGACAGC  GCGGTAAAAG  AAGCGAAAAA
651 AGCCGACAAG  GCTGAAAGCA  AAAAAACAGC  CGAAAAAGAC  CGTTCGGACG
701 CCAAAAAACA  CGAAACGGCA  CAAAAAACCG  ACAAGCGGGA  CAAGACCAAA
751 ACCGCCGAGA  AGGAAAAATC  CGGTAAAAAA  GCCGCCATTG  AGGCAGGTTA
801 TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGGCGG
851 GTATCGATTG  GACCATCACC  GAAATTATGA  CCGACAACGG  CAAAGTTTAC
901 CGGTCCTCAAT  CAAGCAACTA  TAAAAACGCA  AGGGATGCCG  AACGCGATTT
951 GAACAAATTG  CGCGTACACG  GTATCGCCGG  TCAGGTAACG  AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL  SGYEQLKRRN  RRRLVTASCL  VAASCILLAA  ALSSGPAEQT
51  AGETSGVENK  AAGAAQTPAL  KSAADKPQDL  AGEDKPSAAD  SEISEPENVG
101 APLVLINDRL  EDSNIKGLEA  SEKLQQAETA  KTAAPKQAKQ  AAEKVPATAD
151 STDTVAVEKP  KRTAETKPOK  AERTAKAKPK  AKETKTAEKV  ADKPKTAAEK
201 TKPDTAKSDS  AVKEAKKADK  AESKKTAEKD  RSDGKKHETA  QKTDKADKTK
251 TAEKEKSGKK  AAIQAGYAEK  ERALSLQRKM  KAAGIDSTIT  EIMTDNGKVY
301 RVKSSNYKNA  RDAERDLNKL  RVHGIAGQVT  NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
m746      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
              10      20      30      40      50      60

```

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```

          70      80      90      100     110     120
a746.pep   AAGAAQTALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          |||||||:|||||
m746       AAGAAQTALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
          70      80      90      100     110     120

          130     140     150     160     170     180
a746.pep   SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPQKAERTAKAKPK
          |||||||:|||||
m746       SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPQKAERTAKAKPK
          130     140     150     160     170     180

          190     200     210     220     230     240
a746.pep   AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||||||:|||||
m746       AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          190     200     210     220     230     240

          250     260     270     280     290     300
a746.pep   QKTDKADTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAGIDSTITEIMTDNGKVY
          |||||||:|||||
m746       QKTDKADTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAGIDSTITEIMTDNGKVY
          250     260     270     280     290     300

          310     320     330
a746.pep   RVKSSNYKNARDAERDLNKLRVHGIAGQVTNEX
          |||||||:|||||
m746       RVKSSNYKNARDAERDLNKLRVHGIAGQVTNEX
          310     320     330

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

          10      20      30      40      50      60
a747.pep  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR
          |||||
m747      LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR
          10      20      30      40      50      60

          70      80      90     100
a747.pep  HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
          ||| |||||
m747      HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
          70      80      90     100

```

a747/m80195

gi|150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272
 Score = 59.3 bits (141), Expect = 6e-09
 Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR 60
 + PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
 Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTLNKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
 +T + E + GD + ++ EYG RV F
 Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```

1  ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51  CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
101  AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151  CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCGCG
201  ACAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251  AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301  ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351  CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTTACCG
401  TGGGGGTGGG CAGCAGCCTG TTGACGGCC GGTTCGGACT CAAAGACAAA
451  AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCCAACG ATAAGCTGCA
501  AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGC GCCTTCACCC
551  CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAACA CACCGCCCAA
601  ACCGCCGTGA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651  CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701  ACCCAAGGTT TCCGATCCC AAAACCGCCG ACGAGGTTT ATGGACGGGC
751  GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801  TCAGGCAGTC CGCCTTATCC GCCGCTTGT CGAGTTTGG GACAGGACGC
851  CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAAA CAGCGGGGCG
901  CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTCG CCAAAGACCC
951  CGAGGGTGAT ATCAGGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001  GCGATCCCGA ATTCTCAAA AACACTGCC TCTTCGCGG CGCCTACAGC
1051  TATTCTCGCG GACCCGCCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101  CGTCTGCTAT CAGGCAAATC TTGCGGACGG TTTCATCTTC GTGCAAAACC
1151  TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201  TATTTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251  GCTGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```

1  MSQNQPAQPT KRNLFKTALE VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPRQAF SIMCAFEDVTA QSAKQLENLF RTLTARIEFL
101  TQGGEYQDGD DKLPASAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151  KTVHLQEMRD FPNDKLQKSW CDGDLQLQIC AFTPETCQTA LRDIKHTAQ
201  TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251  VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLQEQTG IFGRRKYSGA
301  PMDGKKEADQ PDFAKDPEGD ITPKDSHMLR ANPRDPEFLK KHCLFRFRAYS
351  YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EEYISPFGGG

```


m748.seq

1	ATGAGCAAAA	AACAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAAAC
51	CGCGATCGCA	GCCGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGGCGGCA
101	AAAAACAGGG	CGAAACCGCC	GAACCGCACC	CCGAAAGGCCA	AACTCTCGCC
151	CAAGCCTATC	CCTGCTACGG	CGAACATCAG	CGAGGCATCG	TTACGCGCGCA
201	GCAGGCGTGT	TCGATTATGT	CGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCAGCGTGA	CCGCCCCGAT	CGAGTTTCTC
301	ACCCAAGGCG	CGGAATACCA	AGACGGCGAC	GACAAACTTC	CGCCAGCCCGG
351	CAGCGGCATT	TTGGGCAAA	CCTTCAACCC	CGACGGGTTG	ACCGTTACCG
401	TGGGGGTGGG	CAGACGCCTG	TTTGAACGGC	GGTTCGGACT	CAAAGACAAA
451	AAACCGATT	ATTTGCAGGA	AATGCGCGAC	TTCTCCAACG	ATAAGCTGCA
501	AAAAAGCTGG	TGCGACGGCG	ATTTAGCCTT	GCAAACTGTG	GCCTTCACCC
551	CCGAAACCTG	CCAAGCCGCC	CTGCGCGACA	TCATCAAACA	CACCGTCCAA
601	ACCGCGCTTA	TCCGTTGGAG	TATCGACGGG	TGGCAGCCCA	AATCCGAACC
651	CGCGCGGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCAGGGAC	GGCAGCGGGA
701	ACCCCAAAGT	TTCCGATCCC	AAACCTGCCG	ACGAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	ACAGCCTCGA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGCGAGTC	CGCCTTATCC	GCCACTTTGT	CGAGTTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACGAC	ATTTTCGGGG	GGCGCAAATA	CAGCGGTGCG
901	CCGATGGACG	GCAAAAAAGA	AGCCGACCAA	CCGAGTTTTG	CAACAGACCC
951	CGAGGGTGAT	ATCACGCCCA	AAGACAGCCA	TATACGCCCT	GCGAATCCGC
1001	GCGATCCCCA	ATTCTCCAAA	AAACACCCGC	TCTTCCGGCG	CGCCTACAGC
1051	TATTTCGGCG	GACTCGCTTA	AAGCGGACAG	CTTGATGTGC	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAAACC	TTGCCGACGG	ATTATCTTCT	GTCAAAACC
1151	TCCTCAACCG	GCAAGCCCTG	GAAGAATACA	TCAGCCCTTT	CGGCGGCGGC
1201	TATTTTCTCG	TTCTTCCCGG	CGTGGAAAAA	GCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GTATAA			

m748.pcp

```

1 MSKKQPAQPI RRTLFKTAIA AGAVGAIGGY LGGKKOGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQAAF SIMCAFDVTA QSAKQLENLF RTLTAIEFL
101 TQGGEYQDGD DKLPPAGSGI LGKANFPDGL TVTVGVGSSL FDRGRFLGKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDSLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRSIDG WQPKSEPGAM AARNLLSFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQT D IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHLRFRRAYS
351 YSRGLASSGQ LDVGLVDFVCY QANLADGFFI VQNLLNGEPL EEEYISPFGGG
401 YFFVLPGVEK GGFLGOGIIG V*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPTFR	TLFKTAIAAGAV	GAIGGYLGKKQ	GETAERTAESQ	HSPQAYPCYGE	HQ
g748						
	MSQNQPAQPTK	RNLFKTALAVG	AIGAIGGYFGG	KKQGETAERTA	ESQHSPOAYPC	YGEHQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m748.pep	AGIVTPQQA	FSIMCAFDVTA	QSAKQLENL	FRTLTARIE	FLTQGGEYQD	GGDKLPPAGSGI
g748						
	AGIVTPRQA	FSIMCAFDVTA	QSAKQLENL	FRTLTARIE	FLTQGGEYQD	GGDKLPSAGSGI
	70	80	90	100	110	120
	130	140	150	160	170	180
m748.pep	LGKAFNPDGL	TVTVGVGSS	LFDGREFGLK	DKKPIHLQEM	RDFSNDKLQK	SWCDGDL
g748						
	LGKAFNPDGL	TVTVGVGSS	LFDGREFGLK	DKKTVHLQEM	RDFPNDKLQK	SWCDGDL
	130	140	150	160	170	180
	190	200	210	220	230	240
m748.pep	AFTPETCQA	ALRDIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSD

g748	AFTPETCQTALRDIIKHTAQTA VIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP	190	200	210	220	230	240
m748.pep	KTAD EVLWTGVAANS LDEPEWAKNGSYQAVRLIRHFVEFWDRTP LQEQT DIFGRRKYSGA	250	260	270	280	290	300
g748	KTAD EVLWTGVAANS LDEPEWAKNGSYQAVRLIRRFVEFWDRTP LQEQT DIFGRRKYSGA	250	260	270	280	290	300
m748.pep	PMDGKK EADQPDFAKDPEGDITPKD SHIRLANPRDPEFLKKHRLFR RAYSYSRGLASSGQ	310	320	330	340	350	360
g748	PMDGKK EADQPDFAKDPEGDITPKD SHMLANPRDPEFLKKHCLFR RAYSYSRGPASSGQ	310	320	330	340	350	360
m748.pep	LDVGLV FVCYQANLADGFIFVQNLLNGE PLEEYISPFGGGYFFVLP GVKG GGLGQGLLG	370	380	390	400	410	420
g748	LDVGLV FVCYQANLADGFIFVQNLLNGE PLEEYISPFGGGYFFVLP GVKG GGLGQGLPG	370	380	390	400	410	420
m748.pep	VX						
g748	VX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2565>:

```
a748.seq
1 ATGAGCAAAA ACCAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51 CGCGATCGGA GCTGGAGGAC TCGGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAAACGGG CGAAACCCGC TAACGCACCG CGGAAGGCCA ACATCGCGCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTTCCT
251 AGCACTGGGA AAACCTGTT CGCACCGTGA CCGCCCGCAT CGAGTTTCTC
301 ACCAAGGCGC GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTTACCG
401 TGGGGGTGGG CAGACGCCTG TTTGACGGCC GGTTCGGACT CAAAGCAAAA
451 AAACGATTTC ATTTGCAGGA AATTCGCGAC TTCTCAAACG ATAAGCTGCA
501 AAAAAAGCTG TGCAGCGGCG ATTTGAGCCT CGAAATCTGT CGCTTACACC
551 CCGAAACCTG CCAAGCCGCG CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCGTTTGGC CTTCGCGCAC GGCACGGGCA
701 ACCCCAAAGT TTCCGACCCC AAAACTGCGC ACAGAGTTT GTGACGGGG
751 GTGGCCGCGA ACAGCCTCGA CGAACCGGAG TGGCGCAAAA ACGGCAGCTA
801 TCAGGCAGAT CGCCTTATCC GCCACTTTGT TGAATTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTGGGCG GCGCAATAA CAGCGGCGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGGAAT ACCACGCCCA AAGACAGCCA TATACGCTG GCGAATCCGC
1001 GCGATCCGGA GTTCTCTAAA AAACACCGCC TCTTCGCGCC CGCCTACAGC
1051 TATTGCGCGG GACTCGCCTC AAGCGGACAG CTGATGTGCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCACTTTC GTGCAAAACC
1151 TCCTCAACGC CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGA AAAA GGCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2566; ORF 748.a>:

```
a748.pep
1  MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSP
51  QAYQPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTLTARIEFL
101 TQGGHEYQDGD DKLPPAGSGI LGKAFNPDLG TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCOAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQT D IFGRRKYSGA
301 PMDGKKEADD PDFAKDPGEN TQKLDOSHIL ANPRDPEFLK KHRLFRRAYS
351 YSRGLASSGQ LDVLGVFVCY QANLADGFIF VQNLNNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFGLGOGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSPQAYPCYGEHQ
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGYQDGGDKLPPAGSGI
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGYQDGGDKLPPAGSGI
a748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC
a748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
m748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
a748.pep	KTADEVLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA
m748	KTADEVLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ
a748.pep	LDVGLVFVCYQANLADGFI FVQNLLNGEPLEEYISPFGGGYFFVLPGVEKGGFLGQGLLG
m748	LDVGLVFVCYQANLADGFI FVQNLLNGEPLEEYISPFGGGYFFVLPGVEKGGFLGQGLLG
a748.pep	VX
m748	VX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGGCGGTT	CGGTCGGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGGCTTTCC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTC	AGGCGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTTTTGACC	CGCCACCGCG	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGTGTG	AAGACGACTT
651	CAAAGACGGT	GCGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCTGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC

1221

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801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 CCGCGGGCAG TAAATCAGC GGCAGGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TGCGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCCTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCATA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIIVN
51 DNACEFNLIT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSQVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCCG AGGCGGAGAA AGTCGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCACTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCAGT GGAAGTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAGC CTAAGCTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCTGTGTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACCGC GCGAAAGATG CCGGATTAC CGGCTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGCGGGGAGC TAAATCAGC GCGGAAGAAG ACCGCTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIIVN
51 DNACEFNLIT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSQVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep  MRKFNLALSVMALGLTACQPPEAEKAAPAAASGEAQTANEGGSVSIIVNDNACEFNLIT
          |||
g749      MRKFNLALSVMALGLTACQPPEAEKAAPAAASGETQSANEGGSVGIIVNDNACEFNLIT
          10      20      30      40      50      60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPOPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRIVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

```

1  ATGAGAAAAT  TCAATTTGAC  CGCATTGTCC  GTGATGCTTG  CCTTAGGTTT
51  GACCGCGTGC  CAGCCGCCGG  AGCGGAGAA  AGCTGCGCCG  GCAGCGTCCG
101  GTGAGGCGCA  AACCGCCAAC  GAGGGCGGTT  CGGTCAGTAT  CGCCGTCAAC
151  GACAATGCCT  GCGAACCGAT  GGAAGTACC  GTGCCGAGCG  GACAGGTTGT
201  GTTCAATATT  AAAAACAACA  GCGGCCGCAA  GCTCGAATGG  GAAATCCTGA
251  AAGGCGTGAT  GGTGGTGGAC  GAGCGCGAAA  ACATCGCCCC  CGGACTTTCC
301  GATAAAATGA  CCGTCACCCT  GTTGCCGGGC  GAATACGAAA  TGAATGCGCG
351  TCTTTTGACC  AATCCGCGCG  GCAAGCTGGT  GGTAACCGAC  AGCGGCTTTA
401  AAGACACCGC  CAACGAAGCG  GATTTGGAAA  AACTGTCCCA  ACCGCTCGCC
451  GACTATAAAG  CCTATGTTCA  AGGCGAAGTC  AAAGAGCTGG  TGGCGAAAAC
501  CAAAACCTTT  ACCGAAGCCG  TCAAAGCAGG  CGACATTGAA  AAGGCGAAAT
551  CCCTGTTTGC  CGACACCCGC  GTCCATTACG  AACGCATCGA  ACCGATTGCC
601  GAGCTTTTCA  GCGAACTCGA  CCCCCTCATC  GATGCGCGTG  AAGACGACTT
651  CAAAGACGGC  GCGAAAGATG  CCGGATTTAC  CGGCTTCCAC  CGTATCGAAT
701  ACGCCCTTTG  GGTGGAAAAA  GACGTGTCCG  GCGTGAAGGA  AATTGCAGCG
751  AAATGATGA  CCGATGTCGA  AGCCCTGCAA  AAAGAAATCG  ACGCATGGC
801  GTTTCCTCCG  GGCAAGGTGG  TCGGCGGCGC  GTCCGAACGT  ATTGAAGAAG
851  TGGCGGGCAG  TAAATCAGC  GCGGAAGAAG  ACCGGTACAG  CCACACCGAT
901  TTGAGCGACT  TCCAAGCCAA  TGTGGACGGA  TCGAAAAAAA  TCGTCGATTT
951  GTTCCGTCCG  TTGATCGAGA  CCAAAAACAA  AGCCTTGTTG  GAAAAAACCG
1001  ATACCAACTT  CAAACAGGTC  AACGAAATTC  TGGCGAAATA  CCGGACTAAA
1051  GACGGTTTTG  AAACCTACGA  CAAGCTGGGC  GAAGCCGACC  GCAAAGCGTT
1101  ACAGGCCTCT  ATTAACGCGC  TTGCCGAAGA  CCTTGCCCAA  CTTCCGCGCA
1151  TACTCGGCTT  GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

```

1  MRKFNLTALS  VMLALGLTAC  QPPEAEKAAP  AASGEAQTAN  EGGSVSIAVN
51  DNACEPMELT  VPSGQVVFNI  KNSGRKLEW  EILKGMVVVD  ERENIAPGLS
101  DKMTVTLLPG  EYEMTCGLLT  NPRGKLVVTD  SGFKDTANE  DLEKLSQPLA
151  DYKAYVQGEV  KELVAKTKTF  TEAVKAGDIE  KAKSLFADTR  VHYERIEPIA
201  ELFSELPVI  DAREDDFKDG  AKDAGFTGFH  RIEYALWVEK  DVSGVKEIAA
251  KLMTDVEALQ  KEIDALAFPP  GKVVGGASEL  IEEVAGSKIS  GEEDRYSHTD

```

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	MRKFNLTALS	VMLALGLT	TACQPPEA	EKAAPAS	GGEAQT	ANEGGS	SVSIAV	NDNACE	PMELT
m749	MRKFNLTALS	VMLALGLT	TACQPPEA	EKAAPAS	GGEAQT	ANEGGS	SVSIAV	NDNACE	PMELT
a749.pep	VPSGQVVF	NIKNNSGR	KLEWEIL	KGVMVVD	ERENIAP	GLSDKMT	VTLLPGE	YEMTCG	LLT
m749	VPSGQVVF	NIKNNSGR	KLEWEIL	KGVMVVD	ERENIAP	GLSDKMT	VTLLPGE	YEMTCG	LLT
a749.pep	NPRGKLVV	TDGFKDT	ANEADLE	KLSQLAD	YKAYVQ	GEVKEL	VAKTKTF	TEAVKA	GDIE
m749	NPRGKLVV	TDGFKDT	ANEADLE	KLSQLAD	YKAYVQ	GEVKEL	VAKTKTF	TEAVKA	GDIE
a749.pep	KAKSLFAD	TRVHYER	IEPIAEL	FSELDPV	IDAREDD	FKDGAK	DAGFTG	FHRIEY	ALWVEK
m749	KAKSLFAD	TRVHYER	IEPIAEL	FSELDPV	IDAREDD	FKDGAK	DAGFTG	FHRIEY	ALWVEK
a749.pep	DVSGVKEI	AAKLMTD	VEALQKE	IDALAFP	PGKVVG	GASELIE	EVAGSK	ISGEED	DRYSHTD
m749	DVSGVKEI	AAKLMTD	VEALQKE	IDALAFP	PGKVVG	GASELIE	EVAGSK	ISGEED	DRYSHTD
a749.pep	LSDFQANV	DGSKKIV	DLFRPLI	ETKNKAL	LEKTDTN	FKQVNEI	LAKYRTK	DGFETYD	DKLG
m749	LSDFQANV	DGSKKIV	DLFRPLI	ETKNKAL	LEKTDTN	FKQVNEI	LAKYRTK	DGFETYD	DKLG
a749.pep	EADRKALQ	ASINALA	EDLAQL	LRGILGL	KX				
m749	EADRKALQ	ASINALA	EDLAQL	LRGILGL	KX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

1	GTGAAACCGC	GTTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCCTG
51	TTCGCCCCGA	CCTGCCGCCG	AAAAAACTGT	ATccgCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACggtcgcc	gtgtAcgaCt	ggCGCGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGG	CTATTGCGAG	CCTGCATTTG	ACAAGCGGCG	AACGGTGGGG
301	ACGCTGTTTG	AGCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCGCAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TTGAATGCGC	AGATTGACGC	GCTGTTCGCC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCTGGT	TACAGGCAAC
601	AAGGTGTCCG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCGCG	CTGCCGCCCG	TGGACGAATC	TTTACGCAAC	GAAGGGCACG
701	GGCAGCCCGT	TTCCTTCGAA	TACATCAAAG	AGAAAAACCC	CGGCTGGATT
751	TTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

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```

801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGAAGCGCA
851 AGCAAATCAT CGTCATGCCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG
901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
951 AGAACCCGTT GCGGCGCAGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

```

g750.pep
1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
51 VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
101 TLFEPDCESL HRHNPQFVIT GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS
151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN
201 KVSAGFTQSR LASWIHGDIQ LPPVDESIRN EGHGQPVSEF YIKEKNPGWI
251 FIIDRTAAIG QEGFAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
301 RQLIQAAEQL KAAFEKAEPV AAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

```

m750.seq
1 GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGCTCTGC TGACCGCCTG
51 TTCGCCCCGAA CCTGCCGCGG AAAAACTGT ATCCGCGCGA TCCGCATCTG
101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGGCCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTGAG
301 CCGGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGCGGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTCCGCCA AACGCGCGAA GCCGCCAAAG
551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC
601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCCCTGT GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC
751 CGTACCGCCG CCATCGGGCA GGAAGGCGCG GCGGCTGTCG AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
851 TCATGCTGCG CGCGAACTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
901 CAGGCGGCGG AGCAGTTGAA GGCGGCGGTT AAAAAGGCAG AACCCGTTGC
951 GCGGGGAAA AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

```

m750.pep
1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51 NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAQ IDALFAQTR AAKGKGRGLV LSVTGNKVSA
201 FTQSRLASW IHGDIPLPPV DESLRNEGHG QPVSEFYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
301 QAAEQLKAFF KKAEPVAAGK K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

```

          10      20      30      40      50
m750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA----ATLTVPRTARGDAVVPKNPERVA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g750       VKPRFYWAACAVLPAACSPEPAAEKTVSAAQAASQASTPVATLTVPRTARGDAVVPKNPERVA
          10      20      30      40      50      60

          60      70      80      90     100     110
m750.pep  VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g750       VYDWAALDTLTEPGNVGATTAPVRVDYLQPAFDKAATVGTLFEPDCESLHRHNPQFVIT
          70      80      90     100     110     120

          120     130     140     150     160     170
m750.pep  GGPGEAEYEQAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAELKAQIDALFA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

[illegible]

a750.seq

1	GTGAAACCGC	GTTTTTATTG	GGCAGCCTGC	GCCGCTCTGC	TGACCGCCTG
51	TTCGCCCGAA	CCTGCCGCCG	AAAAAACTGT	ATCCGCCGCA	TCCGCATCTG
101	CCGCCACACT	GACCGTGCCG	ACCGCGCGGG	GCGATGCCGT	TGTGCCGAAG
151	AATCCCGAAC	GCTGCGCCGT	TACAGACTGG	GCGCGTGTGG	ATACGCTGAC
201	CGAATTGGGT	GTGAATGTGG	GCGCAACCAC	GCGCGCCGGT	GCGCGTGGATT
251	ATTTGACAGC	TGCATTTGAC	AAGGCGGCCA	CGGTGGGGAC	GCTGTTCCGAG
301	CCCGATTACG	AAGCCCTGCA	CCGCTACAAT	CCTCAGCTTG	TCATTACCGG
351	GCGGCGGGCG	GCGGAAGCGT	ATGAACAGTT	GCGCAAAAAC	GCGACCACCA
401	TAGATCTGAC	GGTGGACAAC	GGCAATATCC	GCACCAGCGG	CGAAAAGCAG
451	ATGGAGACCT	ATGGCGGGAT	TTTCGGGAAG	GAAGCGCGCG	GCGCGGAATT
501	GAAGGCGCAG	ATTTGACGCG	TGTTCCGCCA	AACGCGCGAA	GCCGCCAAGG
551	GCAAAAGGACG	GCGGCTGGTG	CTGTGCGTTA	GCGGCAACAA	GGTGCTCCGC
601	TTCGGCACGC	AGTCGCGGTT	GGCAAGTTGG	ATACACGGCG	ACATCGGCCT
651	ACCGCTGTGA	GATGATACTT	TACGCAACGA	GGGCGACGGG	CAGCCTGTTT
701	CCTTCGAATA	CATCAAAGAG	AAAAACCCCG	ATTGGATTTT	CATCATCGAC
751	CGTACCGCCG	CCATCGGGCA	GGAAAGGCCG	GCGGCTGTCC	AAGTATTGGA
801	TAACGCGCTG	GTACGCGGCA	CGAACGCTTG	GAAGCGCAAG	CAAAATCATCG
851	TCATGCCTGC	CGCGAACTAC	ATTGTGCGGG	GCGGCTCGCG	GCAATTGATT
901	CAGGCGGGCG	AGCAGTTGAA	GGAGGCGTTT	GAAAAGGCAG	AACCCGTTGC
951	GCGCGGGAAA	GAGTAG			

a750.pep

1	VKPRFYWAAC	AVLLTACSPE	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERVAVYDV	AALDTLTTEL	VNVGATTAPV	RVDYLQPAFD	KAATVGTGLFE
101	PDYEAALHYD	PQLVTITGGP	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ
151	METLARIFGK	EARAELKAQ	IDALFAQTRE	AAKGKGRGLV	LSVTGNKVSF
201	FGTQSRSLAS	IHGDI GLPPV	DESLRNEGHG	QPVSF EYIKE	KNPDWIFIID
251	RTAAIGQEGP	AAAEVLDNAL	VRGTNAWKRR	QIIVMPAANY	IVAGGSRLQI
301	QAAEQLKEAF	EKAEPVAAGK	E*		

Homology with a predicted ORF from *N. meningitidis*

a750/m750 98.8% identity in 321 aa overlap

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASAATLT	VP	TARGDAVV	PKNP	ERVAVYDW
m750	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASAATLT	VP	TARGDAVV	PKNP	ERVAVYDW
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AALDTLTELGVNVGATTAP	VRVDYLQPAFDKAA	TGTLFEPDYEALHRYNP	Q	L	VITGGPG
m750	AALDTLTELGVNVGATTAP	VRVDYLQPAFDKAA	TGTLFEPDYEALHRYNP	Q	L	VITGGPG

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	70	80	90	100	110	120
a750.pep	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
m750						
	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
a750.pep	190	200	210	220	230	240
	AAKGKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDESLRNEGHGQPVSFYEIYE					
m750						
	AAKGKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDESLRNEGHGQPVSFYEIYE					
	190	200	210	220	230	240
a750.pep	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVLNLDNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLI					
m750						
	KNPDWIFIIDRTAAIGQEGPAAVEVLNLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
a750.pep	310	320				
	QAAEQLKEAFEKAEPVAAGKEX					
m750						
	QAAEQLKAAFKKAEPVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTGGTGC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCGTGAA CTGATGTATG
401 TCGGTACGA CCAATTAAAT AATAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTGAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCACTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTAATAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAATCTAA
951 ACCCATACTG GTAGAACCAA ACAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCCTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```

1  MAWSMFATQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMGNG WSVDTSNHSR GGITAGVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKWI PF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKTCDNE KYEKEAF*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq..
  1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATCTTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTC A TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGAAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
  1 MKISRPPEFT LLQQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
 51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFICIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLYFYIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNAL EYVAP QDLLE RLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
  1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATCTTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
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651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCC ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTC GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHEDTRM KRAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKQAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTIFYIYQC DIKRAVADL EHYISDKQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPPK
451 SGNALFYVAP QDLLEKLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTCCTAGT ACGACAGTAC
401 CGGCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNDSWN
101 CGDNIWLIQW FAPLGSHSQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTAA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGCG AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CTTTGCTTGG CTGCCAATGA ATTTTATGCG ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCTGTG GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTGCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCGGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMR FAYDNPSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVIVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAAGTAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGTTCTG GAAAAACAGA
401 AATTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```

1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLSDLN AQFIADGVYQ
101 AKQAFLOQVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```

1 MTANFAQTLV EIQDSLVRV SVVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```

1 MTANFAQTLV EIQDSLVRV SVVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLVRVSVVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLVRVSVVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

1231

	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTA AAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAAAGT TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFS DGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCGGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAATTT CCCGTCGTCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCGGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGGAAATT CCCGCTGCTGCT ACGGCGGCGA ATACGGCCCCG
151  GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTTCCTG CTTACTCATC CATGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCTCAAC GGCATCCCA TGCCCGACTT CCGGCTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACCAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
 651 AAACCACGGC TTA CTCTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTGACAAG
 751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGCTT
 801 CGATAATTTT TCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTGCGGCT GACCACCAAC
 901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
 951 CAACGAACGC ATCACCCTGC CCATTGCAAA CCTTCGCTT GCCCCACAAA
 1001 ACGCAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCAGT TCGACAGCAA CTTCAACGTC GTCGGTAAAA
 1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
 1251 AGGCAAGCTT ATCGCCAACG GACAAGGCAT CAACCAAGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCAAA AAGCTGCTT AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
 1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCTG
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTCACGAA
 1651 TACATCAACC CGCACCAGCA CCGTCGGACC GACTACTTCA TACTCAAACC
 1701 CGGCGGCAAC CCGCGCAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCGCGCGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCCAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCAGCTGTG TGCTCAACGG CGGCATGAAC CTTAACGGGG
 2051 AAGCTTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
 2101 CATGCCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG
 2351 TTTTAAAAGC CGAAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACCCCT
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
 2551 GACGGCGCAC AAATTACCTT GAACCCCGAT TTCGCCAATA ATACACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTTCGGCA
 2651 CATTCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAATGGAAG GGGACAGCCG CGGCGCATTC CAAATCCACG TCAAAAACAC
 2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCATTGTG AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCC TACCGTACAT CCTCCGAAA AACAACAACG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGC GG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
 3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGTGTAAGAA TGGCCGAATC CGAACTTGAC
 3301 AAAGCACGGC AAGGCGGCGA TCGCAAGCC GTCGAAACAG CCCGGCACGC
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAC TATCAGCCGG
 3451 TCGGCCAACA CCGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
 3651 CGGCATCACC GACCGTCTCA GTGTGCGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCgcCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCGG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
  1 MRFTHHTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
 51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQA YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTRDFPYFVR LGSGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQONDSRHMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQGAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRLDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAYVG
651 RPEYRYNGAL NLHYRPKRTD STLLLNGGMN LNGEVLIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQKTPPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLKKAHLYGS IRAGKDTAVR MEADSNWTLN QSSHTGALTIL
851 DGAQITLNPD FANNTNHNRF NTLTVNGTLD GFGTFRFLTG IVRKQNAPPL
901 KLEGDSRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEILSR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQONIWLETG TQQTQDYHSGT
1201 HRPYQQTNNY AHIGIQTGIT DRLSVGTILT DERTNNRFEDE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
  1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
 51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACCGCA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTGGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
  1 NNRNTRYAAL GKRVMGCVET EISGAITPKW QIHAGYSYLH SGIKTAANPR
 51 DDGIFLLVPK HSNLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCCT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCCAG
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTC GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCG GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACC GGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTC
751 GGCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCA CACGTATTTC
851 TCGGCGCGGA TTGGAACAAA TTTAAATGAC ACAGCCACGA CGTGTTTCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCTG TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGC CTTTGCCCTA TAACGGCATA CTTCAGAACG CCCGCGCCG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GGCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACC GCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTTCGTTC TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGCAT TGGGCAAAAC
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTTCG GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGAGGC
1951 GGTTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAATATTC CCGGTTGGA GCGAGCGCTG
2101 ACGGCAAAAC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLNDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQRR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHS HDVFA
301 DLKHYFGNGG YGKVMRYSD RKADSNTYFA GSKLNNTGQA DVAGLGTDIK
351 QKAFAVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSKVALD
401 GFRALPYNGI LQARAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYRMKDKNAAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
		:				
g760	QIHAGYSYLHSQIKTAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPCLKLQINADNIFNRHYARVGSESTFNIPGSESLTANL					
	:				:	
g760	AGMHAGGYATFDAMAAYRFTPCLKLQINADNIFNRHYARVGGTNTFNIPGSESLTANL					
	100	110	120	130	140	150

	709
m760.pep	RYSFX
g760	RYSFX

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAATAT	CATTTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTCACCAGC	GAAGTCGGGC	GCGCCAATTC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTA
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCAG	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTTCG	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGTGA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTTC	AAATTCTGTC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACTCACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCGGCCG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGCGGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTTCG	GCGGCGTGGA

1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
  1 MKISEHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
  51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
 101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
 151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
 201 NKNVAIRLTG EVGRANSERS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
 251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
 301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT L
 351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
 401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
 451 GSSROYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPAPYG RGGYLSIDTL
 501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
 551 NPYIYAVSGK HSRRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
 601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
 651 LPGFARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMFG NPRGYTARVN
 701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
  1 ATGAAAATAT CATTTTATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
  51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
 101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
 151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
 201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
 251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
 301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGCTT
 351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
 401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
 451 CCGTCTCCCG TGCTTTATGG GCGTACCAAC GGCGCGGGTG TCATCAACAT
 501 GGTGAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
 551 ATGGTTCTGT GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
 601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATT C
 651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
 701 CCGTCAAAC TCGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
 751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
 801 CTTCGGACTG CTTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
 851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
 901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
 951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC T
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTGA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGGCGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCCGCGG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAT CGAACGCTTC AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGCGCTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
  1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
  51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
 101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
 151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
 201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
 251 NVERTPDRSP TKSVDREGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
 301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTD NKTLSNLTL
 351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
 401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
 451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
 501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
 551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSIGVMQA KVVEDKENPD
 601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
 651 LPGFARVDAM LGWNHKNVNV TFAAANLENQ KYWRSDSMPG NPRGYTARVN
 701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
	LKWTGQYTYDNVERTPDRSPTKSVDREGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPTKSVDREGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTDNKTLSNLTLNGDYTIGRFE					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTDNKTLSNLTLNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

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```

m761.pep      NHLTVGMDYSREHRNPTLGSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
|||||
a761          NHLTVGMDYSREHRNPTLGSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
              370      380      390      400      410      420

              430      440      450      460      470      480
m761.pep      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
|||||
a761          QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
              430      440      450      460      470      480

              490      500      510      520      530      540
m761.pep      YNKGFAFYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
|||||
a761          YNKGFAFYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTLSAYQIERF
              490      500      510      520      530      540

              550      560      570      580      590      600
m761.pep      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
|||||
a761          NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
              550      560      570      580      590      600

              610      620      630      640      650      660
m761.pep      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSNRNKEVTTLPGFARVDAM
|||||
a761          RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSNRNKEVTTLPGFARVDAM
              610      620      630      640      650      660

              670      680      690      700
m761.pep      LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
|||||
a761          LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
              670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGG ACTTTTACTT TTTTCCATA TATTAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1   MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVOLCTIL FHSQKIYFIT
51  LFLLFIFNEV TKSIIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep
 1 MKWLLNMIMR PIKFSMVNTL LFIVICSSEF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVII LLSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVII LLSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq
 1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GCGCAGCAA CATTCCGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
 251 CAGTGC GCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCACCCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CCGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CCGTGC GCGC CGTTACCAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAAGCA GCCGTTTGA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCAGGCT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CCGGTTAGGG TTGGAAACGG TATTTGCGGA
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMVSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACG GTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCGAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGC GCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAGC CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CTTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACC GGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACCG TATTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMVSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

	10	20	30	40	50	60
m763.pep	MTLLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT					
a763	MTLLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT					
	10	20	30	40	50	60

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m763.pep	70	80	90	100	110	120
	LPEAWRAAQHSADFQASHYQRDAVRARQQAKAAFLPHVSNASYQRQPPSISSTRETQ					
a763						
	LPEAWRAAQHSADFQASHYQRDAVRARQQAKAAFLPHVSNASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
m763.pep	130	140	150	160	170	180
	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
a763						
	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
m763.pep	190	200	210	220	230	240
	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
a763						
	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
	190	200	210	220	230	240
m763.pep	250	260	270	280	290	300
	TDLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763						
	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
m763.pep	310	320	330	340	350	360
	QNSRYPTVSAHVGYNLYTSSAQNNDYHYRGKGMSVGVQLNLPLYTGGEISGKIHEAEA					
a763						
	QNSRYPTVSAHVGYNLYTSSAQNNDYHYRGKGMSVGVQLNLPLYTGGEISGKIHEAEA					
	310	320	330	340	350	360
m763.pep	370	380	390	400	410	420
	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763						
	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
m763.pep	430	440	450	460		
	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763						
	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```
m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTA CTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCA GTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCCTTTTTG CCCGCGCATT TGGAAC TGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGGCGCGT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGACGAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
701 CACAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTGAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```
m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAE EQAFL PAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSA LRHQ AELQSAKAE QKLVSVAIE QKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKS VSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```
a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCA GTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCCTTTTTG CCCGCGCATT TGGAAC TGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGGCGCGT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGACGAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
```

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```

701: CAGCAGACTA CCGCCGTTTG CGGCGCGACA ATTTTATTTT GGAACATGCG
751: TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801: TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851: AGAATCGGGT GCTGAATACG CAGAACCTGA AACCGGATAC GCTGGATGCG
901: CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951: GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001: CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051: CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101: TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151: TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201: AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251: GGTTTATACG GCGGTGGTGT CGTGCGACAA ACATACCTTG AATATTGACG
1301: GCAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

a764.pep (partial)

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAE QKLVSVAIE QKKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

	10	20	30	40	50	60
m764.pep	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVAVHVRDQHVQKQE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVAVHVRDQHVQKQE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m764.pep	TLAELEAVGTDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	TLAELEAVGTDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m764.pep	VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAELQSAKAEQKLVSVAIEQQKTADYRRL					
a764	VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAELQSAKAEQKLVSVAIEQQKTADYRRL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m764.pep	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVPDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m764.pep	DKMDVEVLVLNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT					

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|||||
a764      DKMDVEVLVLNKGDFVEQGDVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
              |||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTGCGG TCGTTGCTGA TGTTCACGGT CATGATCCG CCACAATGAA
201 CGCTGCGGCT GCCAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG TGGAAAAATG GCGTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTTCG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTTGTTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDEIAAI MGHEMTHALH EHGKKNVGGQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLLPVPM PVYEQSVRNK
301 GRVNNKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTCACGGT CAGGATCCG CCACAATGAA
201 TGCTGCGGCT GCCAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG CGGAAAATG GCGTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTTCG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTTGTTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

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51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDGEIAAI MGHMETHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLLEEA DEGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLPVPM PVYEHVSRNK
301 GRVKNRNRX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

m765.pep      10      20      30      40      50      60
MLRCRPKSVLDSGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
|||||
a765          10      20      30      40      50      60
MLRCRPKSVLDSGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
|||||

m765.pep      70      80      90      100     110     120
HDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTSHKFDW
:|||||
a765          70      80      90      100     110     120
QDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTGHHKFDW
|||||

m765.pep     130     140     150     160     170     180
KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHMETHALHEHGKKNVQOK
|||||
a765         130     140     150     160     170     180
KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHMETHALHEHGKKNVQOK
|||||

m765.pep     190     200     210     220     230     240
ILTNTAAQIGTQIILDKKPDNTPELVGLGMDILGTYGLTLPYSRSLLEEADEGMMLMAQ
|||||
a765         190     200     210     220     230     240
ILTNMAAQIGTQIILDKKPDNTPELVGLGMDILGMYGITLPYSRSLLEEADEGMMLMAQ
|||||

m765.pep     250     260     270     280     290     300
AGYHPAAAVRVWEKMNQENDQNGFIYAITSHTPTNNARIENLKRLLPVMPVYEQSVRNK
|||||
a765         250     260     270     280     290     300
AGYHPAAAVRVWEKMNQENDQNGFIYAITSHTPTNNARIENLKRLLPVMPVYEHVSRNK
|||||

m765.pep     310
GRVKNKRRRX
|||||
a765         310
GRVKNKRRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTGCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGCCG GAAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTGGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCG
301 GGTGTGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAAATCCG TTGGAACAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAAGGTT TGACGGCAAA AAACGTGATG GCGCTATGA TTCCCCCGAA
451 GCTGCCGCCG TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLKLKGLK PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKA VYEQKIR LENRAVAGKW ALSQKGF DGK KLMRAYDSPE
 151 AAAVALKMQK LTEQY GIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTGCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTTGGA ATTTTTCGGC
 151 TATTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTTGTCG
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTAAAGCAG TTTACGAACA
 351 AAAAAATCCG TTGGAAAACA GGTGCGTTGC CGAAAAATGG GCTTTGTCTC
 401 AAAAAAGGCT TGACGGCAAA AACTGATGC GCGCCTATGA TCCCCCGAA
 451 GCTGCCGCCG CCGATTAAA AATGACAGAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGG GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTGCAAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLKLKLGKAL PSDAYLRTEH VVWQPEMLGL ARMAAANLNS
 101 GLKYQANPAV FKA VYEQKIR LENRSVAGKW ALSQKGF DGK KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPL	LLLSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQ	PGKIEVLEFF	GYFCVHCHHFD
m767	:					
	10	20	30	40	50	60
g767.pep	70	80	90	100	110	120
	PLLLKLK	GKALPSD	TYLRTEH	VVWRPEML	GLARMAAA	VKL SGLKYQANS
m767	PLLLKLK	GKALPSD	AYLRTEH	VVWQPEML	GLARMAAA	VNL SGLKYQAN
	70	80	90	100	110	120
g767.pep	130	140	150	160	170	180
	LENRAVAG	KWALSQK	GF DGKKLM	RAYDSPEA	AAVALKMQK	LTEQY GIDST
m767	LENRSVAG	KWALSQK	GF DGKKLM	RAYDSPEA	AAAAALKMQK	LTEQYRIDST
	130	140	150	160	170	180
g767.pep	190	200	210			
	VIFNNGFD	GGVHTIK	ELVAKVRE	ERKRQTP	AVQKX	
m767	VIFNNGFD	GGVHTIK	ELVAKVRE	ERKRQTP	AVQKX	
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTGCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTTGGA ATTTTTCGGC
 151 TATTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAATTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTAAAGCAG TTTACGAACA
 351 AAAAAATCCG TTGGAAAACA GGTGCGTTGC CGAAAAATGG GCTTTGTCTC
 401 AAAAAAGGCT TGACGGCAAA AACTGATGC GCGCCTACGA CTCTCCTGCG

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCGCAAA
601 GTCAGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQKS GKIEVLEFFG
 51 YFCVHCHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFQDG KLMRAYDSPA
151 AAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767    96.7% identity in 214 aa overlap

      10      20      30      40      50      60
a767.pep    MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD
            |||
m767        MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD
            10      20      30      40      50      60

      70      80      90     100     110     120
a767.pep    PLLLKLKALPSDAYLRTEHV VVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR
            |||
m767        PLLLKLKALPSDAYLRTEHV VVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR
            70      80      90     100     110     120

      130     140     150     160     170     180
a767.pep    LENRSVAEKWALSQKGFQDGKKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR
            |||
m767        LENRSVAGKWALSQKGFQDGKKLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVVGKYYR
            130     140     150     160     170     180

      190     200     210
a767.pep    VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
            |||
m767        VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
            190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCACGCAG GCAGCCCGCG AAAAACCGGT ATCCGCGGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRAE AALQELKKAG
101 YTNVANHGGY EDLLKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGCG AAAAACCGGT ATCCGCGGCC CAAACCGCGC
101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI VQIVRRIHE AAPDKTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPQKPVSAQAQHSASVWIDVRSEQEFSEGH	LHNAVNI				
m768	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHPAVWIDVRSEQEFSEGH	LHNAVNI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIEAAAPDKDTPVNL	YCRSGRRAEAAALQELKKAGYTNVANHGGYEDLLKGMKX				
m768	VDQIVRRIHEAAPDKDTPVNL	YCRSGRRAEAAALQELKKAGYTNVANHGGYEDLLKGMKX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
 101 AACATTGAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCGC
 201 CATAACAGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI VQIVRRIHE AAPDKTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHSASVWIDVRSEQEFSEGH	LHNAVNI				
m768	MNIKHLITAALIASAAFAAQAPQKPVSAQAQHPAVWIDVRSEQEFSEGH	LHNAVNI				
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIHEAAPDKDTPVNL	YCRSGRRAEAAALQELKKAGYTNVANHGGYEDLLKGMKX				
m768	VDQIVRRIHEAAPDKDTPVNL	YCRSGRRAEAAALQELKKAGYTNVANHGGYEDLLKGMKX				
	70	80	90	100	110	120

1250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTSTA TTTTATTSTT TGTGGGAAGA CATTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCTG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCTTAT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAGAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGCGGCGCA
801 CGTGTCGGCG AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCACGACG CTTATTCTTA
951 CGCCACGCGC GCACGCCCTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCCGACA ATACCCATTT GCAAATTTCC AATTCGCTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CGCGAGCGCA
1151 ACCCCGCGCA CCGTGGCGAC AATTTCGAAC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
1251 CGTGCGGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCG CGCCTGACGC TGTCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNWG YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRKKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WGQEWGSGSL SSLFRLGVAK RHYEKPFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTSTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCTTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACC GATTGTAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGAGGT
201 CCGGGAAAAA GGAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CGCCGTCCG TATGCGTTG GCGGCAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAACA AAGTGACGCG ACGGCGGTCA ATTACCGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTCC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCTTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGCGGGCAG CGGCTGTCT TCGCTGTTGC GCCTCGGCGC

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1251

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1251  GCGGAAACGG  CATTATGAAA  AACCCGGCTT  TTTCAGCGGT  TTAAAGGGG
1301  AAAGGCGCAG  GGATAAAGAA  TTGAACACAT  CCTTGAGCCT  TTGGCACCAG
1351  GCATTGCATT  TCAAAGGCAT  CACGCCGCGC  CTGACGTTGT  CGCACCGCGA
1401  AACGCCGAGT  AACGATGTGT  TCAACGAATA  CGAGAAAAAT  CGGCGGTTTG
1451  TCGAGTTTAA  TAAACGTTT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
  1  LIMVIFYFCG  KTFMPARNRW  MLLPLLASA  AYAETPREP  DLRSRPEFRL
51  HEAEVKPIDR  EKVPGQVREK  GKVLQIDGET  LLKNPELLSR  AMYSAVVSNN
101 IAGIRVILPI  YLQQAQDDKM  LALYAQGILA  QADGRVKEAI  SHYRELIAAQ
151 PDAPAVMRML  AAALFENRQN  EAAADQFDRL  KAENLPPQLM  EQVELYRKAL
201 RERDAWKVNG  GFSVTREHNI  NQAPKRQQYG  KWTFFPKQVDG  TAVNYRLGAE
251 KKWSLKNGWY  TTAGGDVSGR  VYPGNKKFND  MTAGVSGGIG  FADRRKDAGL
301 AVFHERRTYG  NDAYSYTNGA  RLYFNRWQTP  KWQTLSSAEW  GRLKNTRRAR
351 SDNTHLQISN  SLVFYRNARQ  YWMGGLDFYR  ERNPADRGDN  FNRYGLRFAW
401 GQEWGSGSL  SLLRLGAAGR  HYEKPGFFSG  FKGERRRDKE  LNTSLSLWHR
451 ALHFKGITPR  LTLSHRETRS  NDVFNEYEKN  RAFVEFNKTF  *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769    95.1% identity in 492 aa overlap

      10      20      30      40      50      59
g769.pep    LIMVIFYFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLRSRPEFRLHEAEVKPI
            |||||  |||||  |||||  |||||  |||||  |||||
m769        LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPI
            10      20      30      40      50

      60      70      80      90     100     110     119
g769.pep    DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
            |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
            60      70      80      90     100     110

      120     130     140     150     160     170     179
g769.pep    KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVMRMLAAALFEDRQNEAADQFD
            |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVMRMLAAALFENRQNEAADQFD
            120     130     140     150     160     170

      180     190     200     210     220     230     239
g769.pep    RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQQYGNWTFPKQV
            |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQQYKWTFFPKQV
            180     190     200     210     220     230

      240     250     260     270     280     290     299
g769.pep    DGTAVNRYFGAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
            |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        DGTAVNRYLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
            240     250     260     270     280     290

      300     310     320     330     340     350     359
g769.pep    GLAVFHERRTYGNDAYSANGARLYFNRWQTPRWQTLSSAEWGRLKNTRRARS DNTHLQI
            |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        GLAVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARS DNTHLQI
            300     310     320     330     340     350

      360     370     380     390     400     410     419
g769.pep    SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLFRLGVA
            |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGAA
            360     370     380     390     400     410

      420     430     440     450     460     470     479
g769.pep    KRHYEKGFFSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
            |||||  |||||  |||||  |||||  |||||  |||||  |||||

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```

m769      KRHYEKP GFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACC GATTGAGAA GCCGTCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCGGACA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCATTACC GGAATTGAT TGTCGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
501 CAGCGAGAAC GAGGCGGCGG CAGACCAAGT CGACCGCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGCG AAATGGACTT
701 TCCGCGGACA GGTGGACGCG ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGCG AACGACGCTT ATTCTTACAC
951 CAACGCGCGA CGCCTTTATT TCAACCGTTG GCAAAACCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GCGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GCGGAAACGG CATTATGAAA AACCCGCGCT TTTCAGCGGT TTTAAGGGG
1301 AAAGGCGCAG GGATAAGAAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCGCGCG CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKRQYQG KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWGY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGGLDFYR ERNPADRGDN FNRYGLRFAW
401 QQEWGGSGLS SLRLGAAKR HYEKP GFFSG FKGERRRDKELNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

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|||||
m769      EKVPQGQVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
              70          80          90          100          110          120

              130          140          150          160          170          180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
              130          140          150          160          170          180

              190          200          210          220          230          240
a769.pep   KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNINQAPKRQYQKWTFFPKQVDG
|||||
m769      KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNINQAPKRQYQKWTFFPKQVDG
              190          200          210          220          230          240

              250          260          270          280          290          300
a769.pep   TAVNYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250          260          270          280          290          300

              310          320          330          340          350          360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDTHLQISN
              310          320          330          340          350          360

              370          380          390          400          410          420
a769.pep   SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAAKR
|||||
m769      SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGGSLSLRLGAAKR
              370          380          390          400          410          420

              430          440          450          460          470          480
a769.pep   HYEKPGFFSGFKGERRRDKELNNTSLSLWHRALHFKGITPRLTSLSHRETRSNDVFNEYEKN
|||||
m769      HYEKPGFFSGFKGERRRDKELNNTSLSLWHRALHFKGITPRLTSLSHRETRSNDVFNEYEKN
              430          440          450          460          470          480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC ACGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTTG GTTTACAGCG
401 ATAAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTT CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSI FDETA VRKPK
101 EVFKRGTFGA FKSQRIVRY DPKRKAFAYL VYSDKIVQS PKNLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRY Y DPKRKTFA YL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

```

m770/g770 93.5% identity in 186 aa overlap

      10      20      30      40      50      60
g770.pep MNRLLLLSAAVLPTACGSGETDKIGRASTVFNMLGKNDR I EVEGFDDPDVQGVACYISYA
          ||||| ||||| ||||| ||||| ||||| |||||
m770      MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EVEGFDDPDVQGVACYISYA
          10      20      30      40      50      60

      70      80      90      100     110     120
g770.pep KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPK EVFKRGTGF AFKSRQIVRY Y
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m770      KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPK EVFKHGASFA FKSRQIVRY Y
          70      80      90      100     110     120

      130     140     150     160     170     180
g770.pep DPKRKAFA YLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDGVQADTS GKL LAGACI ISNPI
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m770      DPKRKTFA YLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDGVQADTS GNL LAGACMISNPI
          130     140     150     160     170     180

g770.pep KNPDKRX
          :| ||||
m770      ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRY Y DPKRKTFA YL VYSDKIIQGS PKNSLSAVSC

```

1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

```

m770/a770    99.5% identity in 186 aa overlap

              10      20      30      40      50      60
a770.pep     MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
              |||||
m770         MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
              10      20      30      40      50      60

              70      80      90     100     110     120
a770.pep     KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKVEFKHGASFAFKSRQIVRY
              |||||
m770         KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKVEFKHGASFAFKSRQIVRY
              70      80      90     100     110     120

              130     140     150     160     170     180
a770.pep     DPKRKTFAVLVYSKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
              |||||
m770         DPKRKTFAVLVYSKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
              130     140     150     160     170     180

a770.pep     ENPDKRX
              || ||||
m770         ENLDKRX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

```

g771.seq
1  ATGGATTAT TATCGGTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51  GGTGCTGACG ATGCTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCCGAA AACATCCGCA GCCGCCTCCA ACAAAGCATT
151 GCCCATACCC ACCGGAATAAT CTCGTTTGAT GCGGATATAC GGCGCAGGCT
201 TCTGCCCCGC CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 ACGGCGGCGG GGTGCGCGTT TCCGTCAAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCGGATACAG GTTGA AAAAT GGGTGGTTTC
351 GGGTGCGGAT CTTGCCCTGA CGCGCGACAG AAACGGCGCT TGGAAACATC
401 AAGACCTGTT CGACGGCGCG AAACACTCCG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTT CTGCAGCAAC AGCTTATCCT
501 GAAGGAAATC AGCCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCAGT
551 TTGAAAGTTC GGCATACTG GTTTGAGAG AAAGTTCCTT CCGCTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCC AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGGACACGGC ATCACCATT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCGCAAATC CCCGCACTGG CACTCAAAAA CAACAGCATC AAAACCGGCA
851 CGGTCAACGG CACGTTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCTT CAAACCAATT
1001 TCTCCCTCGG CTCGCCGTTG GTTTGGAGTC GGGACAACGG GCTGGACGCC
1051 CCGCGCCTGC ACATATCGAC CCTTCAGGAT ACCGTCGACC GCCTGCCGCA
1101 ACCCGGTTT ATCAGCCGGC TCGACGGTTC GCTGTCCATA CCGAATCTGC
1151 AAAATTGGA TGC CGAATTA AACGGCACAT TCGACCGCCA ACCCGTTGCC
1201 GCAAAATTCA AATATACGCG GGAAGGCGCA CCGCACCTGG AAGCCGCCGC
1251 CGCGCTGCAA AAATTAAACC TCGCCCCCTA TCTTGACGAA TTTCGGCAAC
1301 AAAACGGCAA AATATTCCCC GACATCCTCG GCAGGCTGTC CGGCAACGTC
1351 GAGGCACACC TCAAAATCGG CAGCATCCAA CTCCCCGGCT TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCGGACAA AGACCATATC GCGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GCGGGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA TGCGGTTCATC GACCTGACCG CAAGCGGCGA AAACCGCAAA
1651 CAGCTTATCC GCTCGCTGCA AGGCAGCCTG TCGCTGAATA TTTCCAACGG
1701 CGCGTGGCAC GGCATCGATA TGGACAGCAT TTTAAAAAAC GGCCTTTCCG
  
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1256

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1751  GGGAAATCTC  GGGCAGCACA  CCCTTCTACC  GATTACGCT  CAACAGCGAA
1801  ATTTTCAGACG  GCATCAGCCG  CCACATCGAT  ACCGAACTCT  TCTCCGACAG
1851  CCTCTATGTT  ACCAGCAACG  GCTATACCAA  TCTGGATACG  CAGGAATTGT
1901  CTGAAGATGT  CTTATCCGC  AACGCCGTCC  ATCCGAAAAA  CAAACCGATT
1951  CCCCTGAAAA  TCACCGGTAC  GGTGGACAAG  CCGTCCATTA  CCGTCGATTA
2001  CGGCAGGCTG  ACCGGCGGCA  TCAATTCCGC  CAAAGAGAAA  CAGAAAATCC
2051  TCGAAGACAC  CCTGCTGGAA  CAATGGCAGT  GGCTCAAACC  TAAAGAACCG
3051  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1  MDLLSVFHKY  RLKYAVAVLT  MLLLAAVGLH  ASVYRTFTPE  NIRSRLQOSI
51  AHTHRKISFD  ADIRRRLLPR  PTVILKNLTI  TEPDGGRRVAV  SVKETKIGLS
101 WKNLWSDRIQ  VEKVVVSGAD  LALTRDRNGA  WNIQDLFDGA  KHSASVNRII
151 VENSTVRLNF  LQQQLILKEI  SLNLQSPDSS  GQQFESSGIL  VWRKLSVPWK
201 SRGLFLSDGI  GTPEISPFHF  EASTSLDGHG  ITISTGSPS  VRFNAGGADA
251 AGLGLRADTS  FRNLHLTAQI  PALALKNSI  KTGTVNGTFT  AGGEYARWDG
301 SFKLDKANLH  SGIANIGNAE  ISGSFKTPRL  QTNFSLGSP  VWSRDNLDA
351 PRLHISTLQD  TVDRLPQPRF  ISRLDGSLSI  PNLQWNNAEL  NGTFDRQPVA
401 AKFKYTREGA  PHLEAAAAAQ  KLNLAAPYLDE  FRQNGKIFP  DILGRLSGNV
451 EAHLKIGSIQ  LPGLQLDDME  TYLHADKDHI  ALSRFKSGLY  GGHTEGGISI
501 ANTRPATYRL  QQNASNIQIQ  PLLQDLFGFH  SFSNGNDABI  DLTASGENRK
551 QLIRSLQSSL  SLNISNGAWH  GIDMDSILKN  GLSGKISGST  PFYRFTLNSE
601 ISDGISRHID  TELFSDSLYV  TSNGYTNDLT  QELSEDVLR  NAVHPKNKPI
651 PLKITGTVDK  PSITVDYGR  TGGINSRKEK  QKILEDTLLE  QWQWLKPKPE
701  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1  ATGCGATTTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  CGTGTGACG  ATACTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCACCTT  CACGCCTGAA  AACATCCGCA  GCCGCCTACA  ACAAAGCATT
151 GCACACACAC  ACCGAAAAAT  CTCGTTTGAT  GCGGACATTC  AGCGCAGGCT
201 CCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGGCGACCA  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGCGGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAAATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GCGGCGACCA  GCACCGTCCG  CCTCAATTC  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTGGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AAACGGCATC  GGCCCGCCCG  AAATCTCACC
651 GTTCCATTTT  GAAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701 CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAAATC  CCCGCGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTTACC  GCCGGCGGCG  AATATGCCCG  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACCGG
1051 CCGGCGCTGT  ATGTATCGAC  CCTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCGTTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCGTTGCC
1201 GCGAAATTC  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCC  GACACCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATTCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAGTC  AGGGCTTTAC  GCGGCCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCTG  CAACAGAATG  CAAGCAACAT
1551 CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGCGA  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAACGG
1701 TGCAATGGAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGTC  CGACAATGCC  GCACCCAGCA  CACCTTCCA  CCGATTACCG
1801 CTCAACAGCG  AATATTCAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCGGC  ACGGTGGACA  AACCCTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTCG  CGCAAAGAGA
2051 AACAGAAAA  CCTCGAAGAC  ACCCTGCTGG  AACAAATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTA

```

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep

```

1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFSLNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQNGKIFP DTLAKLSGDI
451 EAHLKIGKVQ LPLQLDDME TYLHADKGIH ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGIH RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap
	10 20 30 40 50 60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIATHRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSIATHRKISFD
	10 20 30 40 50 60
	70 80 90 100 110 120
g771.pep	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVSAD
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
	70 80 90 100 110 120
	130 140 150 160 170 180
g771.pep	LALTRDRNGAWNIDQLFDGAKHSASVNRIIVENSTVRLNQLQQLILKEISNLQSPDSS
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNQLQEQILKEINLNQSPDSS
	130 140 150 160 170 180
	190 200 210 220 230 240
g771.pep	GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHF EASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHF EASTSLDGHGITISTTGSPS
	190 200 210 220 230 240
	250 260 270 280 290 300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGFTAGGEYARWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
	250 260 270 280 290 300
	310 320 330 340 350 360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRONGLDAPRLHISTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
	310 320 330 340 350 360
	370 380 390 400 410 420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAAALQ
m771	TVNRLPQPRFISRLDGSLSVNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
	370 380 390 400 410 420
	430 440 450 460 470 480
g771.pep	KNLNPYLDEFQNGKIFPDILGRSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDIH
m771	KNLNPYLDDVRQNGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGIH

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG----STPFYRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

1	ATGGATTAT	TATCGGTCTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTAGC
51	CGTGCTGACG	ATACTGCTTT	TGGCGGCAAT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCATCTT	CACACCTGAA	AACATCCGAA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACGC	ACCGGAAAAT	CTCGTTTGAT	GCGGATATAC	AGCGCAGGCT
201	TCTGCCCCGG	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	GCGGCGACCG	GACTGCCGTT	TCCGTCCAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCAGATACAG	ATTGAAAAAT	GGGTGGTTTC
351	GAGTGCAGAA	CTTGCCCTGA	CGCGCGACGG	GAAAGGTGTT	TGGAACATCC
401	AAGACCTGAT	CGACAGCCAA	AAACGCCAAG	CCTCAGTCAA	CCGCATTATC
451	GTGAAAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGGAAC	AGCTTATCCT
501	GAAGGAAATC	AACCTCAACC	TGCAATCCCC	CGATTCTCG	GGGCAGCCGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGGGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGGCCCA	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATTACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCGCTTCA	ACGCGGGCGG	AGCGGATGCC
751	GCCGCGCTCG	GCCTGCGTGC	AGACACTTCC	TCCGCAACC	TCCACCTGAC
801	CGCCCAATC	CCTACGCTGG	CACTCAGGAA	CAACAGCATT	AAAATTGAAA
851	CCGTCAACGG	CGCATTTACC	GCCGGCGGCG	AATATGCCCA	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCAC	CAGACCAACT
1001	TCTCCCTCAA	TTCGCCGCTC	GTATGGACGG	AAAACAAAGG	GCTGGACGCG
1051	CCGCGCCTGT	ATGTATCGAC	CCTTCAGGAT	ACCGTCAACC	GCCTGCCGCA
1101	ACCCGATTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCGTA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	AACCGTTGCC
1201	GCGAAATTCA	GATACACACA	TGAAGACGCA	CCGCATCTGG	AAGCCGCCGT
1251	CGCACTGCAA	AAATTGAACC	TGACCCCTTA	TCTTGACGAC	GTGCGGCAAC
1301	AAAACGGCAA	AATATTTCCT	GACACCCTCG	CCAAGCTGTC	CGGCGACATC
1351	GAGGCGCACC	TGAAAATCGG	AAAAGTCCAA	CTTCCCGGCC	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGGCCATATC	GCCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGCGA	CGCGGTCATC	GACCTGACCG	CGGGCGGCGA	AACCCGAAAA
1651	GAGCTTATCC	GCTCGCTTCA	GGGACGCTG	TCGCTAAATA	TTTCCAACGG
1701	TGCATGGCAC	GGTATCGACA	TGGACAATAT	CCTGAAAAAC	GGCATTTCGG
1751	GCAAACTGTC	GCACAAATGC	GCACCCAGCA	CACCTTCCCA	CCGATTACAG
1801	CTCAACAGCG	AAATTTGAGA	CGGCATCAGC	CGCCACATCG	ATACCGAACT
1851	CTTCTCCGAT	AGCCTCTATG	TTACAGCAAA	CGGCTATACC	AATCTGGATA
1901	CGCAGGAATT	GTCTGAAGAT	GTCTTATCC	GCAACGCCGT	CCATCCGAAA
1951	AACAAACCGA	TTCCTTGAA	AATCACCCTG	ACGGTGAGCA	AACCGTCCAT
2001	TACCGTCGAT	TACGGCAGGC	TGACCGGCGG	CATCAATTCT	CGCAAAGAGA
2051	AACAGAAAAT	CCTCGAAGAC	ACCCTGCTGG	AACAATGGCA	GTGGCTCAAA
2101	CCTAAAGAAC	CGTAA			

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1256

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1751 GGAAAAATCTC GGGCAGCACA CCCTTCTACC GATTCACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

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This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1 MDLLSVFHKY RLKYAVAVLT MLLLAAGVLH ASVYRTFTPE NIRSRLQOSI
51 AHTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQPVA
401 AKFKYTREGA PHLEAAAALQ KLNLAAPYLDE FRQNGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGPH SFGNGDAVI DLTASGENRK
551 QLIRSLQGS LSNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

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m771.seq
1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAAGCATT
151 GCACACACAC ACCGGAATAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCGCG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCG CGATTTCGTC GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGGACACGGC ATTACCATTT
701 CACCAACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCGGCGCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCGCTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAATATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAAGTC AGGGCTTTAC GCGCGCCATA CCGAAGGCGG CATCAGCATC
1501 GCTAACACCC GTCCGCGCAC TTACCGCTG CAACAGAAAT CAAGCAACAT
1551 CCAATTCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTCATC GACCTGACCG CGGCGGCGGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGGAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTTGAA AATCACCAGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACCAATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRHKISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRHKISFD					
	10	20	30	40	50	60
g771.pep	ADIRRRLLPRPTVILKNLTITPEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKVVVSGAD					
m771	ADIQRLLPRPTVILKNLTITPEGGDQTAVSVQETKIGLSWKNLWSDQIQIEKVVVSSAE					
	70	80	90	100	110	120
g771.pep	LALTRDRNGAWNIIQDLFDGAKHSASVNRIIVENSTVRLNFLQOQLILKEISLNLQSPDSS					
m771	LALTRDGGVWNIIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNLQSPDSS					
	130	140	150	160	170	180
g771.pep	GQQFESSGILVWRKLSVPWKSRLGFLSDGIGTPEISPFHFESTSLDGHGITISTTGSPS					
m771	GQPFESSGILVWGKLSVPWKSRLGFLSNGIGPPEISPFHFESTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
g771.pep	SFKLDDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDNGLDAPRLHISTLQD					
m771	SFKLDDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAAAAQ					
m771	TVNRLPQPRFISRLDGSLSVNPNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVAALQ					
	370	380	390	400	410	420
g771.pep	KLNLAPYLDEFROQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDHI					
m771	KLNLTPYLDDEVROQNGKIFPDITLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI					
	430	440	450	460	470	480

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNLSGKISG----STPFYRFT					
m771	DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

1	ATGGATTTAT	TATCGGTCTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTAGC
51	CGTGCTGACG	ATACTGCTTT	TGGCGGCAAT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCATCTT	CACACCTGAA	AACATCCGAA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACGC	ACCGGAAAT	CTCGTTTGAT	GCGGATATAC	AGCGCAGGCT
201	TCTGCCCCGG	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	GCGGCGACCG	GACTGCCGTT	TCCGTCCAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCCGA	TCAGATACAG	ATTGAAAAAT	GGGTGGTTTC
351	GAGTGC GGAA	CTTGCCCTGA	CGCGCGACGG	GAAAGGTGTT	TGGAACATCC
401	AAGACCTGAT	CGACAGCCAA	AAACGCCAAG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGGAAC	AGCTTATCCT
501	GAAGGAAATC	AACCTCAACC	TGCAATCCCC	CGATTCTGTC	GGGCAGCCGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGGGAA	AGCTGTCCGT	CCCGTGGAAT
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGGCCCA	AAATCTCACC
651	GTTCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATTACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	CCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCGCAACCC	TCCACCTGAC
801	CGCCCAATC	CCTACGCTGG	CACCTCAGAA	CAACAGCATT	AAAATTGAAA
851	CCGTCAACGG	CGCATTTACC	GCCGGCGGCG	AATATGCCCA	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAC	ACCGCGCCAC	CAGACCAACT
1001	TCTCCCTCAA	TTCGCCGCTC	GTATGGACGG	AAAACAAAGG	GCTGGACGCG
1051	CCGCGCCTGT	ATGTATCGAC	CCTTCAGGAT	ACCGTCAACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCGTA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	AACCGTTGCC
1201	GCGAAATTCA	GATACACACA	TGAAGACGCA	CCGCATCTGG	AAGCCGCCGT
1251	CGCACTGCAA	AAATTGAACC	TGACCCCTTA	TCTTGACGAC	GTGCGGCAAC
1301	AAAACGGCAA	AATATTTCCT	GACACCTCG	CCAAGCTGTC	CGGCGACATC
1351	GAGGCGCACC	TGAAAAATCG	AAAAGTCCAA	CTTCCCGGCC	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGGCCATATC	GCGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	CGCGGTCATC	GACCTGACCG	CGGGCGGCGA	AACCCGAAAA
1651	GAGCTTATCC	GCTCGCTTCA	GGGCAGCCTG	TCGCTAAATA	TTTCCAACGG
1701	TGCATGGCAC	GGTATCGACA	TGGACAATAT	CCTGAAAAAC	GGCATTTCGG
1751	GCAAAACTGC	GCACAATGCC	GCACCCAGCA	CACCCCTCCA	CCGATTCAAC
1801	CTCAACAGCG	AAATTTGAGA	CGGCATCAGC	CGCCACATCG	ATACCGAACT
1851	CTTCTCCGAC	AGCCTCTATG	TTACCGACAA	CGGCTATACC	AATCTGGATA
1901	CGCAGGAATT	GTCTGAAGAT	GTCTTATACC	GCAACGCCGT	CCATCCGAAA
1951	AACAAACCGA	TTCCCTTGAA	AATCACCAGT	ACGGTGGACA	AACCGTCCAT
2001	TACCGTCGAT	TACGGCAGGC	TGACCGGCGG	CATCAATTCG	CGCAAAGAGA
2051	AACAGAAAAT	CCTCGAAGAC	ACCCTGCTGG	AACAATGGCA	GTGGCTCAAA
2101	CCTAAGAAGC	CGTAA			

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
 51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
 401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI
 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSNGDAVI DLTAGGETRK
 551 ELIRSLQSSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDQELSED VLIRNAVHPK
 651 NKPIPKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLEQWQWLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLLAAIGLHASVYRIFTPENIRSRLQOSIAHTRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAHSVQETKIGLSWKNLWSDQIQIEKWVSSAE
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKWVSSAE
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQILKEINLNQSPDSS
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQILKEINLNQSPDSS
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLSDGIGTPKISPFHFEASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLGLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
a771.pep	TVNRLPQPRFISRLDGSLSVPNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
m771	TVNRLPQPRFISRLDGSLSVPNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
a771.pep	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI
m771	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRET					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRET					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPEKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPEKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTTCGGCA	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTGCG	CGGTTGGCGG
101	AAGGCGAGTT	TCACCAGTTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTCACCGGAA	TCATGCGCAC	CACTGCGGAA	TCGATTTTCG
201	GCGCGGGATC	GAACGATTCC	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGGCGACATC	GTCGCCACAC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCCCTG	AGATGCCCGTT
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTTCGAT	TTGACAACCG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGGCG	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGCTT	TGTGTTCTTT	CATCGTGTTT	CCTCTTCGGT	TGAAACCCCG
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGGCGGGGC	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	ERFGRHVNNQ	LHIEKILQHH	TQATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKRQR	FQTAYDVAVD	FDNVQAVQLF	RQRFGNCRQT
201	RADFNDIIR	LRAHGVNDIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFFQIR	TTHRAVLYVS	SCVLEHKCVY	SIRLMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTTCGGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTGCG	CGGTTGGTGG
101	AAGGCGAGTT	TCACCAGTTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTCACCGGAA	TCATACGGAC	GACGGCGGAA	TCCACTTTCG
201	GCGCAGGGTC	GAACGATTCC	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGTTTGCC	GACGATTTTC	TTTTTGCCCTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTTCGAT	TTGACAACCG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGGCG	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC

1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

```

m772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV EREGRYVNOH FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGRNRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

```

m772/g772 85.2% identity in 298 aa overlap

          10      20      30      40      50      60
g772.pep  VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHFQFGEMIEIVRLADTVFHRNHAH
          :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772      MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
          10      20      30      40      50      60

          70      80      90     100     110     120
g772.pep  HCGIDFRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI
          || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772      DGGIHFRRRVERFGRYVNOHFHIEKILQHHAQAQVVAFRGNHTLDHFFLQHKVHIDDI
          70      80      90     100     110     120

          130     140     150     160     170     180
g772.pep  VRHLRQFEQKRRGDVIRQVADDFLFXDAVEIKLQHVAFVNHQFIRKRQRFQTAYDVAVD
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772      VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
          130     140     150     160     170     180

          190     200     210     220     230     240
g772.pep  FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772      FDNVQAVQLFRQRFGRNRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
          190     200     210     220     230     240

          250     260     270     280     290     299
g772.pep  HRVSSSVETPPFRAAGSDSVWAGRNPFFQIRTTTHRAVLYVSSCVLEHKCVYSIRLMSALX
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772      HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX
          250     260     270     280     290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

```

a772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTTC GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTGGC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTACAGCGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIIVACK LFIQIVAYGFA ALVEGEFHEF GEMLEIVRLA
51 DTVFHRNHAD DGRIFHRRGV ERFGRHVNQH FHIEEILQHH AQAQVVAFR
101 RGNHTIDHEF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIIVACKLFIQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD					
m772	MFGAVLRIDADCLQIIIVACKLFIQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRIFHRRGVVERFGRHVNQHFIHIEEILQHHAQAQVVAFRRGNHTIDHFFLQHKVHIDDI					
m772	DGGIHFRRRVERFGRYVNVQHFIHIEEILQHHAQAQVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLFRQRFGNRRQTRTDFNHDIIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTCGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AACTTTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTAC CTAATAATT TAAACATTT GATTATTTT ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```


1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFFK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101  TGVKTSLTPK TADVQRNLS QSEVGKWK GIEGQGMPE DYVGKGLSAN
151  ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGIDK
201  TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSQ
251  NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101  CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251  CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401  TTTCTGCCCG AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501  GGGGAAGTGT GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551  TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAT CGGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
651  GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701  TACGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDDRKLKE
101  HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAALAL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEVIFKIGEC
201  QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101  CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251  CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401  TTTCTGCCCG TGCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501  GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551  TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAT CGGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
651  GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701  TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101  HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEAMFKIGEC
201  QYRLQOKDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRLDYLEGKI				
m774	MKIKLPLFIIWLSVSASCASVSPVAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGKI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGRTYVQK	LDDRKLKEHYLNTEGGSASAHTVETAQN				
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQK	LDDRKLKEHYLNTEGGSASAHTVETAQN				
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGDGG	SIAQRSMYLLQSRARMGNCSVIEIGGRY				
m774	LYNQALKHYKSGKFSAAASLLKGADGGDGG	SIAQRSMYLLQSRARMGNCSVIEIGGRY				
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQKQDIAR	TWRSLIQTYPGSPAAKRAAAVRKRX				
m774	ANRFKDSPTAPEAMFKIGECQYRLQKQDIAR	TWRSLIQTYPGSPAAKRAAAVRKRX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACCGC
101	AGGCAGAGGC	AGGTAGTTTC	GACGCTATTC	CCTATCCCGT	TCCCACTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCTTCCAG	CAGGGCATA	GTCCAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTTGC	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAACCC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGGCGCAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFII	WLSVSAACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLDDRKLK
101	EHYLNTEGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAAS	LLKGADGGDG
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT	APEAMFKIGE
201	CQYRLQKQDI	ARATWRSLIQ	TYPGSPAAGR	AAAAVRKR*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRNIQDMR	LEPQAEAGSSDAIPYPVPTLQDRLDYLEGT				
m774	MKIKLPLFIIWLSVSASCAS-VSPVPAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGK				
	10	20	30	40	50	

1265

```

          70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYL NTEGGSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYL NTEGGSASAHTVETAQ
          60      70      80      90      100     110

          130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGD GGSIAQRSMYLL LQSRARMGNCSVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      NLYNQALKHYKSGKFSAAASLLKGADGGD GGSIAQRSMYLL LQSRARMGNCSVIEIGGR
          120     130     140     150     160     170

          190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQ QKD IARATWRS LIQTPGSPA AKRAAAVRKRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      YANRFKDSPTAPEAMFKIGECQYRLQ QKD IARATWRS LIQTPGSPA AKRAAAVRKRX
          180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAGCCG GTATAGCGAC CCTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTCACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTGC
551 CCCCTTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCG
651 TCGCGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCTG
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCGCT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDITI NNHHTHTNH SDADGKALSM
151 RLTPRPLLS D RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLIV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAGCCG GTATAGCGAC CCTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTCACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTGC
551 CCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCTG
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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1266

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGAC AGGCAAGAAG
851 GCGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCC ACCGAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKLVFEF GTAKPCVINC PKHGNQTCSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTNH SDADGKALSM
151 RLTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH ROEGVLIRIT APDVWTVGTI
301 SASKTSTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790    98.2% identity in 342 aa overlap

          10      20      30      40      50      60
a790.pep    MARRSKTFEEAAAEVEERFGHRGIKLVFEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
m790         MARRSKTFEEAAAEVEERFGHRGIKLVFEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
          10      20      30      40      50      60

          70      80      90     100     110     120
a790.pep    GCPSCGNEQAAKAGIATLRKNHIALEMLKQAVTGMKQERITTQAYNEMTKSVAGSNSII
m790         GCPSCGNEQAAKAGIATLRKNHIALEMLKQAVTGMKQERITTQAYNEMTKSVAGSNSIV
          70      80      90     100     110     120

          130     140     150     160     170     180
a790.pep    LNDVQGDTTINNHHHTHNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
m790         LNDVQGDTTINNHHHTHNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
          130     140     150     160     170     180

          190     200     210     220     230     240
a790.pep    SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMRPADEDIVLIELSDKRLVAHLVID
m790         SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMCPADEIALIELSDKRLVAHLVID
          190     200     210     220     230     240

          250     260     270     280     290     300
a790.pep    IAGRMLIYQTRPSEALDLPESVILGVVLESKNGLCPPHROEGVLIRITAPDVWTVGTI
m790         IAGRMLIYQTRPSEAFDLPEGSTILGVVLESKNGLCPPHROEGVLIRITAPDVWTVGMI
          250     260     270     280     290     300

          310     320     330     340
a790.pep    SASKTSTRPTAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
m790         SASKTSTRPTAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
          310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTA CTGTTT
51  TGGTTTGT TTGGTTT TTGATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCT CTTGGATT CTTGCAGCAT
151 TACCAGCCCTA AATGCCGT GACTATTAT TCGGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GCGGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCCG GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGTGGTTCGG CGGTTATGAT
1351 TTTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTCGGTT ACGGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGCG CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCGCAACCG TTCCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

g791.pep

```

1 MVNYYSAMIK KILTTCTFGLF FGFCVFGVGL VAIAILVTYP KLPSLDLSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRKY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNF D RGSSYRGAEN YIDLKSSEDV EETVSQYLSG
351 LYTVDKMVPV VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYGYT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRILRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

m791.seq

```

1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGATTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACCTGCCG CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GGCAGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT CGGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGCGAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTGTTC GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGT TTAAGGTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTTG ATGTACTAA
1101 AAGAGAAAAT TCGTCATAC AGCTGCCCG CGGCAGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGA AAAAATG
1201 GGGGAGGACC GTATCCGCG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGT GCTGCAGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGC CGCTGGTCG CGGTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGG GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCG TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCG ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTGCG CGCCCAAATG CAACCTTTGG TGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGCA TGTGTCCGT GTTGTACGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGTTT GTCGTTTTA ACCGTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCG TTTGGGTGGA CTATATGCG TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGG ATGAAAATGC CTGAAGGTGT GGTACAGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCCAAC TCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCAAGATA
2351 TGCAGGAAAC GCCGTGCTT CCGAGTAATA CTGTTTCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

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1 MVNYYSAMIK KILTCFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVPV VVLDVTKKKK VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLLQ ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRV QAMRQPGSTF KPFVYSAA LS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNA QAI DPNRAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

g791/m791 97.3% identity in 805 aa overlap

```

          10      20      30      40      50      60
g791.pep  MVNYYSAMIKKILTCFGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
          70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TCGCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 TACGCGTGTCC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGCTGTC
651 CTATAATCCG ATTTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 GAGCGGTTG ATGAGAACT GCATTACGAG CGGTTTGTTC GGAATACTGA
801 TCAGAGTGCT TTATATGTGG CCGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGCGAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCCG GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACAGCA AATCATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGCG GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG GCGCCAAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCCTGGTTT GTCCGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CCGTACGATT
2101 GCGGTGCCCG TTTGGGTGGA CTATATGCGT TTGCGGTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGCGGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1 MVNYYSAMIK KILTTCFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSDV EETVSYQLSG
351 LYTVDKMVPV VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQOYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRLLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKG MKMPEGVVSS NGEYMKERM VTDPLTLDN
751 SGIAQPSPRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10

20

30

40

50

60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFRHWGVDVWGVARAAVGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEYGEDAYTQGFKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDVTKKKNVVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWFGFNPDDVTVAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKGK
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYYMKERMVTDPLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	MKMPEGVVSSNGEYYMKERMVTDPLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTTCG
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAGAGGC GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAC
451 AGGATTTTCG AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACCAAACA GCAGcgggcG aaactgacgg tactcgctcc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcatgggtt cggcaaatTA ccccaagcg aaacggactg
701 attgttccag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKPP AADLTQKQAA KLTVLVPAPF
201 YYSDHPSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCGTTAC CGACAAAGAC
451 AGGATTTTTC AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCCGCTCCC GGTATTTTTA TCAATACCC GCCGCCAAGC
551 TGACCAAACA GCAGGCGGCA AAATGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQKQAA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSALPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK					

m792	WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK	70	80	90	100	110	120
g792.pep	NLFLNESRNYLRKGEEAAITAMMEAVTDKNRIFELYLNSIEWHYGVFGAEASRYFYKKP	130	140	150	160	170	180
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEASRYFYQIP	130	140	150	160	170	180
g792.pep	AADLTQQAAKLTVLPAPFYSDHPKSKRLRNKTNIVLRRMGSANYPKAKRTDCSRYGN	190	200	210	220	230	240
m792	AAKLTQQAAKLTARVPAPPLYADHPKSKRLRNKTNIVLKRMGSAELPESDIDX	190	200	210	220	230	
g792.pep	AAXTGVRTAYVFWDLX	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2685>:

```
a792.seq
1  ATGTTCCGCA TCATCAAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCGCTCG
101 CTGCCCATCG GACTGCCCTTT ATGTCGATCG GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CCGCTTCGAT TGGGGCGGCA TTCAAACGC CATCAGCGCG
301 AACCGGAACA CGGGCAAAAGT GAAGCGGGCG GTTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GGCATATACC GAGCTGATGG AAGCGGTTAC CGACAAGAGC
451 AGGATTTTTG AACTGTATTT AAACCTAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA CGCGCTTCCC GGTATTTTTA TCAAATACAT GCCGCCAAGC
551 TGACCAAAAC GCAGGCGGCA AAACCTGACGG CGGCGGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651 CTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIYT	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRISTN	LKKALIASED	ARFAGHGDFD	WGGIQNAIRR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNSI	ERHWYGVFGA	AASRYFYQIP	AAKLTKQQA	KLTRVVPAPL
201	YYADHPKSRV	LHNKNTNIVLR	RMGSFELPES	DDT*	

m792/a792 99.6% identity in 233 aa overlap

a792.pep	10	20	30	40	50	60
	MFR	I	K	W	L	I
m792	MFR	I	K	W	L	I
a792.pep	70	80	90	100	110	120
	W	M	P	Y	K	R
m792	W	M	P	Y	K	R
a792.pep	130	140	150	160	170	180
	N	L	F	L	N	E
m792	N	L	F	L	N	E
a792.pep	190	200	210	220	230	
	A	A	K	L	T	K
m792	A	A	K	L	T	K

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2687>:

g793.seq

1274

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1   ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTGCG CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTC CGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCGCAA AACGGCAAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 CCGATACGCG CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGCGGCCCCA TCGAACAGGC
1251 GACGATGCTT TTGCGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CCGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGCGGCA
1451 CCGGTACGCG GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAAACCGGC
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCTGTGT ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCAGGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGCG AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1   MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSFIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFHAVIG FTDIDGKQBE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIIILSD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPF RADSEQRNRN
301 AVTDMIPEGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSAREFGAEM YDFYHELIG VMHSGFPFGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQ GK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVAKTG
501 TARKEVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYYGGVVA
551 GPPFKKIMGG SLNILGISPT KPLTAAAVKT PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1   ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTGCG CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTCGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGC GC GATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGCGGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCCGCCGA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTCCGT AACCGAGCCG GCGGCACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGCGCGGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGCGGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

```

m793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSFIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVVLD RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNRRWR RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

```

          10      20      30      40      50      60
g793.pep  MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNFKLEQ
          |||||
m793      MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAMAVLFAGLIARGLYLQTVTYNFKLEQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g793.pep  GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV
          |||||
m793      GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV
          70      80      90      100     110     120

          130     140     150     160     170     180
g793.pep  PVDVLRNKLEQKGKFSFIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG
          |||||
m793      PVDVLRNKLEQKGKFSFIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG
          130     140     150     160     170     180

          190     200     210     220     230     240
g793.pep  FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLDSPRNKAPQNGKDIILSLD
          |||||
m793      FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLDSPRNKAPKNGKDIILSLD
          190     200     210     220     230     240

          250     260     270     280     290     300
g793.pep  QRIQTLAYEELNKAVEYHQAAGTVVVLDARTGEILALANTPAYDPNRPGRADSEQRNR
          |||||
m793      QRIQTLAYEELNKAVEYHQAAGTVVVLDARTGEILALANTPAYDPNRPGRADSEQRNR
          250     260     270     280     290     300

          310     320     330     340     350     360
g793.pep  AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM
          |||||
m793      AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM
          310     320     330     340     350

          370     380     390     400     410     420
g793.pep  QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS
          |||||
m793      QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS
          360     370     380     390     400     410

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1276

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          430      440      450      460      470      480
g793.pep   FGYGLQLSLLQLARAYTALTHDGVLLPLSF EKQAVAPQGKRIFKESTAREVRNLMVSVTE
          |||||
m793       FGYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep   PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||||
m793       PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep   AHGYYGGVVAGPPFFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          |||||
m793       AHGYYGGVVAGPPFFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTGTC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTGAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCAGGGGG AAATCCTCGC CTGGCCAAAT ACGCCCCTCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TCGGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGCGGTTT TACTGCCGGT CAGCTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTCCGT AACCGAGCCG GGCGGCACCG
1451 GTACGGCGGG TGGGTGGAC GGTTCGATG TCGGCGCGAA AACGGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCTTCA AAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNLFKEQ GDNRIVRTQT LPATRGTVSD RINGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYD MGNLFHAVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPD RADSEQRNRN
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSFE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GVTGTAGAVD GFDVGAKTGT
501 ARKFVNNGRY DNKHVATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PFFKKIMGGS LNILGISPTK PLTAAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

	10	20	30	40	50	60
a793.pep	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	PVDVLRNKLKQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLKQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	PVDVLRNKLKQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLKQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	FTDIDGKGQEGLELSLEDSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	FTDIDGKGQEGLELSLEDSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	QRIQTLAYEELNKAVEYHQAKAGTVVVLDDARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLDDARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	QRIQTLAYEELNKAVEYHQAKAGTVVVLDDARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLDDARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	KSSNVGTSKLSARFGAEEMYDFYHELIGVVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGVVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	KSSNVGTSKLSARFGAEEMYDFYHELIGVVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGVVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	HGYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX					
	550	560	570	580		
a793.pep	HGYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTCAT AATGGAACG ATTATTATAT ATGTGATTC
51  CCTGCAAAAC AAGCCGGTCC GCCGCCCGG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GCCCGCATTG CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTCCG CCTTCAAAC
351 CTTCGCGAGC AATTACCGCT GGGCGACCGA GTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGCGGG CAGCGCGAC
451 CCCGTTTCA ATCAGGAAA CCTGCTGCC GTCCAACGCC AGTTGCGCA
501 CAAAGGCATC CGCAATATCA CGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGCGTCAA AAACTGATG CGGCATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGCGGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTG GAAAACGGT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNF
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVF AFAAFKTEFS NYRWATEFES NGTVNDGTLN GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVSGP DHFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVDLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLLNNVRAI AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAC AAGCCGGCCC GCGGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCTTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGCGCAC
451 CCCGTTTTC ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGATCTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTG GAAAACGGT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLWAGSGD
151 PVFNQENLLD AQKQLREQGI LNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPECL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILD MNKRSNLI
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLV ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNVRAL AGYWLGDKEP AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

```

          10      20      30      40      50      60
g794.pep  VRFNHFIMVTIIIVISPAKPVRRPGVPTYPALPYNCFFVYVTDSPMFPKTAASLLLLL
          ||:|||||::|||||||:|:|:|||||||:|||||||:|||||||
m794      VRLNHFIMIAIIIVISPAKPARHSVPTYPALPYNCFFVYVTDLPMPFPKTAASLLLLL
          10      20      30      40      50      60

          70      80      90      100     110     120
g794.pep  ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
          |||:|||||:|||||||:|||||||:|||||||:|||||||
m794      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
          70      80      90      100     110     120

          130     140     150     160     170     180
g794.pep  NYRWATEFKNGTVDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRLMLD
          |||:|||||:|||||||:|||||||:|||||||:|||||||
m794      NYRWATEFKNGTVDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGILNITGHLMLD
          130     140     150     160     170     180

          190     200     210     220     230     240
g794.pep  HSLWGEVGSFDPHFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
          |||:|||||:|||||||:|||||||:|||||||:|||||||
m794      HSLWGEVGSFDPHFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
          190     200     210     220     230     240

          250     260     270     280     290     300
g794.pep  QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
          |||:|||||:|||||||:|||||||:|||||||:|||||||
m794      QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
          250     260     270     280     290     300

          310     320     330     340     350     360
g794.pep  NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSNLIARSVFLKLGSD
          ||:|||||:|||||||:|||||||:|||||||:|||||||
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSNLIARSVFLKLGSD
          310     320     330     340     350     360

          370     380     390     400     410     420
g794.pep  GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          |||:|||||:|||||||:|||||||:|||||||:|||||||
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          370     380     390     400     410     420

          430     440     450     460     470     480
g794.pep  QDFIDTLPIAGTGTDLNRNRFKQSGGLRLKGTGTLNVRALAGYWLGDKPMVAVVVIINSGR
          |||:|||||:|||||||:|||||||:|||||||:|||||||
m794      QDFIDTLPIAGTGTDLNRNRFKQSGGLRLKGTGTLNVRALAGYWLGDKPMVAVVVIINSGR
          430     440     450     460     470     480

          490     500     510
g794.pep  AVSLLPDLNDFVAKNIIISGGDGWLDKLMCKERRAX
          |||:|||||:|||||||:|||||||:|||||||
m794      AVSLLPDLNDFVANNIISGGDGWLDKLMCKERRAX
          490     500     510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCTTATAA TTGCTTTTAT TATGTAACAG ATTTACCTAT GAATTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTGCGATTC CGCAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGGCG CTTTCAAAC
351 CTTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGCGAC
451 CCCGTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCGTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTCTC TCCTCAAACT CGGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAACGG CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTTAC CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

```

a794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG DGLYWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLKL LRGNIPECL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQAM LETAYFSPFA QDFIDTLPIA GTDGLNRNF KQSGGLRLK
451 TGTLLNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

```

a794/m794 98.6% identity in 515 aa overlap

```

a794.pep      10      20      30      40      50      60
VRLNHFIMIAIIIYVISPANPARRHSVPTYPALPYNCFYVTDLPMNFPKTAASLLLLL
|||||
m794          10      20      30      40      50      60
VRLNHFIMIAIIIYVISPANPARRHSVPTYPALPYNCFYVTDLPMNFPKTAASLLLLL
|||||

a794.pep      70      80      90      100     110     120
ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS
|||||
m794          70      80      90      100     110     120
ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS
|||||

a794.pep      130     140     150     160     170     180
NYRWATEFKSNGTVNDGTLGDNLYWAGSGDPVFNQENLLAVQRQLREQGIRNITGHLMLD
|||||
m794          130     140     150     160     170     180
NYRWATEFKSNGTVNDGTLGDNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD
|||||

a794.pep      190     200     210     220     230     240
HSLWGEVGSFPDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAADSTDILTDPPLPHIFA
|||||
m794          190     200     210     220     230     240
HSLWGEVGSFPDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
|||||

a794.pep      250     260     270     280     290     300
QNNLKITASQAACPSIKKLMRASFSNTLKLRLGNIPESCLGKPVGVRMFALDELIRQSFT
|||||
m794          250     260     270     280     290     300
QNNLKITASQAACPSIKKLMRASFSNTLKLRLGNIPESCLGKPVGVRMFALDELIRQSFT
|||||

a794.pep      310     320     330     340     350     360
NHWLLGGGRISDGIGISDTPGAQTLAVAHSKPMKEILTMNKRSNLIARSVFLKLGGD

```

```

|||||:|||||:|||||:|||||:|||||:|||||:
m794 NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDMNKRSNLIARSVFLKLGGD
      310      320      330      340      350      360
      370      380      390      400      410      420
a794.pep GKLPVAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
      370      380      390      400      410      420
m794 GKLPVAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
      370      380      390      400      410      420
      430      440      450      460      470      480
a794.pep QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGT LNNVRALAGYWLGD KPMVAVVVI INSGR
      430      440      450      460      470      480
m794 QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKTGT LNNVRALAGYWLGD KPMVAVVVI INSGR
      430      440      450      460      470      480
      490      500      510
a794.pep AVSLLPDLDNFVANNIISGGDGWLDAKLMCKERRAX
      490      500      510
m794 AVSLLPDLDNFVANNIISGGDGWLDAKLMCKERRAX
      490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1  ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATCGC GCGCTTCTTT GCGCGCTTTT TCGCGCctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TCGTGTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
251 CCCCAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTTGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcg cATTTCgacg tgttgGATTT GGTCGCGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCGG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTCGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tggGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
951 AGGATTGGT ATCGGGGTTT TCGCGCCGCG GGACGGCGGG GCGGATGGCG
1001 CCGACGTAGT TGCCCAGATG CGGGGTGCCG GTGGTGTTA CGCCGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAAa. gatgcgCCGA TTATACCCGA TTTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

```

g900.pep
1  MPSEMPSETW QAEVRTALGL FQRADADRIA .YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQFCQ FGVDFFRRKF FRLAPSQAVG KHLRKFRFRFR
101 RRGEFIDFK QRAFVGLFRL ARLFHVGNDF VDRFLGFFV FPKRNGIAVG
151 FGHFASVQTD QEFDVVDFH FGQGEFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVHQQ NVGSHQNRIT EQTHFHTEIG VFLPVFRIGL NGGFVGVGAV
251 HQTLLGGDAGQ NPVQLHHFGN VALAVEGGAL GVESAGKPSG GNGLGGLVNH
301 LLLVAFDDAV VIGEEEEFG IGVLRRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPSEREK DAPIIPDLPH TSSRQQTfPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1  ATGCCGCTCTG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTGCGGT
101 GCTTCTTTAC GCGCTTTTCG CGCGCTGCC TGCAAAATCT CTTCGATTTG

```

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```

151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CGGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATTT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CCGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGTG GTGCGCTCGG GGTCGAGTCC GCAGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCGGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXFVQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQEFDFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNLRLV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

```

          10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRRAACLQNLFDLRRVGGQ
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900       MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRAACLQNLFDLRRIRGO
          10      20      30      40      50      60

          60      70      80      90      100     110
m900.pep  LVVAFARFGEFGVDFFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEFGVDFKQWAFVGLFRL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900       CVVAFQAQFCQFGVDFFRRRKFFRLAPSAVAGKHLRKFRFRFRRRGEGFIDFKQRAFVGLFRL
          70      80      90      100     110     120

          120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFIDFHFGQGEEFPEA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900       ARLFHVGNDFVDRFLGFFVVFPRKNGIAVGFGHFASVQTDQEFDFVDFHFGQGEFLET
          130     140     150     160     170     180

          180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900       VGEAAGNVARHFDVLDLVAPDGDFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFRIGL
          190     200     210     220     230     240

```

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	240	250	260	270	280	290
m900.pep	HGGFVGMGAVHQ	TLGSDAGQNPVQ	FHHFGSVALAVE	GGALGVESAGKP	SGGNGLGGLVNH	
	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
g900	NGGFVGVGAVHQ	TLGGDAGQNPVQ	LHHFGNVALAVE	GGALGVESAGKP	SGGNGLGGLVNH	
		250	260	270	280	290
	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVI	GEEEEFGFIEVL	RRLRADGGADG	ADVVAQMRDAGG	GYAGQNSFFAH	KNVL
	: : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
g900	LLLVAFDDAVVI	GEEEEFGFIEVL	RRLRADGGADG	ADVVAQMRGAGG	GYAGQNSFFAH	KNVL
		310	320	330	340	350
	360	370	380			
m900.pep	AASMPSEREKDV	PIIPDLPTSSRQ	QTFFPYX			
	: : : : : :	: : : : : :	: : : : : :			
g900	TAAMPSEKDAPI	IPDLPTSSRQQT	FFPYX			
		370	380	390		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

```

1   GAGGTTCCGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51  CACGTACTTT GCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGC
101 CCTGCCTGCA AAATCTCTTC GATTTGCGAA GGGTCGGCGG TCAGCTCGTT
151 GTAGCGTTCG CGCGGTTCGG CGAGTTCGGC GTTGATTTTC GCCGCCAAAA
201 GTTTTTTTGC CTCGCCCCAA GCCAAGCCGT CGGCAAGCAT TTTTCGTAAT
251 TCTGCCGTTT CAGACGGCGT GGAGAAAGCT TTGTAGATTT CAAACAGAGG
301 GCTTTCGTCG GGCTTCTTCG GCTCGCCCGG CTCTTTCATA TTGGTGATGA
351 TTTTGTGAC CGATTTTGG GTTTTTTGT CGTTTTCCCA AAGCGGAATG
401 GTGTGCGCGT AGGATTTGGA CATTTTGCGT CCGTCCAAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATTT TCACTTCGGG CAGTGTGAAG AGTTCGCCGA
501 AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTC AACGTGTTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCAGTCATG AGGATAGGGT AGCTGTACAA ACCCATTTC ACGCCGAAAT
651 CGGGGTCTTC CTGCCGTTT TCCGCATTG CCTGCACGGC GGCTTTGTAG
701 GCGTGGGCGC GGTTCATCAA ACCCTTGGCG GTGATGCAGG TCAGAATCCA
751 GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGCAG GCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGAA TCATCTCCGG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901 GCGGAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951 CGGGGCGGAT AGCACCACG TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001 GTTACGCCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTTGGCGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTGCGC
1101 ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

```

1   EVRTALGLFQ RADTDRTITYF AQ*FACFFTR FLRACLQNLF DLRRVGGQLV
51  VAFARFGEFG VDFRRQKFFC LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101 AFVGLRLRLAR LFHIGDDFVD RFLGFFVFP KRNGVAVGFG HFASVQTNQE
151 FDVFVDFHFG QCEEFP EAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201 GSHEDRVAVQ THFHAIEIGVF LPVERICLHG GFVGVGAVHQ TLGGDAGQNP
251 VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNH LR LVAFDDTVVI
301 GEEEEFGFIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLA
351 SMPSEREKDA PIIPDLPTS SRQQTFFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVRTASGS	FQRADADRIXFYVQ	XFACFFTRFRRACLQ	NLFDLRRVGGQLVVA		
	: : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
a900	EVRTALGLFQ	RADTDRTITYFAQ	XFACFFTRFLRACLQ	NLFDLRRVGGQLVVA		
		10	20	30	40	50
	70	80	90	100	110	120

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```

m900.pep    FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
            |||||:|||||:|||||:|||||:|||||:|||||
a900        FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFHRRRRGESFVDFKQRAVGLLRLARLF
            60      70      80      90      100     110

            130      140      150      160      170     180
m900.pep    HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTDQEFDFIDFHFQGEFPEAVVEA
            |||||:|||||:|||||:|||||:|||||:|||||
a900        HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTNQEFDFVDFHFGQCEEFPEAVVEA
            120     130     140     150     160     170

            190      200      210      220      230     240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
            ||::| ||:||||| | :|::||:|:||||::|: ||||:| ||||| |||||
a900        AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
            180     190     200     210     220     230

            250      260      270      280      290     300
m900.pep    VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHLRLV
            ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHLRLV
            240     250     260     270     280     290

            310      320      330      340      350     360
m900.pep    AFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        AFDDTVVIGEEEEFGFIRVLRRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
            300     310     320     330     340     350

            370      380
m900.pep    PSEREKDVPIIPDLPTSSRQQTFPYX
            |||||:|||||:|||||:|||||:|||||
a900        PSEREKDAPIIPDLPTSSRQQTFPYX
            360     370

```

g901.seq not found yet
g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCCGATT TTTGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTakGyAG TGGCTTGGTG ATGTTTTCCT
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGCGCG GCGACCATGG
251 CATTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGCGTGT CTGCTATCCG GCTTGCCGA GCCGTTGGG
601 GCGGCTTTGG GCTATTTGGT TTGCGAGCCG TTTTGTGCG CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTC TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAACGGGTAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP

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101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCCTTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATPTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTT AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
 401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGAAAAT
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCACC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTTCGC CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG
 701 TCGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

	10	20	30	40	50	60
m901.pep	MPDFSMSNLA	VAFSITLAAG	LFTVLXSG	LMVFSKTP	NPRVLSF	GLAFAGG
a901	MPDFSMSNLA	VAFSITLAAG	LFTVLGSG	LMVFSKTP	NPRVLSF	GLAFAGG
	70	80	90	100	110	120
m901.pep	FSKSSEAF	AEIYDKDH	AFAAATMA	FLAGMG	GIALIDRL	VNPHE
a901	FSKSSEAF	AEIYDKDH	AFAAATMA	FLAGMG	GIALIDRL	VNPHE
	130	140	150	160	170	180
m901.pep	IARVGMMA	AFATAHNF	PEGLATFF	ATLENPA	VGMPALA	IAIAHNI
a901	IARVGMMA	AFATAHNF	PEGLATFF	ATLENPA	VGMPALA	IAIAHNI
	190	200	210	220	230	240
m901.pep	RSRKKTVW	ACLLSGL	AELGALG	YLVLPFL	SPAVFGS	VFGVIAG
a901	RSRKKTVW	ACLLSGL	AELGALG	YLVLPFL	SPAVFGS	VFGVIAG
	250	260	270			
m901.pep	KRYSDGH	ETVYGLT	TGMAVIA	VS	LVLFHFX	
a901	KRYSDGH	ETVYGLT	TGMAVIA	VS	LVLFHFX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTT
151 ACGCCGCGCC TGTCGCCGT CGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGGCTCTG CATCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgCG CGcgcccgTG aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgTC tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgccg
801 catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTCGCA CACCGCCCA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTCGGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFVAGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQQN GGSAFQQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIF GDFGDDGQVL
201 IVVVTQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDL RPE SDVVTRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTTC CCGTcGGGCA TTTCTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTGTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC GATGAGTTTC TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep
 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQGRR
 101 QNTVFGIMFQ IAEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
 201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
 301 RVAGQHFHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
 351 FQKSTPLYIF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

	10	20	30	40	50
m902.pep	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
g902	MPSEPERRHGNTALPFPIAARPTVGFSGKPFKITGKCVLRRRIVQAVDFTPRLFAVGHF				
	10	20	30	40	50
	60	70	80	90	100
m902.pep	VDVPAYVFACDAHTGGVAVKRVYGADVQNSG GAFQCQTQGRRQNTVFGIMFQIAEPRPA				
g902	ADVPAVFACDAHTDGLTIKRVHGADVQNGGS AFGCQTQGRRXNAVFGIMLQIAEKPRPA				
	70	80	90	100	110
	120	130	140	150	160
m902.pep	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPPDRDVTAFGFGDEFVTRFAFVHLRTRASV				
g902	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVDPPGRDVTAFGLGDEFVTRLAFVHLRARAPV				
	130	140	150	160	170
	180	190	200	210	220
m902.pep	DGKGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDG FQNGGNQRLVLHQRATGL				
g902	NGKGGNAIFGDFGDDGQVLI VVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQRATGL				
	190	200	210	220	230
	240	250	260	270	280
m902.pep	DIADFFSGTAHVVDKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSIS				
g902	DVAHFLGGAHIDVDDL RPESDVVTRRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
	250	260	270	280	290
	300	310	320	330	340
m902.pep	ERRVAGQHFHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	ERRIAGQHFHRPTCAKRPTEAAGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
	310	320	330	340	350
	360				
m902.pep	IFX				
g902	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
 51 CGCAGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA

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101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTCCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTGCGTG CGCGTGCCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```

1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRRTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRSALR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLRRT	TVQAVDFTT	CLFAVGHFVD
a902	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLRRT	TVQAVDFTT	CLFAVGHFVD
	70	80	90	100	110	120
m902.pep	VPAYVFACDA	HTGGVAVKRV	YGADVVQNSG	GAFQCQTQGR	RQNTVFGIMFQ	IAEEPRPALR
a902	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNSG	GAFQCQTQGR	RQNTVFGIMFQ	IAEEPRPALR
	130	140	150	160	170	180
m902.pep	AAPYHNAVGG	LFLRRSNVAV	DPDRDVQTA	FGFGDEFVTR	FAFVHLRTR	ASVDG
a902	AAPYHNAVGG	LFLRRSNVAV	DPDRDVQTA	FGFGDEFVTR	FAFVHLRTR	ASVDG
	190	200	210	220	230	240
m902.pep	KGGDAAIFGD	FGDDGQVLM	VVPTQTGFEG	NGYACRTDD	GFQNGGNQRL	VLHQRATGLDI
a902	KGGDAAIFGD	FGDDGQVLM	VVPTQTGFEG	NGYACRTDD	GFQNGGNQRL	VLHQRATGLDI
	250	260	270	280	290	300
m902.pep	ADFFSGTAHV	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA	VQGFSSISER
a902	ADFFSGTAHV	DVDKLRPKAD	VVTRGIRHLL	RIASGNLHGN	NAAFIGKIAA	VQGFSSISER
	310	320	330	340	350	360
m902.pep	RVAGQHFAHR	PTCAKISAKS	AERFVGNAHR	RRCDCGVVDK	IAADVHNGSA	FQKSTPLYIF

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|||||
a902  RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
      310      320      330      340      350      360

m902.pep  X
          |
a902      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCGCTcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcg gcgacatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TCtgcgctcC
301 ATAcgaATCG atcggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTC CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTTCG CTTC AACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDSNGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DHRKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAOWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLGAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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151 CGCAAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCGTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTCACT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTCTATG
701 TTTTCATATG ACGCGGTTTG GCGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACCTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCT CCGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903 . pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNYYVL SEDETPCTRV NYISLDDKTV
51 RKFSFLPSVL MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR SSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAPF XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903 . pep  MQRQQHIDAE LLTDANVRFE QPLEKNYYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
                                     |:::| |:::|:::|:::|:::|
g903        MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
                                     10      20      30

          70      80      90     100     110     120
m903 . pep  MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
: : | : | | : : : : : | : | | | : : : | : : | : | :
g903        LCQTHFVSGKCL HAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKLQLTLM PGYLR
          40      50      60      70      80      90

```

1291

	130	140	150	160	170	180
m903.pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLENLRLPSVKTDIQUIIPSE					
	: : : : : : : : : : : : : : : : : : : : : : :					
g903	SIRIDRSNDDQTHAGRIAAFQNKFPTRSNDDLNLRLDLEQGLENLKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903.pep	EE-GKSDLQIKWQONK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDFYVSYGR					
	: :					
g903	REPNSQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFLGSDMFYVNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903.pep	GLAHKTDLTATGTETESGSRYSVHYSPVKKWLFSFNHNGHRYHEATEGYSVNYDYNG					
	: : : : : : : : : : : : : : : : : : : : : :					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903.pep	KQYQSSLAERMLWRNRLHKTSGVMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAY					
	: :					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRKTSYIDDAELTVQRRKTTGWLAEELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903.pep	LNRWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIIITASLDAAAPFXLGKQOFF					
	: : :					
g903	IGRSTADFKLKYKHGTGMKDALARPEEAFGE---GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903.pep	YATAIQAWNKTPPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
	: :					
g903	YDTSVHAQWNKTPPLTSQDKLAIGGHHTVRGFDGEMSLPAERGWWYWRNDLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903.pep	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
	: : : : : : : : : : : : : : : : : : : :					
g903	LGADVGHVSGQSAKWLSGQTLAGTAIGIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903.pep	YGFNLNYSFX					
	: : : :					
g903	TGFQVGYAFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903.seq

```

1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAAATGT
51  CCGTTTTTCGAG CAACCATTTGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGCG
151 CGCAAATTTT CTTTCTTCTC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAGCCG
251 CGCAACAGAT ACTGATTGTG CGTGGCTACC TCACTCCCA AGCTATTATC
301 CAACCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TCGTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCACT

```

```

601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCGCTTTA TCGTTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTTCATATGG ACGCGGTTTG GTGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTTCG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCACTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51 RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLRPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRES
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRFHKT VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTAR	KFSFLPSVL
	70	80	90	100	110	120
m903.pep	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQAI	IQPQNMDSGI	LKLRVSAGEIG
a903	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQAI	IQPQNMDSGI	LKLRVSAGEIG
	130	140	150	160	170	180
m903.pep	DIRYEEKRD	GKSAEGSISAF	NNKFPLYRNK	ILNLRDVEQ	GLENLRLRPS	VKTDIQIIPSE
a903	DIRYEEKRD	GKSAEGSISAF	NNKFPLYRNK	ILNLRDVEQ	GLENLRLRPS	VKTDIQIIPSE
	190	200	210	220	230	240
m903.pep	EEGKSDLQI	KWQONKPIRES	IGIDDAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
a903	EEGKSDLQI	KWQONKPIRES	IGIDDAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
	250	260	270	280	290	300
m903.pep	AHKTDLTDA	TGTETESGSR	SSVHYSPVK	KWLFSFNHNG	HRHYHEATEG	YSVNYDYNKGQ
a903	VHKTDLTDA	TGTETESGSR	SSVHYSPVK	KWLFSFNHNG	HRHYHEATEG	YSVNYDYNKGQ

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFMLGKQQFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTTCGCCCA
151 GCCGGGCATG GTTTCGTAAG TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTTCGTTCA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCAG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTTCG
901 GCCGATTTTG CTTTGGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGTAAGG CAGGATCAGC GGGCAGGTCG GCGGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

1294

```

51 AGHGFVNRF A GFHRI RTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVLDL A AFQGGG I KPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGI A FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFKA Q FFAVFV FVQ HAGHVG NHRR NARRDFFDNR HHVFRFNRS G
251 VMQVLELDV A IGKDG I QFFT QFFRMQ QIGG ANGAACHFVF VGRADAAAGR
301 ADFAFARCF A AGLVERDVVR QDQRAGR RDF QTAFDV FHAC RVQLVDFAQQ
351 GFGGNDNAR T DEAIQS FVQD TARNQA QNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

m904.seq

```

1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATAACGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGGCC GCAGCGCGT GCGCGTCCGG TTACCGAACC GAATTCGTTG
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAAAT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTCCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTGTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTACAG CAGTTTtTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTTGCCGC GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCaCGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904.pep

```

1 MMQHNRF FSV GAGGDDGDRR AADFFNPFQI CFGVFGQCAV VLHAESGFAP
51 AGHGFVNRL A GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVLDL A AFQGGG I KPA AAACASGYRT EFVS AFCQTY AYFVEQFGRE
151 RARTDARGI A FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFKA Q FFAVFVFLVQ HAGHVG NHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDI V IGKDG I QFFT QFXRMQ QIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF A AGLVERDVVR QDQRAGR RDF QTAFDV FHAC RVQLVDFAQQ
351 GFGGDDNAR T DEAVQTFMQD AARNQA QNGF FAADNQGMAR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

```

              10      20      30      40      50      60
m904.pep    MMQHNRF FSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
              |||||:|||||:|||||:|||||: ||:|:|:| |||||:|
g904         MMQHNRF FAVGAGGDDGDRRAADFFNPFQICFGIGRQCVVAFHADSRFAPAGHGFVNRLA
              10      20      30      40      50      60
              70      80      90      100     110     120

```


1295

m904.pep	GFHRIGTARQDVGFAAVQGFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA
g904	GFHRIRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVDLDGAFQGGGIKPA
	70 80 90 100 110 120
m904.pep	AAACASGYRTEFVS AFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904.pep	CARQTVGRGNEGISAVVDVQORTLRAFKQQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
g904	RAGETVGRGNEGVS AVVDVQORTLRAFKQQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
m904.pep	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHFV FVGRADAAAGR
g904	HHVFRFNRS GVMQVLELDV VIGKDGIOFFTQFFRMQQIGGANGAACHFV FVGRADAAAGR
	250 260 270 280 290 300
m904.pep	ADFAFAARIFAGLVERDVVRQDQRAGRRDFQTA FDVFHACRVQLVDFAQQGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQRAGRRDFQTA FDVFHACRVQLVDFAQQGFGGNDNART
	310 320 330 340 350 360
m904.pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVA ALEAHHAAGFFRQPVNDFTF TLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADDQGMARIVA ALEAHDAAGFFRQPVNDFTF TLVAPLC
	370 380 390 400 410 420
m904.pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTGC TCCGACTTCG TCGAACAAAT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGCCTT ACGCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGGCAGTTGG ACCAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTGTTTCAA CACGCGGGAC ACGTCGTGTA TCATCGGCGT AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTGTCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC TCGGGCTTGG TCGAGCCGCA

```

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```

951 TGTGATAAGG CAGGATCAGC GGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904 . pep

```

1 MMQHNRRFFAV GAGGDDGDRR TADFFNPFI CFIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDLG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHLRG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYNNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

	10	20	30	40	50	60
m904 . pep	MMQHNRRFFSVGAGGDDGDRRAADFFNPFI	CFI	GR	*CVV	AFHAESGFAPAGHGFVNRLA	
a904	MMQHNRRFFAVGAGGDDGDRRTADFFNPFI	CFI	GR	XC	CVVAFHAESGFAPAGHGFVNRLA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m904 . pep	GFHRIGTARQDVGF	AAVVGQFIADADIDGFNAVHYIEFSN	THTGNAVLDLGA	AFQGGGIKPA		
a904	GFYRIRARQDVGF	AAVVGQFVADADIDGFNAVHYIEFGNT	THTGNAVLDLGA	AFQGGGIKPA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQH	LR	TYARACRS			
a904	AAACASGYRTEFVSAFCQTCSDVEQFGRERARTDARGIGFDDAQNIQH	LR	AYARACRS			
	130	140	150	160	170	180
	190	200	210	220	230	240
m904 . pep	CARQTVGRGNEGISAVVDVQRTLRAFQQFFAVFVFLVQHAGHVGNNRR	NARRDFFDNR				
a904	RAGEAVGRSNEGVS	AVVDVQRTLRAFQQFFAVFVFLVQHAGHVGNNRR	NARRDFFDNR			
	190	200	210	220	230	240
	250	260	270	280	290	300
m904 . pep	HHVFRFNLGIVQMLQLDIVIGKDGIQFFTQFXRMQIGGANGAACHFVFVGRADAAAGR					
a904	HHVFRFHLGIVQMLQLDVVISKDGIOFFTQFFRMQIGGANGAACHFVFVGRADAAAGR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m904 . pep	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTA	FDVFHACRVQLVDF	AAQGGFGGDDNART			
a904	ADFAFAARCF	SGLVERDVIRQDQRAGRRDFQTA	FDVFHACRVQLVDF	AAQGGFGGDDNART		
	310	320	330	340	350	360
	370	380	390	400	410	420
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQMARI	VAAL	EAHHAAGFFRQPVNDF	FTFTLVAPLC		
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRI	VAAL	EAHHAAGFFRQPVNDF	FTFTLVAPLC		
	370	380	390	400	410	420

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```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| ||||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTT
51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAATTA CGCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
51 GCTGTGTGCC GCCGGCGCGC TGTTGATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCCG CGATGTCGCG ACGTTTGGA AGATTCTGCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51 GTTGTGTGCC GCCGGTGCGT TGTTGCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGCG ACGTTTGGA AGGTTCTGCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTktGG AAAAACTACA TCGGCAAACC GGCGCACAAAC
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTFA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAQREETL ADDVASVMRS
51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

q907/m907

		10	20	30	40	50	60
g907.pep		MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPPRL					
		: :					
m907		MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPPRL					
		10	20	30	40	50	60
		70	80	90	100	110	120
g907.pep		VFDNPKEGERWLSAMSARLARFVPDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
		:					
m907		VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
		70	80	90	100	110	120
g907.pep		RARIIS					
m907		RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
		130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

```
a907.seq
  1  ATGAAAAAAC  CGACCGATAC  CCTACCCGTC  AATCTGCAAC  GCCGCCGCCT
51  ATTGTGTGCT  GCCGGCGCGC  TGTTGCTCAG  CCCGCTGGCA  CAAGCCGGCG
101 CGCAACGTGA  AGAAACGCTT  GCCGACGATG  TGGCTTCCGT  GATGAGGAGC
151 TCTGTCGGCA  GCATAAATCC  GCCGAGGCTG  GTGTTCGACA  ATCCGAAAGA
201 GGTGAGCGCT  TGGCTGTCCG  CGATGTCGTC  TCGTTTGCCA  AGGTTCGTCC
251 CCGATGAGGA  GGAGCGGCGC  AGGTCGCTGG  TCAATATCCA  GTACGAAAGC
301 AGCCGGGCGC  GTTTGGATAC  GCAGATTGTG  TTGGGGCTGA  TTGAGGTGGA
351 AAGCGCGTTC  CGCCAGTATG  CAATCAGCGG  TGTCGGCGCG  CGCGGCCTGA
401 TGCAGGTTAT  GCCGTTTTTG  AAAAATACA  TCGGCAAAAC  GGCGACAAC
451 CTGTTCGACA  TCCGCACCAA  CCTGCGTTAC  GGCTGTACCA  TCCTGCGCCA
501 TTACCGGAAT  CTTGAAAAAG  GCAACATCGT  CCGCGCACTC  GCCCGTTTTA
551 ACGGTAGCCT  CGGCAGTAAT  AAATATCCGA  ACGCCGTTT  GGCGCGGTGG
601 CGCAACCGCT  GGCAGTGGCG  TTGA
```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

```
a907.pep
1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQREETL ADDVASVMRS
51 SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDDEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRQWR*
```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:			:		:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAI SGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
a907	RQYAI SGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907.pep	ARENGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARENGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTAGA AATGTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYTCY RSYDVLVDVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSQYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIFYTCY RSYDVLVDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10 20 30 40 50 60
g908.pep MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLLIYQNGPHLEMF

```

1300

```

      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m908  MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMFD
      10          20          30          40          50          60

      70          80          90          100         110         120
g908.pep  GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
m908      GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      70          80          90          100         110         120

      130         140         150         160
g908.pep  PDSIVYTD CYRSYDVLDVSEFSHFSFAETSFSYQSQHTFCRTTKPYX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m908      PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      130         140         150         160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

a908.seq

```

1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA AC GCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

a908.pep

```

1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAAY YFHLRLLLIY
51  QNSPHLEMFD GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPPIIREQVK PDSIVYTD CYRSYDVLDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

m908/a908 98.2% identity in 166 aa overlap

```

      10          20          30          40          50          60
m908.pep  MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMFD
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a908      MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMFD
      10          20          30          40          50          60

      70          80          90          100         110         120
m908.pep  GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
a908      GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      70          80          90          100         110         120

      130         140         150         160
m908.pep  PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a908      PDSIVYTD CYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      130         140         150         160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

g909.seq (partial)

```

1  atgcgtaaaa ccgtacttat cCTgaccatc tccgccgccc ttttgcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```

1301

```

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
201 caacccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggagagg gacggggggg ggcgggtgaa cagggcagaa
301 acgggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTTGTCTGGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGKKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGKKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNR	X		
	:		::	::	:	
g909	ERRAVLRNQK	RGKPTRRAAT	LGKPSFRAR	DGGGRVNRAE	TGEKRSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTTGTCTGGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFLEFLT AAALLSGCAW ETYQDNGKKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGKKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
a909	MRKTFLEFLT	AAALLSGCAW	ETYQDNGKKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQ	TGNNADEEHRQHWQKPKFQNRX	
a909	ERHAVLPNQ	TGNNADEEHRQHWQKPKFQNRX	
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCCG
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDH GKPVEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```

g910/m910
10      20      30      40      50      60
g910.pep MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW
          |||||:|:|:|||||
m910     MKKLLLAADVSLSAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDH
          10      20      30      40      50      60

70      80      90
g910.pep GKPVEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          |||||
m910     GKPVEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```


1303

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLVAVVSLAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDADDDHW					
	: : : : : :					
a910	MKKLLLVAVVSLAATAFAGDSAERQIYGDYPFEQNRTKAVKMLEQRGYQVHDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	: : : : :					
a910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCTTGATCGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GCGCGGCGCT
101 TCGGCGGTTT GGACAAACT TACGCCGTTT ATGCCGATTT CCGCGACATC
151 GCGGCTTTGA AGGTCAATGC CCCCCTCAA TCCGAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CCGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACAGTT
401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTT GGACAAACT TACGCCGTTT ATGCCGATTT CCGCGACATC
151 GCGGCTTTGA AGGTCAATGC CCCCCTCAA TCCGAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CCGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACAGTT
401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTGCG
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep    MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911        MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
            10      20      30      40      50      60

            70      80      90      100     110     120
g911.pep    SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911        SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
            70      80      90      100     110     120

            130     140     150     160
g911.pep    ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAEX
            ||||||||||||||||||||||||||||:||||||||||
m911        ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
            130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTCG TCCTGATTGG
51  CGCGCGCGCG GTTGCTTTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCGCGTCAA TCCGAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

            10      20      30      40      50      60
m911.pep    MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911        MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
            10      20      30      40      50      60

            70      80      90      100     110     120
m911.pep    SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911        SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
            70      80      90      100     110     120

            130     140     150     160
m911.pep    ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
            ||||||||||||||||||||||||||||
a911        ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
            130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAAat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGCGACGC GGCTTCTGCA

```

1305

```

151 CGCCCAAAAG CCGAAGCCTA TGCGGTTCCC TATTTGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
451 GGCAAATACC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCT GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQNATQVLT ILKSGDAASA
51  RPKAEAYAVP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
1  ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGCGATGTC CAACACCGCT
151 CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCT GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
1  MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQNATQVLS ILKNGDANTA
51  RQKAEAYAIP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

g912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGQIRQNATQVLTILKSGDAASARPKAEAYAVP					
	: : : : : : :					
m912	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYS GTMLKFKNATVNVKDNPIVN					
	: : : : : :					
m912	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYS GTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGGKEIIVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI IKAK					
	: : : : : :					
m912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI IKAK					
	130	140	150	160	170	180
	190					
g912.pep	GIDGLIAELKAKNGGKX					

1306

m912
 190
 GVDGLIAELKAKNGGKX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq
 1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
 51 CCGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
 101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
 151 CGCCAAAAAG CCGAAGCCTA TGCATTCCC TATTTGATT TCCAACGTAT
 201 GACCGCATTG GCGGTCGGCA ACCCTTGCGC CACCGCGTCC GACGCGCAA
 251 AACAAGCGTT GGCCAAAGAA TTCAAACCC TGCTGATCCG CACCTATTCC
 301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
 351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGC
 401 TACCCGGGCA AAAACCGGTC AACATGGACT TCACCACCTA CCAAAGCGGC
 451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
 501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
 551 GACTGATTGC CGAGTTGAAG GCTAAAACG GCAGCAAGTA A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep
 1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
 51 RQKAEAYAIP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTY
 101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
 151 GKYRTYNVAI EGASLVTYR NQFGEI IAK GVDGLIAELK AKNGSK*

m912/a912 98.0% identity in 196 aa overlap

	10	20	30	40	50	60
m912.pep	MKKSSLSIALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP					
	: : : : :					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m912.pep	YDFQRM TAL AVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN					
	: : : : :					
a912	YDFQRM TAL AVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m912.pep	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEI IAK					
	: : : : :					
a912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEI IAK					
	130	140	150	160	170	180
	190					
m912.pep	GVDGLIAELKAKNGGKX					
	:					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq
 1 atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
 101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
 151 GCCGCGCGCG GCTACCGCAA AGTTACGCGG AAACCCGTCC GCGCCGGCGT
 201 GTCCAATTTT TTTAACAACC TGC GCGACGT GGTCAGTTTC GGCAGCAATA
 251 TCTTGC GTTT GGACatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
 301 atCAATACCA CCTTCGTTT GGcgcGGCTC ATTGATATTG CCGGcgcGGg
 351 cgcgcttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
 401 GctgGAAAAa cagcaATTAT TCTGTgttgc CCGtcttagg cccgtccacc

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc catacccttg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctccctcgatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
  1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVTP KPV RAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGKNSNY FVLPVLPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWGTT AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQAEAAEGAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
  1 ATGAAAAAAA CCGCCTATGC CTTCTCTCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCCCCCT
151 GTCGCGCGCG GCTACGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCCTTT GGACATCAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGC GCGGCAG ACCGGTGCAA CACCTGCCGA AGgTACGGA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
  1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
 51 AARGYRKVAP KPV RAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGKNSNY FVLPVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
      10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||||:|||||
m913      MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVFKFNDQADRYIFAPAARGYRKVAP
          |||||:|||||

      70      80      90     100     110     120
g913.pep  KPV RAGVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||
m913      KPV RAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          |||||:|||||
          70      80      90     100     110     120

```

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPLVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPLVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1   ATGAAAAAAA CCGCCTATGC CTCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCGCGCGCGG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGCACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCCGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1   MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPLVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVRAVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVRAVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPLVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPLVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTGTG CACCAGAGGA TGCCGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTTCACGAT TTTTTCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTGG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TGCGGGTCAG
651 GAACATTTTC ATTTGTTTCG GCGTGGTGTG TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAAGCTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMRVNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALEQCSCSADXSASTIFCTRGCRRTSSPVKWKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRRTSSPVKWKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMRVNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCTG TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTCG
451 TAGGCTTCGA CGATTTTTTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCACGCG
551 CATCTTTTAA TCCCGATTTC ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCAATTTG TCGGGCGTGG TGTTTTGCGC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAG CGTCCTGCCG CGCATATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPN DLMFLGRSIWLV
201 SPVMTAFAPK PMRVNIFIC SGVVFCASSR MMYAPLSVLP RI*
  
```


1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDFPCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga ttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPWFSTVK QMFGYTKLPE EPKIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGC.tG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCCG ACACATATGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

```

m915.pep
  1 MKKTLAIVA VSALSXRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					
g915	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g915	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```

a915.seq
  1 ATGAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

```

a915.pep
  1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCTT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAGAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTGGGTGG
851 ATTCTTTCGT GATTCGAAA GATGCGAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGACGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

```

1314

```

751  GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851  ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901  TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

```

m917.pep
1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	:					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m917.pep	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	:					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
	:					
g917	EMMRLMDGVDPDHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m917.pep	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m917.pep	RGDTCVTIGFGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m917.pep	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
	: : :					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

1315

```

m917.pep    ALKFMVRQWQDVKAGKX
            |||||
g917        ALKFMVRQWQDVKAGKX
            370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

```

a917.seq
1  ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAGC
51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAATTT TACAACGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG
251 GTTACGACAT TGTGCGGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAATAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

```

a917.pep
1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLNIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

m917/a917 99.7% identity in 376 aa overlap

```

          10      20      30      40      50      60
m917.pep  MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG
          |||||
a917      MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG
          10      20      30      40      50      60

          70      80      90     100     110     120
m917.pep  IKVTYDVYDSDETLESKVLVTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
          |||||
a917      IKVTYDVYDSDETLESKVLVTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
          70      80      90     100     110     120

          130     140     150     160     170     180
m917.pep  EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG
          |||||
a917      EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG
          130     140     150     160     170     180

          190     200     210     220     230     240
m917.pep  QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA
          |||||

```

1316

a917	QCGISYLDAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRFRTSSGFIDDLA
	190 200 210 220 230 240
	250 260 270 280 290 300
m917.pep	RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMMPKEGVGIWVDSFVIPKDAKNVANAHK
a917	RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMMPKEGVGIWVDSFVIPKDAKNVANAHK
	250 260 270 280 290 300
	310 320 330 340 350 360
m917.pep	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
a917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
	310 320 330 340 350 360
	370
m917.pep	ALKFMVRQWQDVKAGKX
a917	ALKFMVRQWQDVKAGKX
	370

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

g919.seq

1	ATGAAAAAAC	ACCTGCTCCG	CTCCGCCCTG	TACGGcatCG	CCGCCgccAT
51	CctcgCCGCC	TGCCAAAgca	gGAGCATCCA	AACCTTTCCG	CAACCCGACA
101	CATCCGTCAT	CAACGGCCCC	GACCGGCCGG	CCGGCATCCC	CGACCCCGCC
151	GGAACGACGG	TTGCCGGCGG	CGGGGCCGTC	TATACCGTTG	TGCCGCACCT
201	GTCCATGCCC	CACTGGGCGG	CGCaggATTT	TGCCAAAGC	CTGCAATCCT
251	TCCGCCTCGG	CTGCGCCAAT	TTGAAAAACC	GCCAAGGCTG	GCAGGATGTG
301	TGCGCCCAAG	CCTTTCAAAC	CCCCGTGCAT	TCCTTTCAGG	CAAAGcGgTT
351	TTTTGAACGC	TATTTACGCG	cgtGGCaggt	tgcaggcaAC	GGAAGcCTTG
401	Caggtacggt	TACCGGCTAT	TACGAACCGG	TGCTGAAGGG	CGACGGCAGG
451	CGGACGGAAC	GGGCCCGCTT	CCCGATTTAC	GGTATTCCCG	ACGATTTTAT
501	CTCCGTCCCG	CTGCCTGCCG	GTTTGCGGGG	CGGAAAAAAC	CTTGTCGCA
551	TCAGGCAGac	ggGGAAAAAC	AGCGGCACGA	TCGACAATGC	CGGCGGCACG
601	CATACGCGCG	ACCTCTCCCG	ATTCCCCATC	ACCGCGCGCA	CAACGGcaat
651	caaaGGCAGG	TTTGAaggAA	GCCGCTTCTT	CCCTTACCAC	ACGCGCAACC
701	AAAtcaacGG	CGGCgcgcTT	GACGGCAAag	cccCCATCCT	CggttacgcC
751	GAgaccCcG	tcgaacttTT	TTTCATGCAC	AtccaaggCT	CGGGCCGCCT
801	GAAAACCCcg	tccggcaaat	acatCCGCAt	cggatagcc	gacAAAAACG
851	AACAtccgTa	tgtttccatc	ggACGctaTA	TGGCGGACAA	AGGCTACCTC
901	AAGctcgggc	agACCTCGAT	GCAGGgcac	aaagcCTATA	TGCGGCAAAA
951	TCCGCAACGC	CTCGCCGAAG	TTTTGGGTCA	AAACCCAGC	TATATCTTTT
1001	TCCGCGAGCT	TGCCGGAAGC	GGCAATGAGG	GCCCCGTCCG	CGCACTGGGC
1051	ACGCCACTGA	TGGGGGAATA	CGCCGGCGCA	ATCGACCGGC	ACTACATTAC
1101	CTTGGGCGCG	CCCTTATTTG	TCGCCACCGC	CCATCCGGTT	ACCCGCAAAG
1151	CCCTCAACCG	CCTGATTATG	GCGCAGGATA	CAGGCAGCGC	GATCAAAGGC
1201	GCGGTGCGCG	TGGATTATTT	TTGGGGTTAC	GGCGACGAAG	CCGGCGAACT
1251	TGCCGGCAAA	CAGAAAACCA	CGGGATACGT	CTGGCAGCTC	CTGCCCAACG
1301	GCATGAAGCC	CGAATACCGC	CCGTGA		

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

g919.pep

1	MKKHLLRSAL	YGIAAAAILAA	CQSRSIQTFP	QPDTSVINGP	DRPAGIPDPA
51	GTTVAGGGAV	YTVVPHLSMP	HWAAQDFAKS	LQSFRLGCAN	LKNRQWQDV
101	CAQAFQTPVH	SFQAKRFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDGR
151	RTERARFPIY	GIPDDFISVP	LPAGLRGGKN	LVRIRQTGKN	SGTIDNAGGT
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVELFFMH	IQGSGRLKTP	SGKYIRIGYA	DKNEHPYVSI	GRYMA DKGYL
301	KLGTSMQGI	KAYMRQNPQR	LAEVLGQNPS	YIFFRELAGS	GNEGVPV GALG
351	TPLMGEYAGA	IDRHYITLGA	PLFVATAHPV	TRKALNRLIM	AQDTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	QKTTGYVWQL	LPNGMKPEYR	P*

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFR	AALYGIAAA	ILAACQSK	SIQTFFQ	PDTSVING	PDPRVGI
	PDPA	GTTVGGG	GAV			
	:	:	:	:	:	:
g919	MKKHLLR	SALYGIAAA	ILAACQSR	SIQTFFQ	PDTSVING	PDPRVGI
	PDPA	GTTVAGG	GAV			
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHL	SLPHWAAQ	DFAKSLQ	SFRLGCAN	LKNRQGWQ	DVCAQAFQ
	TPVH	SFQAKQ	FFER			
	:	:	:	:	:	:
g919	YTVVPHL	SMPHWAAQ	DFAKSLQ	SFRLGCAN	LKNRQGWQ	DVCAQAFQ
	TPVH	SFQAKR	FFER			
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
	: :					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	: :					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	: :					
g919	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
	: :					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	: : :					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1   ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGCGCG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 TCCCTGCCCC CTGCTGCCC GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAACC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG

```


1319

```

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATT TTGGGGATAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1  MKKYLFRAAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
     51  GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
    101  CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
    151  RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
    201  HTADLSQFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
    251  EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
    301  KLGQTSMQGI KAYMQQNPQR LAEVLGQNPS YIFFRELTS SNDGPVGALG
    351  TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
    401  AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919  98.6% identity in 441 aa overlap
              10      20      30      40      50      60
m919.pep    MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              |||||
a919         MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m919.pep    YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
              |||||
a919         YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
              70      80      90      100     110     120

              130     140     150     160     170     180
m919.pep    YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
              |||||
a919         YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
              130     140     150     160     170     180

              190     200     210     220     230     240
m919.pep    LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
              |||||
a919         LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
              190     200     210     220     230     240

              250     260     270     280     290     300
m919.pep    DGKAPILGYAEDPVLEFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
              |||||
a919         DGKAPILGYAEDPVLEFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
              250     260     270     280     290     300

              310     320     330     340     350     360
m919.pep    KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
              |||||
a919         KLGQTSMQGIKAYMQQNPORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
              310     320     330     340     350     360

              370     380     390     400     410     420
m919.pep    VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
              |||||
a919         VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
              370     380     390     400     410     420

              430     440
m919.pep    QKTTGYVWQLLPNGMKPEYRPX
              |||||
a919         QKTTGYVWQLLPNGMKPEYRPX
              430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCCGTCAAA AACAAAGCA
151 GGCTGGAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAAACCGT ATGTTTCGGTA AAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCTT GGAAATCGTC
301 CCGCTGGACA ATCccgccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtggtc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGCGccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttccc
551 CCGATcaaAG CCTGTGccga AAACAggcga ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTA EY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAaCCGG TCGGACAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTGCAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng)
 from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920.pep				PMQLVTEKGKENMIQRGT	YNYQYRSNR	PKV
m920	GGEYLKADLGYGEFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQRGT	YNYQYRSNR	PKV			
	40	50	60	70	80	90
g920.pep						
m920	DGSYLVTAIEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT					
	40	50	60	70	80	90
g920.pep						
m920	DGSYLVIAIEYQPTFWKXKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT					
	100	110	120	130	140	150
g920.pep						
m920	KPVGQNLEIVPLDNPADIVHGXRFKVRVLFGRGEPLPNATVTATFDGFDTS	SDRSKTHKTEA				
	100	110	120	130	140	150
g920.pep						
m920	KPVGQNLEIVPLDNPANIHVGERFKVRVLFGRGEPLPNATVTATFDGFDTS	SDRSKTHXXEA				
	160	170	180	190	200	210
g920.pep						
m920	QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRKQANYTTLT	FQIAHSHHX				
	160	170	180	190	200	
g920.pep						
m920	QAFSDSTDDKGEVDIIXLRQGFWKANVEHKTDFPDQSVKQKQANYSTLT	FQIGHSHHX				
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920.seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCCCACGCC	CACCGCGTCT	GGGTCGAAAC	CGCCCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCTGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCAGT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTTCTGGTC	AAAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAAACA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTTCG
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGCGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGCA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920.pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRHLHIFS	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFDT
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVK
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATS	SAHAHRVWVETA	HTHGGEYLKADL	GYGEFPELEPIAK	DRLHIFS	
	:	:	:	:	:	:
a920	XKKTLTLLAVSALFAASA	HAHRVWVETA	HTHGGEYLKADL	GYGEFPELEPIAK	DRLHIFS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQ	RGTNYQYRSNR	PKDGSYLVIAEYQ	PTFWSKXKAGWKQ	AGIKE	
	:	:	:	:	:	:
a920	KPMQLVTEKGKENMIQ	RGTNYQYRSNR	PKDGSYLVIAEYQ	PTFWSKNKAGWKQ	AGIKQ	
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGK	NIVNVGHESAD	TAITKPVGQNLEI	VPLDNPANIHV	GERFKVRVL	
	:	:	:	:	:	:
a920	MPDASYCEQTRMFGK	NIVNVGHESAD	TAITKPVGQNLEI	VPLDNPANIHV	GERFKVRVL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTAT	FDGFDTSDRSK	THXEAQAFSD	STDDKGEVDI	IXLRQGF	WKANVEH
	:	:	:	:	:	:
a920	FRGEPLPNATVTAT	FDGFDTSDRSK	THKTEAQAFSD	STDDKGEVDI	IPLRQGF	WKANVEH
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQ	KQANYSTLT	TFQIGHSHHX			
	:	:	:			
a920	KADFPDQSVQCQ	KQANYSTLT	TFQIGHSHHX			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCGTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCTG
401 GTAAAAACAT TGTC AACGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATS AHP HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQ RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 QKQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCC CACCGCTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTGGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1  MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIPLR QGFWKANVEH KTDFFDQSV
251 KQQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFRSKNAGWKQAGIKE					
	70	80	90	100	110	120
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTTDGKGEVDIPLRQGFWKASVEY					
	190	200	210	220	230	240
m920-1.pep	KTDFFDQSVCKQKQANYSTLTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260	269			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1  TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCACGCC CACCGCTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTGGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```
a920.pep
1  *KKTLLTLLAV SALFAASAHV HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*
```

m920-1/a920 98.9% identity in 267 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLLTLLAVSALFATS	SAHAHRVWVETAHTHG	GEYLKADLGYGEFPELE	PIAKDRLHIFS		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	10	20	30	40	50	60
m920-1.pep	KPMQLVTEKGKENMIQR	GTNYQYRSNRPVKDGS	YLVIAEYQPTFWSKNK	AGWKQAGIKE		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	70	80	90	100	110	120
m920-1.pep	MPDASYCEQTRMFGKN	IVNVGHESADTAIITK	PVGQNLEIVPLDNPAN	IHVGERFKVRVL		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	130	140	150	160	170	180
m920-1.pep	FRGEPLPNATVTATFD	GFDTSDRSKTHKTEAQ	AFSDSTDDKGEVDIIP	LQRQGFWKANVEH		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	190	200	210	220	230	240
m920-1.pep	KTDFPDQSVCKQKQAN	YSTLTTFQIGHSHHX				
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX				
	250	260	269			
m920-1.pep	KADFPDQSVCKQKQAN	YSTLTTFQIGHSHHX				
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX				
	250	260				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```
g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacggA aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTTCG
151 CATTTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGTGGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GGCGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```
g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```
m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGTGGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

1325

251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GCGGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng)

from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	: :					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTTCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GCGGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

1326

	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTGTG GACGATGAAG TCGGGAAGG GATTTTTC CAGGCGGAAT
251 GGCAGGATTT TTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtggtcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAt acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501 TTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTATATG CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTAtat gaagCAGCAC GGTGGCGCA CgggcggTAA
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901 ggcacatccc ccggggaaaC GCTCGCAGAT GATGAAAAGg cgGTTTGTt
951 CAAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTTG GGCTTGAACA
1001 ATTTTATATC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051 gtcaggGACA TTGCCAATTC GCTCGGCGGC CCGGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KKEsrPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVKGDFS QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFRtGNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201 EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGEkTAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMVvTA
351 VRDIANSLGg PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAATT CGGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCGC GCCGGGTTT TCCAAAAAGA ATTGGTCGAG

```



```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGC GATGTTTCG CCTTAAAGG
651 CAGCTATGCG GGCACAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACC GGCG GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KESRPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFFDKAAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

	10	20	30	40	50	60
m922.pep	MKKRKILPLA ICLAALSACTAMEARPPRANEAQAPRAVEMKESRPAFDAAAVFDAAAVP					
g922	MEKRKILPLA ICLAALSACTAMEARTPRANEAQAPRADEMKESRPAFDAA-----AVP					
	10	20	30	40	50	
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDDEVGKGDFSQA EWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
g922	TGNSGRAKFHGARRFYAENRAVIDDVAQKYGVPaelivaiIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m922.pep	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
	250	260	270	280	290	300
m922.pep	DGDGHRDIWGNVDVAASVAN YMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVDVAASVAN YMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m922.pep	ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					

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	300	310	320	330	340	350
		370				
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1   ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTG
51  TGCCTGTACG GCGATGGAGG CACGCCCCGC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCGCTGGTA
351 TGTGTTCCGC ACGGGAAATT CGGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCGC GCCGGGTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTAAAGG
651 CAGCTATCGG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GTTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTTGTTC AACTGGAAC CGCACCCGGC GTGTTTGAAT
1001 ATTATTTGGG CTGAACAAT TTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1   MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAAY
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKEEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWGRT GGKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEAQAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep    ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
            190      200      210      220      230      240

            250      260      270      280      290      300
m922.pep    DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKALTRTV
            ||||||||||||||||:||||||||||||||:||||||||||||||||||||
a922        DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGEKALTRTV
            250      260      270      280      290      300

            310      320      330      340      350      360
m922.pep    ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMVYTVAVRDI
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMVYTVAVRDI
            310      320      330      340      350      360

            370
m922.pep    ANSLGGPGLX
            ||||||||
a922        ANSLGGPGLX
            370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTCTGTGC
51 CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGA CTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTGTG
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51 GKRRIP EHLR LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTGC
51 TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCGCGTATT TCGGCAGCAT GACATTCAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGA CTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTCGCCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAAC TCGGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRAIR
51 GQRRIP EHLR LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

```

      10          20          30          40          50          60
g923.pep MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRAVRGKRRIPEHRL
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||: |||||
m923      MKRQAFFKLMAACAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRIPEHRL
      10          20          30          40          50          60

      70          80          90         100
g923.pep LLPALFGGWGTGAYLGSRMFRHKHTAKKRFVVLFRLTVSGNVLATCILID-----
|||||:||: ||: ||: || | :||| ||||| ||||| ||||| ||||| |||
m923      LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLTVSGNVLATLILIIYSGLNLNQYGVAS
      70          80          90         100         110         120

              110         120
g923.pep -----YFVPPELFFVKLGQHLX
              |||||:||: |||
m923      PCRTICTVCGFVALSXFLLIHYIYFVPPPEFFVKLGQNTX
      130         140         150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

```
a923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCGTCT
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACCT TACGGCATCG ACAAACGCGC TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTCCG
201 CGGTTGGGCG GCGCATACT TGGGCAGCAG GATATTCAGG CATAAAACGG
251 CGAAAAAGCG TTTTGTTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAAGC ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGTCTGCGG TTCGTGCGCC
451 TTGTCTGAT TTTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep
1 MKRQAFKKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRAVR
51 GKRRIPHEHL LLPALFGGWA GAYLGSRIFR HKTAKKRFV LFRLTVSGNV
101 LATLILYISG LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHXY YFVPPEFFVK LGQNT*

m923/a923 84.6% identity in 175 aa overlap

```

a923      84.6% identity in 175 aa overlap
          10          20          30          40          50          60
m923.pep  MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL
          |||||
a923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRAVRGKRRRIPEHRL
          10          20          30          40          50          60

          70          80          90          100         110         120
m923.pep  LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS
          |||||
a923      LLPALFGGWAGAYLGSRIFRHKHTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS
          70          80          90          100         110         120

          130         140         150         159
m923.pep  PC-----RTICTVCGFVALSXFLLIHXYFVPPEFFVKLGQNTX
          |
a923      PXAQRERFSKVLKHQVNRFTICTVCGFVALSXFLLIHXYFVPPEFFVKLGQNTX
          130         140         150         160         170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gccGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51 KINVFTGKEE SLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

```

m925-1.seq
1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CCGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CCGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CCGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

```

m925-1.pep..
1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNLYFL
51  NKIHVVVTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNRSIPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNLYFLNKIHVVVTGKE					
g925-1	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNLYFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKKCGQT					
g925-1	ESLLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNRSIPALLX					
g925-1	AQAYLDARNALPSNQTYQQRQAIEQLKRRFEAEFDELEKEIKCNK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

```

a925-1.seq
1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CCGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CCGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTATG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

```

a925-1.pep
1  NKINVFTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51  KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNLYFLNKIHVVVTGKEESMLLSEKDGALSINTGIGE			
	30	40	50	60
	70	80		
	40	50	60	70
	80	90		

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
              |||||||||||||||||||||||||:|:|:|
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GGCGGGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GGCGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSGGQVRTL QLNNGNLNR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep  MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
m926      MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
              |||||||||||||||||||||||||||||||||||||||:|:|:|
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRWGASPNVATE

```

1334

||:||||| |||||:|:| :|
 m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq
 1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
 101 GCAGTTTCAC GGCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
 151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
 251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCGCA
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
 501 GAACATCAGG CTGGTTTTC ACGAGATTGG TATGCCGTCT GAAACCGAAA
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep
 1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
 101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
 151 ADSSGGQVRTL QLNNGNLNR LVFTEIGMPS ETETQEQCAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFSAEGRRLAVKAEGKGSYANFDWTYQ					
	:					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEGKGSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGGKGNVYQESAELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGGKGNVYQESAELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
	:					
a926	ETETQEQCAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq
 1 atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
 51 CAGCCcgcga GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGGCCA
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtacgat
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

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```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAActCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGA AACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTQYSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAAACCT ACGCACCAGG ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCCAAA ACTCGTCGCA
601 TCCATCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC
651 ACCACCTTCA CACAACGCAA CATCGCGGAC GTACTCATCA CTTTGTAAAA
701 CGAAGCCAAC TACGTCAGCr AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVVARDFYKEYN					
	10	20	30	40	50	60
	70 80 90 100 110 120					
g927.pep	HLFVGTQYSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130 140 150 160 170					
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180

1336

	180	190	200	210	220	230
g927.pep	YGYGLKANNGNEQEAQKLVASILKNTFPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS					
	:					
m927	YGYGLKTTNGNEQEAQKLVASILKNTFPVFENGGRXPPP-SHNATSATYSSLLKTKPTTS					
	190	200	210	220	230	
	240					
g927.pep	AKNX					
m927	AKNX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```
a927.seq
1  ATGAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```
a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*
```

m927/a927 99.2% identity in 242 aa overlap

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	:					
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	:					
a927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	:					
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTFPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
	:					
a927	YGYGLKTTNGNEQEAQKLVASILKNTFPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GTTAGCCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAacgctggG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAct GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCcgat TATGCagtcg attgCcggCA GttacggctC
501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTttgg
551 tcaattaTCA TTCcaatCCC atttcgctcg ctAtggctat taCTGcaact
601 gCCCCcaaCC CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
651 tttccgctCTT TCttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccggcg
701 ttatcgccctt TTtcgTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGCTCTGAG
801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTtaAATA Aactcggact gattaaatGG TTCTCCGAG TGTGGCGGA
1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTGCGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGATATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep

```

1  MKLGFKPIPL AIAAVLCA LV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  VMPLGALSII AVGLVA VTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTA H
401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAct GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

```

451 GCGGCGATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCTGTTATG CCTTTGATT TATATTTwyT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGG CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCGGC GGTGGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMCKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFAA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
	70 80 90 100 110 120					
g929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
	130 140 150 160 170 180					
g929.pep	FGRKTLGIGYSLALSELLLAPVTSPNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMCKY					
m929	FGRKTLGIGYSLALSELLLAPVTSPNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMCKY					
	130	140	150	160	170	180
	190 200 210 220 230 240					
g929.pep	LALVNYHNSNPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSNPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNAVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGG LGVSGTAAGVILVLA MYAHYMFAS TTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGG LGVSGTAAGVILVLA MYAHYMFAS TTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTG GTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GCGGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTAC AGTCTGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGA
1101 AAGTGTCCGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

a929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
 151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFIGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV					
a929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV					
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVAPALITGN					
a929	PLILYFLYPPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVAPALITGN					
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAAVSLNAPAM					
a929	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTGT TGCCATTAAC GAAAGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACAC
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTCGG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 ACGGCCATCT GTGGTGCAAT GGCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCOA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 CGCAAAACCT CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTG AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAGAA
701 GTTACAACAC TGATTTCCGC TTCAACCGCC TGTTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACCC ACAGGTTGGT
851 TGGCAGAACT TTCCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGC GCGCGGCC
951 TGAAGAAAGC TTTGGCGAAG GCACGTACAG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCACAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKLCP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDSN GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGTPEDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGRYHQH VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETYSYIDD AELTVQRKRT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGTSRMKI WTASADVNTF FQIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDSLW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```

m930-1.seq

1	ATGAAACTTC	CTTTATCCTA	TTTGCTTAAT	ATTCGCTTTT	TGCTTTGGTG
51	CTGCTTATTG	GCAGCGTATCA	TTGCTCCTGC	TACTTTGTTG	GCCTCCCCCA
101	ACCCTGCCGA	AATCCGTATG	CAGCAAGATA	TTACGACAACG	CCAACGCGAA
151	GAGCAGTTGC	GGCAAAACAT	CGACGCTGAA	AGCAGTTGTC	GTTTGCATCA
201	AAAAAACACG	GGGGAACCG	TTAATCAGTT	GATGGGCGAT	GATCCAGACC
251	AACCGTGTTT	TGCCATTAC	GAAGTGGTGT	TGGAAGGGCA	ACACCATGCT
301	CGGTTTCAGT	TTGCCCTAAA	ACGTGCCTTG	CGCGAAACGG	GTTTTCTAGGC
351	TGGCAAGTGT	CTGCATGCGG	GCACACTTAA	CTCAACTATG	TCCTTAGCAC
401	AAAATGCTTT	GATCGGCAGG	GGATATACCA	CGACCCGTAT	CTTGGCTGCG
451	CCACAGGATT	TGAATAGTGG	CAAGCTTTCA	TTAACCCCTG	TACCGAGCTA
501	TCTGCGCTCC	ATACGAATCG	ATCGGTCTAA	CGATGATCAA	ACCCATGCGAG
551	GACGTATTGC	AGCAATTCAG	AACAAATTTT	CCACC CGTC	GAAACGATCTG
601	TTGAATCTGC	GTGATTTGGA	ACAAGGACTG	GAAAATCTCA	AACGTCTCCC
651	GACTGCGGAT	CCTGATCTCC	AAATCGTTCC	CGTAGAGGGA	GAACCAAAACC
701	AAAGTGGTGT	CGGTGTGCAA	TGGCGGCAAC	GTCTGCTGCC	CTACCGTGTG
751	AGTG TG GGA	TGGATAATTC	GGGTAGTGAG	GGCAGAGGAA	AATACCAAGG
801	AAATATCACT	TTCTCTGCCG	ACAATCCTTT	GGGACTGAGT	GATATGTTCT
851	ATGTAAATTA	TGGACGTTTG	ATTGGCGGTA	CGCCCGATGA	GGAAAGGTTTT
901	GACGGCCATC	GCAAAGAAAG	CGGATCAAAC	AATTACGCCG	TGACATTATTC
951	AGCCCTTTTC	GCTAAATGGA	CATGGCGATT	CAATCACAA	GGATACCGTT
1001	ACCATCAGGC	AGTTTCCGGA	TTATCGGAAG	TCTATGACTA	TAATGGAAAA
1051	AGTTACAATA	CTGATTTTCGG	CTTCAACCGC	CTGTTGTATG	GATATGCCAA
1101	ACGCAAAACC	TATCTCGGTG	TAAAGCTGTG	GATGAGGGAA	ACAAAAGGTT
1151	ACATTGATGA	TGCCGAACGT	ACTGTACAAC	GGCGTAAAC	TGCGGGTTGG
1201	TTGGCAGAAC	TTTCCACAA	AGAATATATC	GGTCGCAGTA	CGGCAGATTT
1251	TAAGTTGAAA	TATAAACCGC	GCACCGGCTA	GAAAGATGCT	CTGCGCGCGC
1301	CTGAAGAAGC	TTTGGCGCAA	GGCACGTCAC	GTATGAAAA	TTGGACGGCA
1351	TCGGCTGATG	CAAAATCTCC	TTTTCAAAATC	GGTAAACAGC	TATTTGCCTA
1401	TGACACATCC	GTTCATGCAC	AATGGAACAA	AACCCCGCTA	ACATCGCAAG
1451	ACAACTCTGC	TATCGCGCGA	CACCAACCG	TACGTGGCCT	CGACGGTGAA
1501	ATGAGTTTTG	CTGCCGAGCG	GGGATGGTAT	TGGCGCAACG	ATTTGAGCTG
1551	GCAATTTTAA	CCAGGCCATC	AGCTTTATCT	TGGGGCTGAT	GTAGGACATG
1601	TTTCAGGACA	ATCCGCCAAA	TGGTTATCGG	GCCAAACTCT	AGTCGGCACA
1651	GCAATTTGGGA	TACCGGGGCA	GATAAAGCTT	GGCGGCAACC	TGCATTACGA
1701	TATATTTTACC	GGCCGCGCAT	TGAAAAAGCC	CGAATTTTTT	CAATCAAGGA
1751	AATGGGCAAG	CGGTTTTCAG	TGGGCTATA	CGTTTTTAA	

m930-1.ppt

1	MKLPLSYLPN	IRFLSWCCLL	AGIIPATL	ASPNPAEIRM	QODIQQRQRE
51	EQLRQTMQPE	SDVRLHQKNT	GETVNQLMGD	DSSQPCFAIN	EVVLEGEHHA
101	RFQFALKRAL	RETGFQAGKC	LHAGNINQIM	SLAQNALIGR	GYTTTRILAA
151	PQDLNSGKLQ	LTLIPSYLRS	IRIDRSNDQ	THAGRIAAFO	NKFPTRSNDL
201	LNLRDLLEQGL	ENLKRPLTAE	ADLQIVPEG	EPNQSDVVVQ	WRQRLLPYRV
251	SVGMDNSGSE	ATGKYQGNIT	FSANPLGLS	DMFYVNYGRS	IGGTPEDESF
301	DGHRKEGGSN	NYAVHYSAPF	GKWTWAFNHN	GYRYHQAVSG	LSEVYDYNKG
351	SYNTDPGFNR	LLYRDAKRKT	YLGVKLWMRE	TKSYIDDAEL	TVQRRKTAGW
401	LAELSHKEYI	GRSTADFKLK	YKRQGTGMKDA	LRAPEEAFGE	GTSRMKIWTA
451	SADVNTPEFI	GKQLFAYDTS	VHAQWNKPLD	TSQDKLAIIG	HHTVQGFEDGE
501	MSLSAERGWY	WRNDLSWQFK	PQHQLYLTPG	QGVHSGQSAK	WLSGQTLVGT
551	AIGIRGQIKL	GGNLHYDIFT	GRALKKPEFF	QSRKWSGFO	VGYTF*

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHRARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI					
	:					
g930-1.pep	GKCLHAGDINQIMSLAQNALIGRGYTTTRI					
	10		20		30	
m930-1.pep	150	160	170	180	190	200
	LAAPQDLNSGKQLQLTLPISYLRISIRIDRSNDDQTHAGRIAAFQNKFPTRSDLLNLRDLE					
	:					
g930-1.pep	LAAPQDLNSGKQLQLTLPMPGYLRISIRIDRSNDDQTHAGRIAAFQNKFPTRSDLLNLRDLE					
	40	50	60	70	80	90
m930-1.pep	210	220	230	240	250	260
	QGLLENLKRLLPTAEADLQIVPVEGEPNQSDVVVQWRQRLLPYRVSVGMDNSGSEATGKYQG					

1343

```

g930-1.pep  QGLENLKCLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDSNGSEATGKYQG
              100      110      120      130      140      150

m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDYNKSYNTDFGFNRLLYRDAKRKTYLGVKLMWRETksYIDD
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDYNKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETksYIDD
              220      230      240      250      260      270

m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  AELTVQRRKTTGWLAEKSHKGYIGRSTADFKLKYKHGTGMKDALARPEEAFGEGTSRMKI
              280      290      300      310      320      330

m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390

m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450

m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
g930-1.pep  IFTGRALKKPEYFQTKKWVTGFQVGYSTX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCG GTTGTGTGCG
551 GGCAGTACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

m931.seq

```

1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACcA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

m931.pep..

```

1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLD ESKASKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	70	80	90	100	110	120
	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
	: :					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	130	140	150	160	170	180
	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVVPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

a931.seq

```

1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACA CTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC

```

451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFEGG FKPWPDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTTC CACTCACCGC

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```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTG ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCGCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCGCGTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1  MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPQCA HQQGFHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1  ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51  ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCC TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATTCAC ACGGGCAGGC AACCAAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 yCAGCAGGGA TTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCCG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTThT GCATTTGTTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1  ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51  TGXRRRAVYL RPIDRKLAAA KPGRRGRRV YRQAGKQIH TGRQPRQSRR
101 PARACSLPSV RTPQCAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

m934.pep
                                     10      20      30
                                     RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
g934
                                     |||:|||||||||||||||||||||||||||||
                                     10      20      30      40      50      60
m934.pep
                                     40      50      60      70      80      90
                                     PAEAQANGNNGQPVTKXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
g934
                                     ||:||||||||||||| ||||||||||||||| ||||||||||||||| |||
                                     70      80      90     100     110     120
                                     PAQAQANGNNGQPVTKRRAAVYLRPIDRKLAAAKPDWRGRRVYRQAGKQIHTGGQPR
                                     100     110     120     130     140     150

```

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```

m934.pep  QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
          ||||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934       QPRRPSRACCLPSVRTPQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
          130      140      150      160      170      180

          160      170      180      190      200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
          ||:||||| |||||:||||| :|||:||||| ||||| ||||| ||||| |||||
g934       RQKAVNPARQCRLKGFQTAFLLGALLCCRLIFRRHFVSKRLMSGWQFX
          190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2869>:

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCAG
351 GCAACCAAGA CAGTCCCCTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGC CAATTACCGC CGCCCCGCCA TGCGCGGTTT CGGCAGAAGG
551 CGGTAAATCC GGCGTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTCGGGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2870; ORF 934.a>:

```

a934.pep
1  MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAEAQANGNN GQPVTX*RRR AVYLRPIDRK LAAAKPGRRG
101 GRRVYRQRAG KQIHTGRQPR QSRRPARACR LPSVRTSQCA HQQGFEHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPPRHARF RQKAVNPACQ CRLKGFQTAF
201 LYLLGTLCC RLIFRRHFVS KSLMSGWQF*

```

m934/a934 94.1% identity in 205 aa overlap

```

m934.pep                                10      20      30
                                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
a934                                ||||| ||||| ||||| ||||| ||||| ||||| |||||
                                10      20      30      40      50      60
MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI

          40      50      60      70      80      90
m934.pep  PAEAQANGNNGQPVTGXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934       PAEAQANGNNGQPVTXXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
          70      80      90      100     110     120

          100     110     120     130     140     150
m934.pep  QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934       QSRRPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
          130     140     150     160     170     180

          160     170     180     190     200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
          ||:||||| |||||:||||| :||||| ||||| ||||| ||||| |||||
a934       RQKAVNPACQCRLKGFQTAFLLGTLCCRLIFRRHFVSKSLMSGWQFX
          190     200     210     220     230

```

g935.seq not found yet

1348

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGTT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGT CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCT
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGGTCA ATAATGCCGC CTACCGCGC AACCGTGTT ATGCCGGTTG
1251 GCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTTCTC GACAGAGCGC
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID.2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFFLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFGSGISPAV
201 NRNANNAAPQ YCRONGGROI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNAROTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGTT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGT CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAATT
501 GGATTTGCCG GCGCCGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGGTCAT ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGCTG
1251 GCGCGAGGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTGC
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

a935.pep

```

1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVEGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPPYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

m935.pep	10	20	30	40	50	60
	MLYFRYGLV VWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGLV VWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	70	80	90	100	110	120
	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	130	140	150	160	170	180
	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	190	200	210	220	230	240
	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	250	260	270	280	290	300
	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

1350

	310	320	330	340	350	360
m935.pep	GSDGFD AKTKRVNNRRLPPYMLAHGVG VQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935						
	310	320	330	340	350	360
	GSDGFD AKTKRVNNRRLPPYMLAHGVG VQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935						
	370	380	390	400	410	420
	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVASAYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935						
	430	440	450	460	470	480
	WRQLGGLNSRVASAYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	490	500				
m935.pep	GRTESNPYAKRRNSEVFVSADWRFX					
a935						
	490	500				
	GRTESNPYAKRRNSEVFVSADWRFX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAATC CGTCATCGAC CGcgcgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGA CACGTCCAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAcgcT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```


Homology with a predicted ORF from *N.gonorrhoeae*

m936/g936

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCTCTAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTCTG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTGCGCTACA
251	ACCGCCACCT	GCTGTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTG	AGATTGCACG	TTCGGAACG	CGCCCGGAAG	GCGTGTACAA
351	CTACATTACC	GTGCGCTCCC	TGCCGCGCAC	TGCCGCGCAC	ATCGCGGGCG
401	ACACTTGGA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTACCCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

1	<u>MKPKPHTVRT</u>	<u>LTAAVLSLAL</u>	<u>GGCVSAVVGG</u>	<u>AAVGAksAVD</u>	<u>RRTGAQTDD</u>
51	<u>NVMALRIETT</u>	<u>ARSYLQNNQ</u>	<u>TKGYTPQISV</u>	<u>VGYNRHLLLL</u>	<u>GQVATEGEKQ</u>
101	<u>FVGQIARSEQ</u>	<u>AAEGVYNYIT</u>	<u>VASLPRTAGD</u>	<u>IAGDTWNTSK</u>	<u>VRATLLGISP</u>
151	<u>ATQARVKIVT</u>	<u>YGNVTVYMG</u>	<u>LTPEEQAQIT</u>	<u>QKVSTTVGVQ</u>	<u>KVITLYQNYV</u>
201	QR*				

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD	RRRTTGAQTD	DDNVMALRIETT			
a936						
	10	20	30	40	50	60
	MKPKPHTVRTLTA	AVLSLALGGCVSAVV	GGAAGAKSAVD	RRRTTGAQTD	DDNVMALRIETT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYL	RQNNQTKGYTPQIS	VVGYNRHLL	LLGQVATEGEKQFVGQIAR	SEQAAEGV	NYNIT
a936						
	70	80	90	100	110	120
	ARSYL	RQNNQTKGYTPQIS	VVGYNRHLL	LLGQVATEGEKQFVGQIAR	SEQAAEGV	NYNIT

m936.pep VASLPRTA

1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcAACCA CCGgcgcgca AACCgATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGA A CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCgACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGA A CACATCCAAA GTCCGCGCCA CGCTGTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSVD RRTTGAQTDDNVMALRIETT
g936-1      |||||
          10      20      30      40      50      60
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
g936-1      |||||
          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
g936-1      |||||
          70      80      90      100     110     120
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
g936-1      |||||

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CTTTGCCCTC GCGCGCTGCG TCAGCGCAGT CGTCGGCGCG GCGGCGGTCTG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAAGG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVS AVVGG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGAKSAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLALLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLALLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAA
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACCTTGCTT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCAGACC GAAATTcAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTtACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACtCGacg GCAACGGCAA

```

1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTCACCG
551 CCGCCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCCGCG CAGGTTTCGG TTTCACCAA ACCGCGGCTT TAAACGCATC
801 CGCACGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAAGTG AAATTGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETSL TYLNSENSRA
51 ALASPVYIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIY
101 SGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTSLDDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLK KQPDRIDGKK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGCGCGAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENN
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTN DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVOHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETSLYLNSENSRAALASPVYIQ
          || || :| :: ::|| : :|||:|||||:|||||:|||||:|||||:|:|:|
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60
          60      70      80      90     100     110     119
g937.pep  TGSASFIPVPTEIQENGSTNDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR

```

	: : :	
m937	TGATSFIPITPEIQENGSNNTDMLVGTGLGRYGLTGNTDIYSGSYLWHEERKLDGN SKTR	
	70 80 90 100 110 120	
g937.pep	120 130 140 150 160 170 179 NKRMSDISAGISHTFLKDGNPALIAFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV	
	:	
m937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV	
	130 140 150 160 170 180	
g937.pep	180 190 200 210 220 230 239 LSLTAAAYRINGSKTLSDDVKYKAGNYWMLNPNISFAANDRISLTGGIQLWLKGQPDRI DGK	
	: : :	
m937	LSLTAAAYRINGSKTLSDGI RYKSGNYLLLNPNISFAANDRISLTGGIQLWLGRQPDR TDGK	
	190 200 210 220 230 240	
g937.pep	240 250 260 270 280 289 KESARNTSTYAHFGAGFGFTKTTAALNASARFNVSQSSELKLG VQH TFX	
	: :	
m937	RESSRNTSTYAHFGAGFGFTKT TALNASARFNVSQSSELKFGVQH TFX	
	250 260 270 280	

```
a937.seq
1 ATGAAGCGCA TCTTTTGGCC GGCCTTGCCC GCCATCTGCG CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAACCT GGAACCTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 CCCGAACTTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCG AAGAAAACGG CAGCAATAAC GATATGCTCG
251 TTGGCACGCT CGGTTTGC GC TACGGACTGA CCGGGAATAC GCACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTCGCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCG TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCGCTCGTG CTCTCATTTA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCTTTCAAG CAACACCAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCTTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA
```

```
a937.pep
1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51 AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLRL YLGTGNTDIY
101 GSGSYLWHEE RKLDBGNGTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTSSNNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL KQGPDRDLGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
a937	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPITPEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
a937	:					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRDVGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRDVGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTALNASAREFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTALNASAREFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAGATAT TGCAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTCGCC
601 AACTTTATCC AAGGTTTGGC TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQQPKSGEA NPENPELGA KIYRGGLSDK KVPACMSCHG PSAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEDLLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDILNVSIFYAKQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

g950.seq

```

1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCCGG GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAAGCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

g950.pep

```

1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

m950.seq

```

1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

m950.pep

```

1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAG SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
              10      20      30      40      50      60
              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |:|||||
g950          SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

a950.seq

```

1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
  1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

              10      20      30      40      50      60
a950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
              |||||
m950           MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
              10      20      30      40      50      60

              70      80      90      100
a950.pep      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              |||||
m950           EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
  1 ATGATTATGT TACCCGCCCG TTTCACATATT TTATCTGTCC TCGCAGCAGC
 51 CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTGT ACCTGTGTTG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTGCG TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTGCAGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTAATGAC GTTGCGTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGGCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGTCTGTT
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTTCA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGCG
1201 AGGGTGCAGG AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GGCGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCCGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCGACGGC
1551 ATACCAAATC AACCCGGACG ATACCCGCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GGCGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
  1 MIMLPARFTI LSVLAAALLA GOAYAAGAAD VELPKEVGKV LRKHRRYSEE
```



```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHL DGLE EVLAQSDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSKLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDdTAVNDS IGWAYYLLKG AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTGCGGCGAG TGGGCGAGCG
201 GGTTAATCAG ATATTTACGT TGCTGGGAGG GGAACCCGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGGACGAA GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAA GCAATCGGA GCTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTT AATGACGTTG
751 CGTCTGACTG CACGCAAATA TCCCGAAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGTCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTTGGAGG CCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGGCAAAAC CGAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCAGGG TGCGGAAACT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTGCAAG CTGCCCGATA
1301 AACGGGAGG TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCCGTCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAGTGTG
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTCAGAT CTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTGGAC GAAGGTTTCG CCTGTGCTCA
1551 GACGCATAC CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGCGTA TTACCTGAAA GGCACGCGG AAAGCGCGCT GCCGTATCTG
1651 CCGTATTCTG TTGAAAACGA CCCCAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGG ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAC CTCGGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GOVSAAGGGA GDMKQPEVG KVFRKQQRYS
51 EEIKNERAR LAAVGERVNQ IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQWR QIEPIPGKAL KRAGWLRNVL
151 RERGNQHL D LEEVLAQADE QNRRVFLLL AQAAVQQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RL TARKYPEI LDGFFEQTD T QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YKVRQWLKK VSAPEYLFDK GVLA AAAAVE LDGGRALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALSK LPDKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQRSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQTAY QINPD TAVN DSGWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQORYSEEEIKNERAR					
g951	10	20	30	40	50	
	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	60	70	80	90	100	110
	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDLGLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIQKWRQIEPIPGEAQKRAGWLRNVLRERGNQHLDLGLEEVLAQSDDVQKRRIFLLL					
m951.pep	190	200	210	220	230	240
	AQAQVQDGLAQKASKAVRRAALKYEHLEPAAVADVFSVQGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAQVQGGVAQKASKAVRRAALKYEHLEPAAVADAVFGVQGREKEKAIEALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRRAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLEHNPANLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRLPEQQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRLPEQQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIQMLALSCLPKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	420	430	440	450	460	470
	SKIQMLALSCLPKREALIGLNIIAKLSAAGSTEPLAEALQRSIIYEQFGKRGKMIAD					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNLGYSLLSBSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTA AHLTGDKKIWRETL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTA AHLRGDKKIWRETL					
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTATCTCT GTGCTCGCGG CAGCCCTGCT
51  TGCCCGGCGAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAAACGAAC GCGCACGGCT TCGGCGAGTG GCGAGCGGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAGGGG CAGCGGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GGCGGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGGA
451 AATCAGCATC TAGACGGACT GGAAGAAAGT CTGGCTCAGG CGGACGAAGG
501 ACAGAACCGC AGGGTGTTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GCGCTTGAGA
601 TATGAACATC TGCCCGAAGC GCGGGTTGCC GATGTGGTGT TCAGCGTACA
651 TGGACCGGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTCT GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCTT TGAACGTGCT GTTGAACGCG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAACCCG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGGCGG
1151 CTGTCGAGTT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CGGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTTGTC
1251 CAAAATACAG ATGTTGCGCC TGTCGAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCCTGCCCG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GTTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAATGA TTTCAGATCT TGAAAGGCGC TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAGAG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCGTTT
1651 GAAAACGACC CCGAGCCCGA AGTTGCCGCC CATTGCGGCG AAGTGTGTG
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTCG CCCAACCTTC CCGAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPKEVGKVFR KQORYSEEEI
51  KNERARLAHV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDLGLEEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDEILP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILAAANRKEG ASVIDGYAEK AYGRGTGEOR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYLLS
501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDPEFEVAA HLGVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAG--AADAKPPKEVGKVFRKQORYSEEEIKNERAR
          ||| || :|||:|:|:|:| ||| |::| | ||||| ||||| |||||
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKKEVGKVFRKQORYSEEEIKNERAR
          10      20      30      40      50      60
a951.pep  LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

m951	LAAVGERVNVQIFTLGLGETALQKQGAGTALATYMLMLERTKSP EVAERALEMAVSLNAFE	70	80	90	100	110	120
a951.pep	QAEMIIYQKWRQIEPIPGKAQKQKAGWLRNVLRERGNQHL DGL EEVLAQADEGQNR RVFLL	120	130	140	150	160	170
m951	QAEMIIYQKWRQIEPIPGKAQKQKAGWLRNVLRERGNQHL DGL EEVLAQADEGQNR RVFLL	130	140	150	160	170	180
a951.pep	AQA AVQDGLAQKASKAVRRRAALRYEHLPEAAVADVVS VQGREKEKAIGALQRLAKLDT	180	190	200	210	220	230
m951	AQA AVQDGLAQKASKAVRRRAALKY EHLPEAAVADVVS VQGREKEKAIGALQRLAKLDT	190	200	210	220	230	240
a951.pep	EILPPTLMTLRLTARKYPEILDGFFEQTD TQNLSAVWQEMEIMNLVSLHRLDDAYARLNV	240	250	260	270	280	290
m951	EILPPTLMTLRLTARKYPEILDGFFEQTD TQNLSAVWQEMEIMNLVSLHRLDDAYARLNV	250	260	270	280	290	300
a951.pep	LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD	300	310	320	330	340	350
m951	LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD	310	320	330	340	350	360
a951.pep	YTKVRQWLKKVSAPEYLF DKGVLAAAAVELDGGRAALRQIGRV RKLPEQQGRYFTADNL	360	370	380	390	400	410
m951	YAKVRQWLKKVSAPEYLF DKGVLAAAAVELDGGRAALRQIGRV RKLPEQQGRYFTADNL	370	380	390	400	410	420
a951.pep	SKI QMFALSKLPDKREALRGLDKIIEKPPAGSNT ELQAEALVQRSVVYDR LGKRKKMISD	420	430	440	450	460	470
m951	SKI QMLALSKLPDKREALRGLDKIIEKPPAGSNT ELQAEALVQRSVVYDR LGKRKKMISD	430	440	450	460	470	480
a951.pep	LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYY LK	480	490	500	510	520	530
m951	LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYY LK	490	500	510	520	530	540
a951.pep	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVW TQAAHLTGDKKI WRETL	540	550	560	570	580	590
m951	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVW TQAAHLTGDKKI WRETL	550	560	570	580	590	600
a951.pep	KRHGIALPQPSRKPRK	600	610				
m951	KRHGIALPQPSRKPRK	610					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

g952.seq (partial)

1	..TTGCTTTATC	GTTTGAATGC	TGCACCGATG	TTTAACGATA	ATCCTGTGTG
51	TTACGGA AAA	ATCAAATGC	AGAGTTGGAA	AGCGCGCGG	GATTTCAATA
101	TTGTAAAGCA	GGATTGGAT	TTTTCCTGCG	GGCGGCTTC	GGTGGCGACG
151	CTTTTGAACA	ATTTTACGG	GCAAAAGCTG	ACGGAAGAAG	AAGTGTTGGA
201	AAAATCGGGT	AAGGAACAGA	TGCGCGCGTC	GTTTGGAGAT	ATCGCGCGCA
251	TTATGCCCGA	TTTGGGTTTT	GAGGCGAAGA	GCTATGCCCT	GTGCTTCGAA
301	CAGCTCGCGC	AGTTGAAAT	CCCCGTCATC	GTGTATCTGA	AATACCCGAA
351	AGACGACCAT	TTTTCGGTAT	TGCGCGGAGT	GGATGGCAAT	ACGGTTTTTG
401	TTGCCGACCC	GTGCGCGGGT	CATGTTTTCA	TGAGCAGGGC	GCAGTTTTTG
451	GAGGCTTGCG	AAACCCGTGA	GGGAAATTTG	GCAGGCAAAA	TTTTGCGCGT
501	CGTGCCGAAA	AAAGCGGAGG	CGATTTCAAA	TAAATTGTTT	TTACACATC
551	ATCCCAAGCG	GCAGACGGAG	TTTGCAGTCG	GACAGGTAAA	ATGGTGCGGT

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)
 1 ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
 51 LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
 101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
 151 EAWQTREGNL AGKILAVVPE KAEAISNKL FTHHPKRQTE FAVGQVKWWR
 201 AY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGGCGGGA TTTCAATATT
 151 GTAAAGCAGG ATTTGGATT TTTCTGTGGG GCGGCTTCGG TGGCGACGCT
 201 TTTGAACAAT TTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
 301 ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
 451 GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTTTGGA
 501 TGCTTGCGAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep
 1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
 101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTOH
 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

		10	20	30	40
g952.pep		LSYRLNAAPMFNDNPVVYVKIKLQSWKARRDFNIVKQDLD	FSCG		
m952	MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYVKIKVQSWKARRDFNIVKQDLD	FSCG			
	10	20	30	40	50
	50	60	70	80	90
g952.pep	AASVATLLNNFYGQKLT	EEVLEKLGKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ			
m952	AASVATLLNNFYGQTL	TEEEVLKKLDKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ			
	70	80	90	100	110
	110	120	130	140	150
g952.pep	LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSPGHVMSRAQFLEAWQTREGNLAGKI				
m952	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSPGHVMSRAQFLDAWQTREGNLAGKI				
	130	140	150	160	170
	170	180	190	200	
g952.pep	LAVVPKKA	EAISNKLFFTHHPKRQTEFAVGQVKWWRAYX			
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE				
	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG AAAGGCGGGA TTCAATATT
151 GTAAAGCAGG ATTTGGATT TTCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTCAATG AGCAGGGCGC AGTTTTNGGA
501 TGCTTGSCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

a952.pep

```

1 MMKFKYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

	10	20	30	40	50	60
a952.pep	MMKFKYVFL	LACVVVSLSYRL	NAAAPMFNDN	PVVYGKIKVQ	SWKERRDFNI	VKQDLDFSCG
m952						
	10	20	30	40	50	60
	70	80	90	100	110	120
a952.pep	AASVATLLNN	FYGQTLTEEE	VLKKLDKEQM	RASFEDMRRI	MPDLGF EAKG	YALSFEQLAQ
m952						
	70	80	90	100	110	120
	130	140	150	160	170	180
a952.pep	LKIPVIVYLK	YRKDDHFSVL	RGIDGNTVLL	ADPSLGHVSM	SRAQFXDAWQ	TREGNLAGKI
m952						
	130	140	150	160	170	180
	190	200	210	219		
a952.pep	LAVVPKKAET	ISNKLFFTHH	PKRQTEFAVG	QIRQARAE		
m952	:					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

g953.seq

```

1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCGCCACAC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCGCCGT GCCAACCTGC AAAGCGGTTT GCAACCCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAACCTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACATCGA CCGACCAAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

```
g953.pep
  1 MKKIIFAALA AAAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
 51 GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF
101 VSTKFNENGK KLVSVVDGNTL MRGKTAPVKL KAEKFNCYQS PMAETEVC GG
151 DFSTTIDRTK WGVLDLVNAG MTKNVRIDIQ IEAAKQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

```
m953.seq
  1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCACGGC AAAAACTGG TTTCCGTTGA
351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCGTCAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

```
m953.pep
  1 MKKIIFAALA AAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KLVSVVDGNTL TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
151 GDFSTTIDRT KWGMDLVNVV GMTKSVRIDI QIEAAKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

```

      10      20      30      40      50      60
m953.pep  MKKIIFAALAAAIASTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g953      MKKIIFAALAAAAGVTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK
          10      20      30      40      50

      70      80      90      100     110     120
m953.pep  RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKLVSVVDGNTL
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g953      RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIRFVSTKFNENGKLVSVVDGNTL
          60      70      80      90      100     110

      130     140     150     160     170     180
m953.pep  TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDLVNVGMTKSVRIDI
          ||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g953      TMRGKTAPVKLKAKEFNCYQSPMAETEVC GGDFSTTIDRTKWGVLDLVNAGMTKNVRIDI
          120     130     140     150     160     170

m953.pep  QIEAAKQX
          |||::|::|
g953      QIEAAKQX
          180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

```
a953.seq
  1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCACGGC AAAAACTGG TTTCCGTTGA
```

1366

```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAAATTCAT CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GGCGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
  1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

```

a953/m953    97.3% identity in 187 aa overlap

a953.pep      10      20      30      40      50      60
               MKKIIIAALAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          10      20      30      40      50      60
               MKKIIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK

a953.pep      70      80      90      100     110     120
               RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          70      80      90      100     110     120
               RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL

a953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKAEKFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953          130     140     150     160     170     180
               TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI

a953.pep      QIEAAKQX
               |||||
m953          QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
  1 ATGAAAAAGT TTTATTTTGT GCTGCTGCGC TTGGGTTTGG CAGCGTGTGG
 51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTA CTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAACAGGC TGC GCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAATCA ATGCAAGAAT GCCGTAAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
  1 MKKFYFVLLA LGLAACGQEQ SOKADAEQYF FANKYQFADE KQAFYFERAA
 51 RFRVLQQLGL GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDL D KESYQNYRKS MQECRKTITE
151 AEANLPKK*

```


a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
  1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAATAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAAAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacagtc ttgtggtcgg
801 ctatgatgcy gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaattattat tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaaccc tatcatgcgc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
  1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
 51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRKGIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMRPMGMK ANSLVVG YDA DGLPQKVYWS VDNGKKPQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
  1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAATAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCTGATT TTCTTTGAAC
1051 TTGGAATAA TGGAATAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
  1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNAFV
 51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRKGIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```

1368

251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFRNA					
m957						
	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
m957	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
m957	WQPDGVSFDDAAGRKGIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
m957	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSVDNGKKPQSVEYYLKNGNLF					
	250	260	270	280	290	300
g957.pep	310	320	330			
m957	IAQSSTVTLKTDGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCAGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCCTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCCAAGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGACTCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
```

1369

```

951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYI ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

```

a957.pep      10      20      30      40      50
MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
|||||
m957          10      20      30      40      50      60
MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVFPKNPNAFVAKLARLFRNA

a957.pep      60      70      80      90      100     110
DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYIALAVRLSRLKEKAKWFHVTEQEHGEEV
|||||
m957          70      80      90      100     110     120
DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYIALAIRLSRLKEKAKWFHVTEQEHGKEV

a957.pep      120     130     140     150     160     170
WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
|||||
m957          130     140     150     160     170     180
WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV

a957.pep      180     190     200     210     220     230
WQPDGVSVDASGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
|||||
m957          190     200     210     220     230     240
WQPDGVSVDAAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKEKNRIAS

a957.pep      240     250     260     270     280     290
DSRDSVIFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF
|||||
m957          250     260     270     280     290     300
DSRNSVIFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF

a957.pep      300     310     320     330     340     350
IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR
|||||
m957          310     320     330     340     350     360
IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR

a957.pep      360     370
YAEAAARRSGGRRDLSHX
|||||
m957          370
YAEAAARRSGGRRDLSHX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTGGGCACG CATTGCGCCG CCGATACCGT TCGGCGCGAA GAGGCGGACG

```

```

101 GGCCTGTCTGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTTGA CCCTCGGTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCGGAG AGAACCGAAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCCGGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TGCAGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAAGTCGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGC CTCCAACAGG ACGGTACGCT GATTCTGGGC
451 GAAACCCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTG
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTTCGGCGG CGTTCCTCTT TTCTATACGC CTGGGCGGA CTTCCCGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCTTTTCG TCCCTTATTA TTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GGCGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCGG GCGGGCGGGA GGCAGCCTGA ATGCCGCGCT TTCGGTTCAG
1201 AATACACAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTTACGAA
1401 CAGCTGGGGC TACGTCGGCC CCAAACTCGG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGGCGG AAAGCATCCC GCAGCGTCGG GCGCGTTTGT
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATATTCTCTG CAAATCTCAA AACGACCTGC CCAATTTTCA TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCCGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTCGCTCC GCGGCGATAG
1901 GCGGGCGTTT CACCCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCCGAAA
2001 AGTGTGAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGCGGACGG TTTCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCTGTC GCTACAAC
2151 CGGTTTGTAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGCGGCG GTGACGCCCA ACCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCGGTC TTTTTCAC TTCAGTTGAA
2301 AACCCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCGG
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

```

1 LARLFSLKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQQASESAQA
51 SDLTLLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGTLLRG
151 ELTYNLDDQ TGEAHNVNME TEQGGRRLLQS VSRTAEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNIIDGGT FERNTRLFGG GVVQTIIEPL FYNYPKASQ NDLPNFDSSE
551 SSFGYQLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIQG
601 KFYFKDDAVM LDGVSVKNP SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDQDGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRYV
751 TGENTYKNAV FFSLLQLKDL SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51 CTTCCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

```

```

151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGTGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACC GAGCCGCCGT CCAAGGCAGC GGC GAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTGT CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGCTCG AACGCAACCG
351 GACGACCCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCGATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCAA
601 TTCAACACCT GTTCCGCGCG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTGCAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG GCGCGTTCCC ATTTTCTACA CCCCTTGGCG GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTCTT CCGTTCCTTA TTATTTC AAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACGAAGAA ATCGCGGCA ACGTCAACCT CAACCGCCCT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GCGGCGAGCC TGAATGCCGG CTTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGTACAAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCCAAATCG CCGTTCGCA CAATTACCC GATTACGCCA CGACAGCCG
1351 CAAGACGGCA GCCGCTGGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATTT TCAACATCGA CAGCGCGCA ACTTTTGAGC GGAATACGG
1551 GATGTTTCGGC GGAGAAGTCC TGCAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCGGCC GTGCAAAGCC
1751 GTATTTTGA CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCGGCTT CTTATCCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACGCGCGC AGAATACGC CGTCGGTGCA AGCTACGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCGCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCAAAA AACCAGATA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGG GCGTGACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCCCGG CTATATACC GCCCACTCTC TTTCCGCGG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLFLSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PLSLSLSTG LFCNSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQDGLTIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGRRRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VSLVPPYYFN LAPNLDTFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVREPKLGLH ATYYSLNREF SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGVSVGKPK RNRSDWVFAF SGSSIGSRFYL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKVL NARYKYGRNE KIYLSKDSGY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLG GAELYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRKN
801  RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

[illegible]

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLAGEYKSSSCGCGWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g958           EAKKPIEVLAGEYKSSSCGCGWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      MDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||
g958           MDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCAGCG TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTACCGCAGC GCACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCGG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACCTGAC GGAAACCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCCG CGGCGTTCCT ATTTCTACA CCCCTTGGGC GGAATTCCTG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCGCCCGG
801 TTCCGACGGC GTTCCCTTTT CCGTCCCTTA TTATTTCAAC CTGCCCCCA
851 ATCTCGATGC CACGTTCGCG CCCGGCGTGA TCGCGCAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATT TCCGACGCTC TCAGGCGGGT
1051 GTCGATTTCG ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GGGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCCGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCGGATTG CGCAAAAAC ACCGGCAGGG
1301 CGCAATCCG CGTGTCGGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAACAGCGCA GCCGCCTCGT CGTCTATCCC GACATCAAA TGGGATTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC TCGACTGCAC GCCACCTATT
1451 ACAGCTTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGG GCGCGAGTCC TGCAAACCTT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAACG TCGGCTACGG GCAGCTTTT TCGTGAACAC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATCTT ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCGG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTTCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCTGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCT GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1   LARLFSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTSLSLSTGC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGTLIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGRRRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP

```

```

251 LDGNRKSGLL VPSLSAGSDG VSLSVYYFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLRNR VWLDYGGRAA GGSNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYQQLF RENLYYGNDR INTANSLSAA VQSRILGAT GEERFRAGIG
601 QKFYFKNDVA MLDGSGVKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAELYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRKN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	10	20	30	40	50	60
	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
a958.pep	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQQVRAEGNVVVERNRTTL					
m958	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQQVRAEGNVVVERNRTTL					
a958.pep	130	140	150	160	170	180
	NADWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVRMETEHGGRRLO					
m958	130	140	150	160	170	180
	NTDWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVMEIEQGGRRLO					
a958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAVFGGVP					
m958	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAVFGGVP					
a958.pep	250	260	270	280	290	300
	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVYYFNLAAPNLDATFAPGVIGERGAV					
m958	250	260	270	280	290	300
	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVYYFNLAAPNLDATFAPSVIGERGAV					
a958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
m958	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
a958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLRNRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
m958	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLRNRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
a958.pep	430	440	450	460	470	480
	PRLSADWRKN TGRAQIGVSAQFTRFSDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
m958	430	440	450	460	470	480
	PRLSVWRKN TGRAQIGVSAQFTRFSDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
a958.pep	490	500	510	520	530	540
	ATYYSLNRFSGQEARRVSRTLPINIDSGMTFERNTRMFGGVLQTLLEPRLFYNYIPAKS					
m958						
	ATYYSLNRFSGQEARRVSRTLPINIDSGATFERNTRMFGGEVLQTLLEPRLFYNYIPAKS					

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	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
m958	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
m958	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
m958	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
m958	730	740	750	760	770	780
a958.pep	790	800				
m958	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDHGHG DDDHGHAHQ HGKQDKIISR
51  AQAEEKAAR VGGKITDIDL EHDGGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDHGHG DDDHGHAHQ HNKQDKIISR
51  AQAEEKAAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHL	LLTSAAT	ALLSIS	APALAH	HDGHG	DDDHG
g959	MNIKHL	LLTAAAT	ALLGIS	APALAH	HDGHG	DDDHG
	10	20	30	40	50	60

	70	80	90	100	109
m959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQ
g959	VGGKIT	DIDLEH	DDGRPH	YDVEIV	KNGQ
	70	80	90	100	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

1	ATGA	ACTTCA	AACGC	CTTCT	CTTG	ACCGCC	GCCGC	AACCG	CACT	GATGGG
51	CATT	TCCGCC	CCGCA	CTCG	CCCAC	CACGA	CGGAC	ACGGC	GATG	ACGACC
101	ACGG	ACACGC	CGCAC	ACCAA	CACAG	CAAAAC	AAGAC	AAAAT	CATC	AGCCGC
151	GCCCA	AGCCG	AAAA	AGCAGC	GTTGG	CGCGT	GTCGG	CGGCA	AAAT	CACCGA
201	CATCG	ATCTC	GAAC	ACGACA	ACGGC	CGTCC	GCACT	ATGAT	GTCG	AAATCG
251	TCAAAA	ACGG	ACAGG	AATAC	AAAGT	CGTTG	TCGAT	GCCCG	TACCG	GCCGC
301	GTGAT	TTCT	CCCGC	CGCA	CGACT					

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

1	MNFKR	LLLLTA	AATAL	MGISA	PALAH	HDGHG	DDDHG	HAAHQ	HSKQ	DKIISR
51	AQAEK	AALAR	VGGKI	TIDL	EHNGR	PHYD	VEIVK	NGQ	EYKVV	VDARTGR
101	VISSR	RDD*								

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKR	LLLLTA	AATAL	MGISA	PALAH	HDGHG
m959	MNIKHL	LLTSAAT	ALLSIS	APALAH	HDGHG	DDDHG
	10	20	30	40	50	60

	70	80	90	100	109
a959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQ
m959	VGGKIT	DIDLEH	DDGRPH	YDVEIV	KNGQ
	70	80	90	100	

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

1	ATGC	AAGTAA	ATATT	CAGAT	TCCCT	GTATG	CTGT	ACAGAC	GCGGG	AGTGT
51	TAAG	CCCCC	TTGTT	TGAAG	CTCCG	CGGCT	CCTG	CCGAGC	TTCAC	CGACC
101	CCGT	TGTGCC	CAAGC	TCTCT	GCTCC	CGGCG	GCTA	CATTGT	CGACA	TCCCC
151	AAAG	GCAATC	TGAAA	ACCGA	AATCG	AAAAG	CTGG	CAAAC	AGCCG	GAGTA
201	TGCCT	ATCTG	AAAC	AGCTCC	AAGTA	GCGAA	AAAC	GTCAAC	TGGA	ACCAGG
251	TGCA	ACTGGC	TTAC	GATAAA	TGGGA	CTATA	AGCA	GGAAG	CTTA	ACCAGA
301	GCCG	GTGCAG	CGATT	ATCGC	GCTGG	CTGTT	ACCG	TGGTTA	CTGC	GGGCGC
351	GGGA	GTGGA	GCCG	CACTAG	GCTTA	AACGG	CGCA	GCGCCA	GCAG	CGGCGC
401	ATGC	CGCCT	TGCCT	CACTC	GCTTC	TCTCAGG	CTTC	CGTATC	GCTCA	TCAAC
451	AATA	AAGGCG	ATGTC	GGCAA	AACCT	GTAAG	GAAC	TGGGCA	GAAG	CGGCAC
501	GGTA	AAAAAT	CTGTT	TGTAG	CGGCG	GCAAC	GGCA	GGCGTA	TCCA	ACAAAC

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551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAACAAC
601 CTCAACGTTA ACCTGGCCAA TGCGGGCAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAACGCGG TAGAAAAATA TGCGGTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTGC GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGTCAAG GAAGTTTAG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAATA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAAT GAAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDPVVPKLS APGGYIVDIP
51 KGNLKEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIIALAV TVVTAGAVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKV LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAUVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDETL
401 DWNDAKAVID IIVGTGLNRA NKGEAAQVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNPNFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFDD NGNFKFVLNM DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGTGCTT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTAA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAAAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCAATGA AGCCAAACAG ACGGCCGAAG AAACCAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGGCCG
701 AAGTGCCGCG TGGCAGAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCTTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKAV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

```

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEAENDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKVKAETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPNVGR FNVTAAVGGY KSESAVAIGT GFRTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet

a961.pep not found yet

g972.seq not found yet

g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

m972.seq

```

1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

m972.pep

```

1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE D GSGKTFYVGR KKNRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFPICRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVYHQNV D YD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

a972.seq

```

1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGC GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTAA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC-ATCAAAATGT
1251 AGATTATGAT TATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
  1 LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGK GK LLEIP QRRGKQDGVF
 51 VDWFISFTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHF GGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTLNLTFE
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVYHQNVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKT XSKSSERMSEVEYFSHFISDGK GK LLEIPQRRGKQDGVFVDWFISFTFHE					
a972	LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGK GK LLEIPQRRGKQDGVFVDWFISFTFHE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m972.pep	DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
a972	DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RT RITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RT RITRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKKLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKTLNLTFE					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972						
	310	320	330	340	350	360
	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
a972						
	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972						
	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgteggg gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcgaagaagc cgacaccatc ggcggttTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTatc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEADTI GGLVIQELGH LPVRGEKVL I
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCGGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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651 CTTCCGGCAGC GAATACAGCA KCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCGTC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLLRLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	:					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLEKVLDFAELEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	:					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
	:					
g973	EQFHLKSVLRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	: : : : :					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGTEYGSEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX			!		
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCC
 51 ACTCGCCCGC GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAATATAT
 351 GTTCAACCCC GAGCAGTTC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCCGTC GCGGCGAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFGT EYSSEEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	: : : : :					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFGT EYSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTGAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCAGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAACAACCC CGGCCAAAGG AATGGAATTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTTT TGCCAAAGAG GGCGGACAGG CTGCGAAATA
801 A

```


This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

g981.pep

```

1  MKKWIAAALA CSALALSACG GQGKDAAPA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK KMNKVGVTG
151 HTGDFSUSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

m981.seq

```

1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTACGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTAA AACACGGCG ATGCGGACGT TGTGATGTCG
301 GGCCTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCCTAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGT TTCCTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTTACG CCAAATATTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

m981.pep

```

1  MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK NMNKGVTG
151 YTGDFSUSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQGKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMMSGVTITDDRKQSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPGKKVSSSEDLKMNKVGVTGYTGDFSUSKLLGNDNPKIARFENVPLIIKE					
g981	ITQVVLVPGKKVSSSEDLKMNKVGVTGHTGDFSUSKLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSVVSDDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVVSDDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
 51 TGCCTGCGGC GGTGAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCC GCCTTG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
  1 MKKWIAAALA CSALALSACG GQKDAAPA ANPKVYRVA SNAEFAPFES
 51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KISSSEDLK NMNKVGVTG
151 YTGDFSUSKL LGNDNPFIAR FENVPLIIKE LENGGLDSVV SDSAVIANVY
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQKDAAPAANPKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQKDAAPAANPKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	ITQVVLVPGKGVSSSEDLKNMNKVGVTGYTGDFSUSKLLGNDNPFIARFENVPLIIKE					
a981	ITQVVLVPGKGVSSSEDLKNMNKVGVTGYTGDFSUSKLLGNDNPFIARFENVPLIIKE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVSDSAVIANVYKNNPTKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1  atcgcacgcg  aaaacccctcg  attcgacaat  cgattcctcc  aaaaaatggt
51  caacggcgTg  aatatatttgc  cggccgcCga  ttgggtagcC  ttgGGcgCgCA
101 AAGGCCGCAA  CGTGGTGGTT  GACCGCGCTT  TCGGCGGCCC  GCACATCACC
151 AAAGACGGCG  TAACCGTCGC  CAAAGAAATC  GAACTGAAAG  ACAAGTTTGA
201 AAATATGGGC  GCGCAAATGG  TAAAAGAAGT  CGCGTCCAAA  ACCAAcgaCg
251 tagCCGgcga  cggtagcact  accgCCACCG  TATTGGCACA  ATCCATCGTT
301 GCCGAaggcA  TGAAATACGT  TACCGCCGGC  ATGAACCCGA  CCGATCTGAA
351 ACGCGGCATC  GACAAAGccg  ttgCCGCTtt  ggttgAAGAg  cTGA AAAACA
401 TCGCCAAACC  TTGCGATACT  TCCAAAGAAA  TCGCCCAAGT  CGGCTCGATT
451 TCCGCCAACT  CCGACGAACA  AGtcgGCGCG  ATTATCGCCG  AAGCGATGGA
501 AAAAGTCGGC  AAAGAAGgcg  tgattacCGT  TGAAGACGGC  AAATCTTTGG
551 AAAACGAGCT  GGACGTGGTT  GAAGGTATGC  AGTTCGACCG  CGGCTACCTG
601 TCCCCTTACT  TTATCAACGA  CGCGGAAAAA  CAAATCGCCG  GTCTGGACAA
651 TCCGTTTGTT  TTGCTGTTCG  ACAAAAAAAT  CAGCAACATC  CGCGACCTGC
701 TGCCCGTGTT  GGAACAAGTG  GCGAAAGCCA  GCCGCCCGCT  GTTGATTATC
751 GCTGAAGACG  TAGAAGGCGA  AGCCTTGGCG  ACTTTGGTCG  TGAACAACAT
801 CCGCGGCATC  CTGAAAACCG  TTGCCGTCAA  AGCccccggc  tTCGGcGACC
851 GCCGCAAAGC  GATgctgcaa  gaCATCGCCA  TCCTGACcgg  cggcgTagtG
901 ATTtccGAAG  Aagtcggcct  GTCTTTGGAA  AAAGcgactT  TGgacgaCTT
951 Gggtcaaacc  aaACGcatCG  AAATCGGtga  agaaaacact  ACCGTCATcg
1001 acgGCTTCGG  CGACGcagcC  CAAAtcgaag  cgCGTGTTCG  CGAAATCCGC
1051 CAACAAATCG  AAACCGCGAC  CAGCGATTAC  GACAAAGAAA  AACTGCAAGA
1101 GCGCGTTGCC  AAAGTGGCAG  GAGGCGTGGC  AGTGATCAAA  GTCGGCGCGG
1151 CGACCGAAGT  CGAAATGAAA  GAGAAAAAAG  ACCGCGTGGG  AGACGCGCTG
1201 CACGCTACCC  GCGCAGCCGT  TGAAGAAGGC  GTGGTTGCAG  GCGGCGGCGT
1251 AGCCCTGTTG  CGCGCCCGTG  CCGCTTTGGA  AAACCTGCAC  ACCGCAATG
1301 CCGACCAAGA  CGCAGGCGTA  CAAATCGTAT  TGC CGCCGT  TGAGTCTCCG
1351 CTGCGCCAAA  TCGTTGCCAA  CGCAGGCGGA  GAACCCAGCG  TGGTGGTGAA
1401 CAAAGTGTG  GAAGGCAAAG  GCAactacgG  TTACAACGCa  ggctcCGCG
1451 AATACGgcga  CATGATCGGA  ATGGGCGTAC  TCGACCCTGC  CAAAGTAACC
1501 CGTTCCGCGC  TGCAACACGC  CGCGTCTatC  GCCGTCTGA  TGCTGACGAC
1551 CGACTGCATG  ATTGCCGAAA  TCCCTGAAGA  AAAACCGGCT  GTGCCGATA
1601 TGGGGGGAAT  GGGCGGTATG  GCGGCATGA  TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1  IASQNLRFDN  RFLQKMVNGV  NILPAADWVA  LGAKGRNVVV  DRAFGGPHIT
51  KDGVTVAKEI  ELKDKFENMG  AQMVKEVASK  TNDVAGDGT  TATVLAQSIV
101 AEGMKYVTAG  MNPTDLKRG  DKAAALVEE  LKNIAPCDT  SKEIAQVGS
151 SANSDEQVGA  IIAEAMEKVG  KEGVITVEDG  KLENELDVV  EGMQFDRGYL
201 SPYFINDAEK  QIAGLDNPFV  LLFDKKISNI  RDLLPVLEQV  AKASRPLLI
251 AEDVEGEALA  TLVVNNIRGI  LKTVAVKAPG  FGDRRKAMLQ  DIAILTGGVV
301 ISEEVGLSLE  KATLDDLQGT  KRIEIGEENT  TVIDGFGDAA  QIEARVAEIR
351 QQIETATSDY  DKEKLQERVA  KLAGGVAVIK  VGAATEVEMK  EKKDRVEDAL
401 HATRAAVEEG  VVAGGGVALL  RARAALLENLH  TGNADQDAGV  QIVLRAVESP
451 LRQIVANAGG  EPSVVVNKVL  EGKGNYGYN  GSGEYGMIG  MGVLDPKAVT
501 RSALQHAASI  AGLMLTTDCM  IAEIPEEKPA  VPDMGGMGM  GGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1  ATGGCAGCAA  AAGACGTACA  GTTCGGCAAT  GAAGTCCGTC  AAAAAATGGT
51  AAACGGCGTG  AACATTCTGG  CAAACGCCGT  CCGCGTAACC  TTGGGCCCCA
101 AAGGTCGCAA  CGTAGTCGTT  GACCGCGCAT  TCGGCGGCCC  GCACATCACC
151 AAAGACGGCG  TAACCGTCGC  CAAAGAAATC  GAACTGAAAG  ACAAGTTTGA
201 AAATATGGGC  GCGCAAATGG  TGAAAGAAGT  TGCGTCCAAA  ACCAACGACG
251 TGGCAGGCGA  CGGTACGACT  ACCGCCACCG  TACTGGCGCA  ATCCATCGTT
301 GCCGAAGGTA  TGAAATATGT  TACCGCAGGT  ATGAATCCGA  CCGACCTGAA
351 ACGCGGTATC  GATAAAGCCG  TCGCCGCTTT  GGTGACGAA  CTGAAAAACA
401 TCGCCAAACC  TTGCGACACT  TCTAAAGAAA  TCGCCCAAGT  CGGCTCTATT
451 TCCGCCAACT  CCGACGAACA  AGTCGGCGCG  ATTATCGCCG  AAGCGATGGA
501 AAAAGTCGGC  AAAGAAGCGC  TGATTACCGT  TGAAGACGGC  AAGCTTTGG
551 AAAACGAGCT  GGACGTAGTT  GAAGGTATGC  AGTTCGACCG  CGGCTACCTG
601 TCTCCTTACT  TCATCAACGA  TGCGGAAAAA  CAAATCGCTG  CTTTGGACAA

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1386

```

651 TCCGTTTGTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGGC TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GGCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```

m982.seq
  1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
  51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
 101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCG GCACATCACC
 151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTGAAG ACAAGTTTGA
 201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACGACG
 251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
 301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
 351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
 401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
 451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
 501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGCG AAGTCTTTGG
 551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
 601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA
 651 TCCGTTTGTG TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
 701 TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
 751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
 801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGGC TTCGGCGACC
 851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
 901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
 951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GGCGGCATGA TGTAA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m982/g982    95.8% identity in 544 aa overlap

              10      20      30      40      50      60
m982.pep    MAAKDVOFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
              :|:::| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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g982	IASQNLRFDNRFLQKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
	70 80 90 100 110 120
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
	130 140 150 160 170 180
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	:
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
	190 200 210 220 230 240
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	:
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
	250 260 270 280 290 300
m982.pep	AKASRPLLIIEADVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
g982	AKASRPLLIIEADVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
	310 320 330 340 350 360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	: :
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
	370 380 390 400 410 420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
	430 440 450 460 470 480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA
g982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA
	430 440 450 460 470 480
	490 500 510 520 530 540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
g982	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEEKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq	1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
	51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
	101	AAGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCC	GCACATCACC
	151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
	201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
	251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
	301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
	351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GTTTGAAGAG	CTGAAAAACA

1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTG TTGCTGTTTC AAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTAA AGCTCCGGGC TTCGCGGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTC CGAAATCCCG
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GCGCGTGGC AGTAATCAA GTCGGTGCCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCGC
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```

1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG DKAAALVEE LKNIKPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAIVK VAAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVNKKVL EGKNGYGYNA GSGEYDMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

```

m982/a982 99.3% identity in 544 aa overlap

```

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90     100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG
          70      80      90     100     110     120

          130     140     150     160     170     180
m982.pep  DKAAALVDELKNIKPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
          |||
a982      DKAAALVEELKNIKPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
          |||
a982      KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

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	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLGKNGYGYNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
	490	500	510	520	530	540
m982.pep	GMMX					
a982	GMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGCGAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCGACTT	TGCCCAACTG	GTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCGCTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTTCGCAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGCGGTGA	TTATTGAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAgcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agcccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986. pep
  1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT NTHVAGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986. seq
  1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCAGACAAG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCC GCCCCC GCGCACCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCGTTCTAC
301 GAATTTTTC AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GCGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCTG CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCCCGCG
651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGCGA TTCATGGGCA TTCTCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTTCG CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCCG
951 TTTGACAAA GCCGCGCGCG CACTGATTGC CAAAATCCTG CCCGCGACCC
1001 CCGCAGAACG TGCCGCGCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GCGCGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCGG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGCAAC ACGCTGTTTA TCGCATTAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986. pep.
  1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT NTHVVTGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

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Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSM LLPDFAQL					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSM LLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVI IQEVS YGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVI IQEVS YGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGCGACGA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GGNGGATTGA ACTTCGTTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTTCGGCTT GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAAACCCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTATGG TCGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTGGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAC CCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPAVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPNSGGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIFI DVAMNVAEQL KNTGKVQRGQ

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1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSM LLPDFAQL					
a986	VFKKYQYLALALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSM LLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPAVVNIQAAPAPRTONGSSNAETDSPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTA KLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTA KLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGF DNSVTAGIVSAKGRSLPNESYTPFIQT DVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGF DNSVTAGXVSAKGRSLPNESYTPFIQT DVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq

1 ATGAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTC TCTGTTTCATG

1394

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51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201 AGCCTTTGCC GCGCGCGCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttggacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCGCCT GATCAGCGAC AGCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

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1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNSTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNI*V RLFPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSYGVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAAILLS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCGCGCGCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAAACA TGCCGTCCCC GCCACAAAAG ACAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTTCATGAA AGCCCCAAA TCGCAGAAC GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCG CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGA TCGCCGAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLDDN NTRGLDDLL ALDHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDNRNR LQWHDPATRK TYPNEPEAKL WKRIAAILK
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m987/g987 97.8% identity in 508 aa overlap

      10      20      30      40      50      60
m987.pep MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
g987      MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY
      10      20      30      40      50      60

      70      80      90     100     110     120
m987.pep LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLDDN
g987      LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLDDN
      70      80      90     100     110     120

      130     140     150     160     170     180
m987.pep NTRGLDDLLALDHPNIEVRLFNPFVLRKWRALGYLTD FRLNRRMHNKSFTADNRATI
g987      NTRGLDDLLALDHPNIXVRLFNPFVLRKWRALGYLTD FRLNRRMHNKSFTADNRATI
      130     140     150     160     170     180

      190     200     210     220     230     240
m987.pep LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGDIG
g987      LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGNIG
      190     200     210     220     230     240

      250     260     270     280     290     300
m987.pep KGLQALGYNETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
g987      KGLQALGYNETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR
      250     260     270     280     290     300

      310     320     330     340     350     360
m987.pep RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA

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1396

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|||||
g987      RKPP IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDRHNRLQWHD PATRK
          |||||
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDRHNRLQWHD PATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA AAKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51 TTCTTCATGG TTGCCCCCAC TGGAGAACG GACGGAAAGC CGTCATTTC A
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACG A
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTT C
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGCGG CAACATCGGC AAGGGTCTT AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGTTT CACCCTATT CGTCCCAACA AAATCCGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACC CAACCA TGCCGTCCCT GCCACAAAG ACAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTT ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCG CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDNRHNR LQWHPATRK TYPNEPEAKL WKRIA AKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSWLPPEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSWLPPEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLDFPRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSSVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSSVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
a987	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTFPAYAYRVTLDNRHNLQWHPATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDNRHNLQWHPATRK					
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987	TYPNEPEAKLWKRIA AKILSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgagggcg
251 CagtTTGCGc gGCggaag ctgGATTGG TCAATGccg Cgtcagggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcy tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCg ggtatggaCC GCAGGGGccg ccgcGAaggg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAt cgAAATTGCC GTGCGCAAGC ATCATTGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAATC CGcgaAAAA ATtcccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCTT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGCGCG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGCGCA ATGTTTGCgC GCGCGATTTT CTGTTGAAAA
1451 ACAAAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGCG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCT GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAA GCCGTATTGA ACCGAAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGCGTGAA ATATTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTGCG GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGCGGCGG GGAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATCGGC AAAGTAAGGG GAAGGGCGCT
2301 GCCTGCCGTT GCCGAATCGG GGAAGAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFQFAVP LMPMDEGDFV LYERQMRGVM HGDVTVVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVAREFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPFRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYYMRDKVGE IFEGKISRGV
651 ANFGIFVTLD DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1      ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51     CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101    ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151    TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTATCCTG AGCAAAACCG
201    GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251    GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301    AGTGAAGCGT GTGCCAAAGC TGCAGAAAAA ATTCCCGTCC ATGTACGCAA
351    AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
401    TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451    GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
501    TGTCGCCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551    CCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601    AACGGCATTG GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651    CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701    CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGA
751    TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCC
801    TTACAAACTC TTCAAATCC TTCAGAAAAA GCGTTTTCGA CGCGGCGCGG
851    TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901    ATCGAAAAAA TCGTCCCCGT GTGCCGCAAC GATGCCACA AGCTGATTGA
951    AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA
1001   ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051   CTCGCCACCC TCGCGAGCA GTCGGTCTG TTGGGGCTTC AACTTGCGCG
1101   CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151   AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201   CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCC
1251   CGAAGCATAC GCCCACTTCA CCTCGCCAT CCGCCGCTAT CCCGACCTGA
1301   CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351   AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401   TGCCGACGAC GCCAGCCGCG ACGTGAAAA CTGGCTGAAA ACCTATTATA
1451   TGC GCGATAA GGTGCGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC
1501   AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551   GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601   TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGGACAGG
1651   GTTGCCGTCC GGGTCGCCCC TGCCGATTTG GATGACGGAA AAATCGATT
1701   TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751   CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
```

1400

1801 GCCGAGAAAA AACAGCCCC AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADGMEIEIA VRKHHLPHQF
 101 SEACAKAAK IPVHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOTYTP
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGD	TVTVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED				
	130	140	150	160	170	180
m988.pep	40	50	60	70	80	90
	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
g988	KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA					
	190	200	210	220	230	240
m988.pep	100	110	120	130	140	150
	VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK					
g988	VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK					
	250	260	270	280	290	300
m988.pep	160	170	180	190	200	210
	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV					
g988	VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV					
	310	320	330	340	350	360
m988.pep	220	230	240	250	260	270
	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL					
g988	ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL					
	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
g988	FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
g988	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE					

1401

	490	500	510	520	530	540
m988 . pep	400	410	420	430	440	450
	LLQVMMRLSMQQAVYEPHCDGHEFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	LLQVMMRLSMQQAVYEPHCEGHEFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRYTYP					
	550	560	570	580	590	600
m988 . pep	460	470	480	490	500	509
	KKSQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKIS-GMTSFGIFVTL					
g988	NKSQALGVHTSFCERRADDAGRDVENWLKTYMRDKVGEIFEGKISRGVANFGIFVTL					
	610	620	630	640	650	660
m988 . pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
m988 . pep	570	580	590	600	610	629
	IAGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVLSASAKPAGAAGKGSKTTAEKKTARCGKVRGRGVPVAESGKKAKKP					
	730	740	750	760	770	780
m988 . pep	630	640				
	VPIKVKKRKGKSX					
g988	VPIKVKKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988 . seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GCGCGACAAA TTGGATTGCG TCAAATGCCG TGTCAGGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCTGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGGAAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACC
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA GTTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGTCTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGA
1201 TGGCTTTTCA GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT GTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGCGGCAA ACGTTTGC GCAGGATTTC CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTT CGCAACCAT TGGGGCCAC GCCCGAAAA
1501 CTCGCCGCTT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1601	AAGGCAGGCC	GGATGCCGAA	TTGCTGCAAG	TCATGATGTT	GCGCTCCATG
1651	CAACAGGCGG	TTTACGAACC	GCATTGCGAC	GGACACTTTG	GTCTTGCCTA
1701	CGAAGCATAC	GCCCACTTCA	CCTCGCCCAT	CCGCGGCTAT	CCCCGACCTGA
1751	CCGTACACCG	CGCCATCAAA	GGCGTGTTGA	ATCACGCAAC	CTACACGCCA
1801	AAAAAAAAGCT	GGCAGGCTTT	GGGCGTGCAT	ACCTCGTTCT	GTGAGCGCCG
1851	TGCCGACGAC	GCCAGCCGCG	ACGTGGAAAA	CTGGCTGAAA	ACCTATTATA
1901	TGCGCGATAA	GGTCGGCGAA	GTATTCGAAG	GTAAAAATCTC	CGGATGACC
1951	AGTTTTGGTA	TCTTTGTAAC	ACTGGACGGC	ATCCACATTG	ACGGCTTGGT
2001	GCATATCAGC	GATTTGGGCG	AAGACTATTT	CAACTCCCG	CCCCAAATCA
2051	TGGCAATCGA	AGGCGAACGC	AGCGGCATCC	GTTTCAACAT	GGGGACGAGG
2101	GTTGCCGTCC	GGGTCGCCCC	TGCCGATTTG	GATGACGGAA	AAATCGATT
2151	TGTCCTGATT	GCCGGGGGGA	GCGGCAGGGG	GCGGAAAGTT	AAATCATCCG
2201	CGTCTGCCAA	ACCGGCAGGG	ACGGCGGGGA	AAGGGAAGCC	GAAAACCGCC
2251	GCCGAGAAAA	AAACAGCCCG	AGGCGGCAAA	GTAGGGGAA	GGGGCGCGTC
2301	TGCCGCGCGA	GAATCGAGGA	AAAAGGCAAA	GAAACCGGTT	CCGATTAAGG
2351	TAAAAAAACG	GAAAGGCAAA	TCATAA		

a988.pcp

m988/a988 97.0% identity in 641 aa overlap

	10	20	30
m988.pep	TVLDIVERAQSKVVGRFYMDRGVAILEPED		
a988	LYERQMRGIMHGDIVTVRPAGMDGRGRREGTVLDIVERAQSKVVGRFXMDRGVAILEPED		
	130	140	150
	160	170	180
m988.pep	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA		
a988	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA		
	190	200	210
	220	230	240
m988.pep	VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK		
a988	VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK		
	250	260	270
	280	290	300
m988.pep	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPLPENLSNGICSLNPDV		
a988	IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPLPENLSNGICSLNPHV		
	310	320	330
	340	350	360
m988.pep	ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVVKWISDGDHPYKAQIDTLYKL		
a988	ERLCVVCMDMVITYAGNIKEYRFYPAVMRSHARLTYNQVVKWLSGGIEHPFKTQIDTLYKL		

1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPD					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGGDNPSPKDYAALAGQFKGRPD					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTL					
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTL					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKP					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKP					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq
 1 ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
 151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATTT CCGTCAACGC
 201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
 251 TTACCGGGCT TCCCGTCCAA GGTCTCTAAA ACGGCAAAAT CACCAAAACC
 301 ACGGTCGCAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
 351 CGTGGGCTTG GCGGTGTACG TCCCTTTCGG CTCTGCCACC GAATACGAAA
 401 AAGATTCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
 451 GCCGTCGAAC CTGTGCGCGC GTGAAACTC AACGAACGCC ATTCTTTCGG
 501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAACTGCGC AAATATGCCG
 551 ACTGAGGAAT CCCAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
 601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
 651 CAGCGATTGG GCGGTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
 701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
 751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACACAGTG
 801 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
 851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC TTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGT TTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGGTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGGCGACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

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This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAQIKAD GHADVKGS DW GVG YQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGM YK
301 VSDKADLFGD VTWRHSR FN KAELFFEKEK NIANGKKS DR TTITPNWRNT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSA GM
401 KYHIGKNHV V DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CAREKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGCGCG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC
301 AAAATCACCA AAACCAACGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAAC TAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGGCA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTT TTG
1001 AAAAAAGAAA AACCCTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKT TVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAIELT
201 AKPPKPNGVA EAAKIQADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGM YKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKT VV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
	:				
m989	MTPSALKKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
	:				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
	: :				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
	: : : : : :				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYSKVSHTLKGDAEWAADGAAAKQWNDNMLTPLGYTANEKASVKIOTPES				
	: : :				
m989	NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIOTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMVKVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK				
	: : :				
m989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	: :				
m989	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	410
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq
 1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
 201 GATTTCGTC AACGCCACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
 251 ATTCCGCCAC CGACTTTACC GGGCTCCCG TCCAAGGTC GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGGCGAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAACATA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTTC GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGCG AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCAC ATCCACATCA ACGACACCAG CTACCGCAGC GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGCGCGT CTTCCGCACG TTTCAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```

1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVGVNYSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSAREFN
451 HADIIGLQYT YKFK*

```

m989/a989 93.1% identity in 467 aa overlap

```

          10      20      30      40      50      60
m989.pep  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10      20      30      40      50      60

          70      80      90     100     110     120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70      80      90     100     110     120

          130     140     150     160     170     180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
          130     140     150     160     170     180

          190     200     210     220     230     240
m989.pep  SAELRKYADWGIIKSAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
          |||:|||||: ||: | ||: | :||: |:|||||:|||||:|||||:|||||
a989      SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFGYQLAWMWDI
          190     200     210     220     230

          250     260     270     280     290     299
m989.pep  NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
          |||:|||||:|||||:|||||: ||: | ||: | :||: |:|||||:|||||
a989      NDRARVGVNYSKVSHTLKGDAEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSDRTTITPNWRNTYKV					
	300	310	320	330	340	350
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
	360	370	380	390	400	410
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
	420	430	440	450	460	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATG TTCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTCCAG CGGTAAAACC GATCAAATTT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTGCGT
851 TTAAACAAA TTACCGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGACGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TAGCCCCAAC AGGCTTATGC GGCAAATACT TTGTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCAG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTGCGAAAA GGCAATAATG TCGGTTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGCGG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTCCGGC AAAAACCCTT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGG
1701 AATGGACGCG GAAAAACAGA CGTGCGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCCGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKNYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGGAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGTA VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAACC GATCAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGAAGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCTCG
1051 CAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGC GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGCGAGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTGGAAGAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGAAGTC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCTT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACCG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKNYN SGILAVDNMP VVKKYITD TY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*F

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGNYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m990.pep	KFSTLKQTMPLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m990.pep	ALTFEDKVSQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
a990	ALTFEKVSGVVLERRPENLKTLDGRKLIAAKADSNSFQKQNYRQGLYELLKQC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
a990	RSHQNIRGGAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
	370	380	390	400	410	420
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNVRFYLQPPAQFTYLGVNNGGFTDSEGTAAGLLGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQPPAQFTYLGVNNGGFTDSEGTAAGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACCTGAC  GGGACGTGGG  TTTCGACGCG  CCCGTTCCGC  GACGGGCATC
201 GCGGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCT  TCACGTCATC  GACGGCGACG  GCGCGAAACA  TAAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GCGCGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATTCCGTGGG  CGAATGGTTG  GGCATTGTTG
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLMLQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GCGCGGCGAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GCGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCCTG
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCCGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GCGCGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGTTG
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLMLQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVS VRVFD TDRYQREVAQVSVGKTD LNL MQVDGA AWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVS VRVFET DRYQREVAQV SAGKTD LNL MQVDGA AWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAE RERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX					
g992	ADYADAQIQAE RERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```
a992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTTCGCTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGCGCG  TTGCCGTACT  CGACGTACTC
151 GGC GCGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGCGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAATCCCG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTTCGACAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTGCGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGCGCG  CGTGGCATT
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```
a992.pep
1  MFRRRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTG YGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGT VSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFD TDRY  QREVAQVSVG
151 KTD LNL MQVQ  DGA AWHYKSY  AKEQQDKADF  ADYADAQIQ A  ERERKGLWKA
201 KNPQAPWAYR  RAGRS GGGNK  DWM DAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

1412

```

a992.pep      LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF
              |||
m992          LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
              |||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGGA
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAG CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCTCTGC TTGCCTACGA GCAAATGAAA
301 CTGGCGGGCG AGGGTTTGA GCGCTGCGC CGTGGCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCAGAG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AACATACGC GCAGCCACGA AGTAATCCAA GAAACCTTT CCGTGC GCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGCGC CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGCGC
701 ATTCAGACGG CATTTTCGCG ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLGSFQG PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCG ATGGTGGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCGCCTGCG TGCTTACGA ACAGATGAAG
301 CTGGCGGGCG AGGGTTTGA GCGCTGCCC CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCGGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AACACACGC GCAGCCACGA AGTAATCAA GAAACCATCT CCGTGC GCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGCGC
701 ATTCAGACGG CATTTCCGCG ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLGSFQG PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLEFP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			
g993	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQ	MEAYQFDLAAEYLLMA			
	10	20	30	40	50	60
m993.pep	70	80	90	100	110	120
g993	70	80	90	100	110	120
m993.pep	130	140	150	160	170	180
g993	130	140	150	160	170	180
m993.pep	190	200	210	220	230	240
g993	190	200	210	220	230	240
m993.pep	249					
g993	249					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

```

1  CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGAAGA
101 TTACCGAACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCCTGC TGGCTTACGA GCAGATGAAG
301 CTGGCGGCAC AAGGGTTGGA TGCGCTTCCT CGTGCGGGCC GGGATTTCCG
351 ATGGGCATAC CTGCCACTGG AAATGCGCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAGGCGTGGC TGAGTATTTT GTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTTATCAAA GAAACCATCT CCGTGCGCGC
501 GCAAAATGACG GCAATCCTGC GCCGTTTGAA CAAACACGGG ATATGCAGGT
551 TTCACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTCTCAAC
601 TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGTGTTGTCG GAATCGTACA
651 GGAAGTCGGT TTCGAGAGAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCGGGC ACACGGGGCG GGC CGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

```

1  LKVVLSFQGLDLLLYLIRKQ NIDVLDIPMVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTEVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNKHG ICRFHDLFNP EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFQGLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			
m993	LKVVLSFGQPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GGC GCGTTGC  TTCTTACCGC
51  CTGCGGCAGA  AAATCCGCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTGCTTGC  CTTGGGCGAT  TCGCTCACCT  TCGGCTACGG  AGCAAACCCC
151 GCGCAATCCT  ACCCGCGCA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACGTCCGC  GCAAGCCCTA  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCCAAGCTTG  TGATTGTCCG  CATAGGCGGC
301 AACGACTTTC  TGC GCAAGT  TCCCGAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAATATCAT  GAAACCGTGC  AAAAGGAAAA  CATCCCGGCC  GTCCTCGTCG
401 GCGTGCCGCA  CATCACA CTG  GCGCGTTGT  TCGGGCATTT  GAGCGACCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGT  TGTTCCGCGG
501 CGCGTGGGCG  GAAATTTTGG  GCAATAATAA  TCTGAAATCC  GACCAATATC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTCG  CCGAAAATTT  GAATCAATTT
601 TTGAGAAAAC  ATGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGD TSAQAL  SRLPALLARK  PKLVIVGIGG
101 NDFLRKVPEE  QTRANIAKII  ETVQKENIPA  VLVGVPHITL  GALFGHLSDH
151 PLYEDLSEY  GIPLFGGAWA  EILGNNNLKS  DQIHANGKGY  RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GGC GCGTTGC  TGCTTACCGC
51  CTGCGGCAGA  AAATCCGCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTACTTGC  CTTGGGCGAT  TCGCTTACCT  TCGGCTACGG  CGCAAACCCCT
151 GCGCAATCCT  ACCCGCGCA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACATCTGC  CCAAGCCCTG  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCCAAGCTTG  TGATTGTCCG  CATAGGCGGC
301 AACGACTTTC  TGC GCAAGT  TCCCAAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAATATCAT  GAAACCGTGC  AGAAGGAAAA  CATCCCGGCC  GTCCTCGTCG
401 GCGTGCCGCA  CATCACA CTG  GGTGCGTTGT  TCGGGCATTT  GAGCGATCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGC  TGTTCCGCGG
501 CGCGTGGGCG  GAAATTTTGG  GCGATAATAA  TCTGAAATCC  GACCAATATC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTTG  CCGAAGATTT  GAATCAATTT
601 TTGAGAAAAC  AGGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGD TSAQAL  SRLPALLARK  PKLVIVGIGG

```


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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLS DH
 151 PLYEDLSEY GIPFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYP AQLQK					
g996						
	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYP AQLQK					
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANI AKII					
g996						
	70	80	90	100	110	120
	LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANI AKII					
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITL GALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
g996						
	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITL GALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGNNNLKS					
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996						
	190	200				
	DQIHANGKGYRKFAENLNQFLRKHGFRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCAGCAGAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAGT	TCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAATCATC	GAAACCGTGC	AGAAGGAAAA	CATCCCCGCC	GTCCTCGTCG
401	CGGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTTGTC	CGAGGAATAC	GGCATTCCCG	TGTTCCGGCG
501	CGCGTGGGCG	GAAATTTTGG	GCGATAATAA	TCTGAAATCC	GACCAAATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATTT
601	TTGAGAAAAC	AGGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGD TSAQAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANI AKII	ETVQKENIPA	VLVGVPHITL	GALFGHLS DH
151	PLYEDLSEY	GIPFGGAWA	EILGDNNLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYP AQLQK					

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```

|||||
m996      MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK
              10      20      30      40      50      60

              70      80      90      100     110     120
a996.pep   LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
|||||
m996      LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
              70      80      90      100     110     120

              130     140     150     160     170     180
a996.pep   ETVQKENIPAVLVGVPHITL GALFGHLS DHPLYEDLSE EYGIP LF GGAWAE ILGDNNLKS
|||||
m996      ETVQKENIPAVLVGVPHITL GALFGHLS DHPLYEDLSE EYGIP LF GGAWAE ILGDNNLKS
              130     140     150     160     170     180

              190     200
a996.pep   DQIHANGKGYRKFAEDLNQFLRKQGFRX
|||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGFR
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCGCGC TTGTCCGCCG CCGTCACCTT GCGCGGCAC GCGGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGTGT TCGCCTGAT GAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGCG GCTCAACACG CCTTTGGA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCTTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCG GCGCTCCTGC CCGAAGGCAC GCCGGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCG CCGCCCGCTG ACcGGCATtg CCGAcggcAC
951 ggCaCaatgG CTGCTTTgCc cgGGGCAGGc tccggactgc CcccaaAacg
1001 aagTCTCCGc cGTCAAttagc GTTTCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLPD NGQHILLGAY RGVLRMLMTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGQVLT
201 KKS GSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTFEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGIADGTAQW LLC PGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCAGGA CTGTCCGCCG CCGTCACCTT GCGCGGCAC GCGGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGTGT TCGCCTGAT GAAACCATC GGTTCGATC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGA

```

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```

551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CAGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCCTGC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCGCCGCCG GACTTGTGCT GGTTCACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 IQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGDLT
201 KKS GSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGAFAFNR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DLWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g997.pep	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGG IQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGG IQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSGDLTKKSGSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGDLTKKSGSDYLLPKQDLGAIVAE PALADLQRLGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR					
	250	260	270	280	290	300
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFAFNR					
m997	AEPVRLPAPLTGLADGTQWLLCRGRL-GLPENEVSAVISVSDRVGAFAFNR AWADKAHAD					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCCGGC TTGTCCGCCG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCCG CAGCGGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAATAACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTGTCTG
401 CCATATATGC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTTGG AGCCCTTGG TTGGGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGTGACG
601 AAAAAATCCG CGAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 TCGTCGAACG CGCATATGC CGTCTGAACA CCTCCCGGA CGGGAAGTG
751 CTGCTCAACG GCGAACCTTT CGATGCCGCC GTCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGCTA TCTGCGCTAT
901 GCGGAACCCG TCCGCTTGCC TGCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCGCCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACC CGAAGCGTGC GCGTCATCAC CGAAAAACG GCCACAACG
1151 CAGCCGATGC CCCGCCCGG GATTTGTCGT GGTTCACCG GCACCGCATC
1201 TTCCCGCGG GCGACTACCT CCACCCAGAC TACCCGCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGLADGTQWQ LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAQDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVRLRMKTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

a997.pep      250      260      270      280      290      300
RLNTLPDGGKVLVNGEPFDAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR
|||||
m997      RLNTLPDGGKVLVNGEAFDAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR
           250      260      270      280      290      300

a997.pep      310      320      330      340      350      360
AEPVRLPAPLTLGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWDKVDHDL
|||||
m997      AEPVRLPAPLTLGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWDKAHADL
           310      320      330      340      350      360

a997.pep      370      380      390      400      410      420
KRILPHLGEPEAVRVITEKRATTAADAPPPDLWLHRHRIFPAGDYLHPDYPATLEAAVQ
|||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLWLHRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

a997.pep      430
SGFASAEACLQSLSDAVX
|||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA  AAAAATTGAT  TTCCGCAATT  TGTGTTTCAA  TTGTTTATC
51  AGCCTGCAAC  CAACAATCAA  AAACGGCACA  AGCCGAAGAA  CCTGTCCAAA
101  GTATCCAGGC  TGCTGATTGT  ACCGCCCAA  TGGACATCAC  AGTTGAACAA
151  TATCTCATCA  ATTTGGAGCA  AGCATTTAAA  ACTCAGAACG  TCTCAACAAA
201  AATCCATAAT  AAAAATATTG  TCAAGACCGA  TTGTGGTTAT  GACCTTACTT
251  TGGTAATGGA  TTTTGGGGCG  ATTGCGCTCA  AACTGGACGA  GCAGCAAAAA
301  ATTAGAGCTA  TCTCAGTAGG  CTACATTTTA  AAAACCGACG  GAGAGAAAGG
351  ACAAAATCTA  GTCAATAATG  CCATAAATGG  ATTACACAGT  ATTCAGGCAG
401  TTCTGTCTTT  AACTACCACA  GACAAATTGG  GCGAATCGGA  AGCAGGAAAA
451  CAACTTTTTA  CAGCTTTAAC  CGAAGTCGTC  AAAGAATCCA  ATCAGACAGG
501  AGCAACAGCG  CAAAAGACG  TTCCGGCAGA  TGGTATTTTA  TATAGCGTTG
551  TTTTGGAAAA  AGAAACAAAC  ACCATTGCAA  TAATCGGCAG  AAAACAACCC
601  TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI  CVSIVLSACN  QSKTAQAE  PVQSIQAADC  TAPMDITVEQ
51  YLINLEQAFK  TQNVSTKIHN  KNIVKTD  DLTLMDFGA  IALKLDEQK
101  IRAISVGYIL  KTDGEKGQNL  VNNAINGL  IQAVLSLTTT  DKLGESEAGK
151  QLFTALTEVV  KESNQTGATA  QKDVPADG  YSVVFERETN  TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

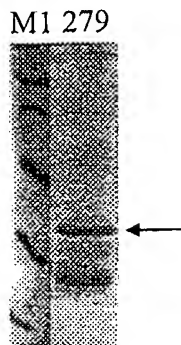
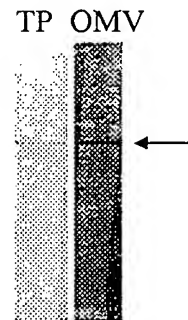
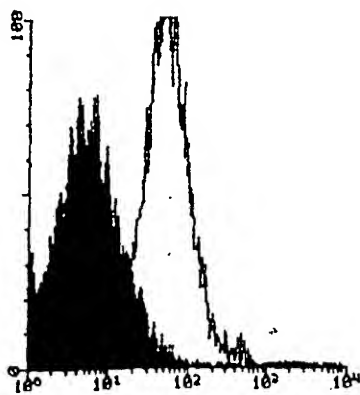
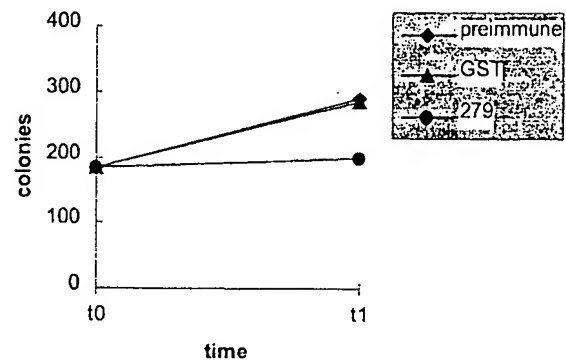
1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

Fig. 2

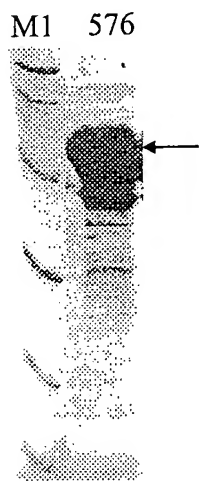
279 (10.5 kDa)**A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****279**

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 3

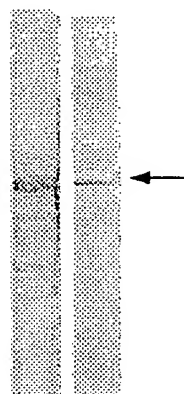
576 (27.8 kDa)

A) PURIFICATION

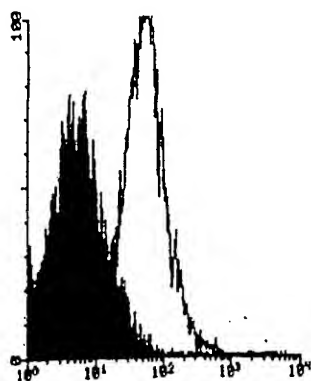


B) WESTERN BLOT

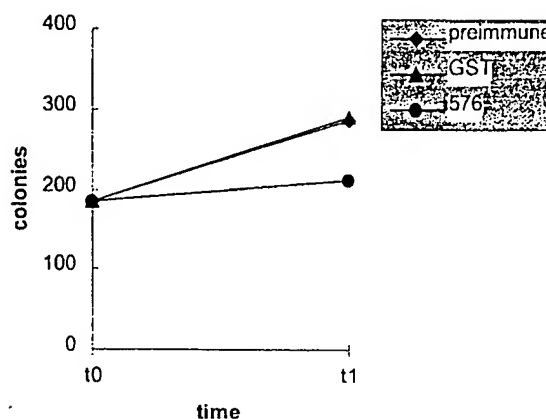
TP OMV



C) FACS



D) BACTERICIDAL ASSAY

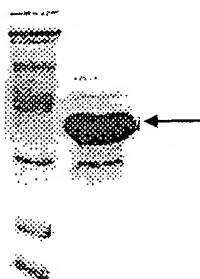
E) ELISA assay: positive

576

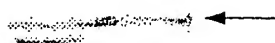
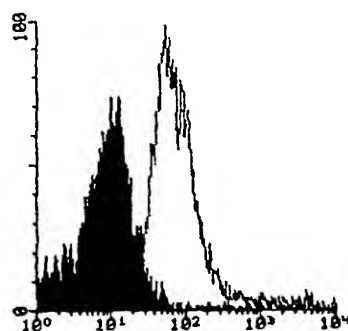
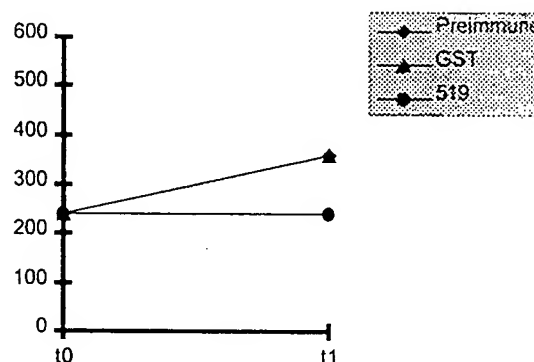
The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**Fig. 4****A) PURIFICATION**

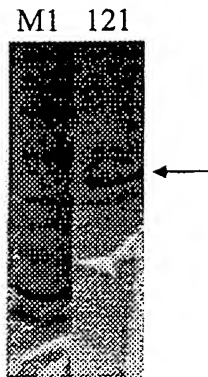
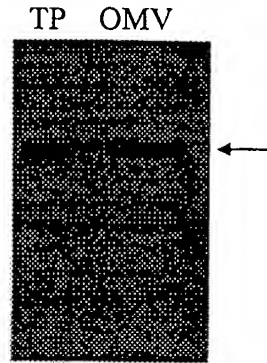
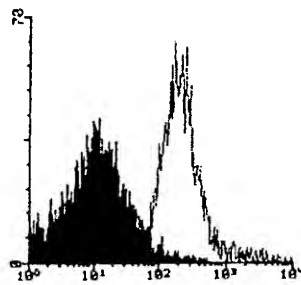
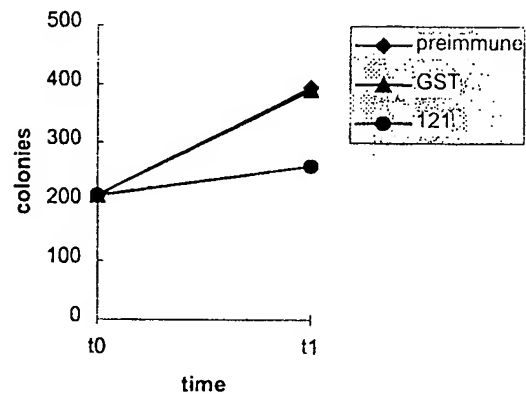
M1 519

**B) WESTERN BLOT**

TP OMV

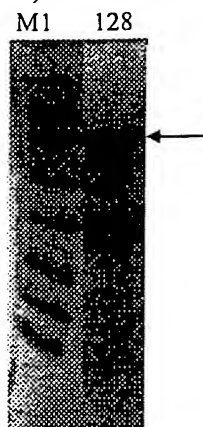
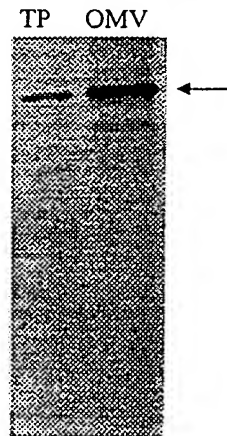
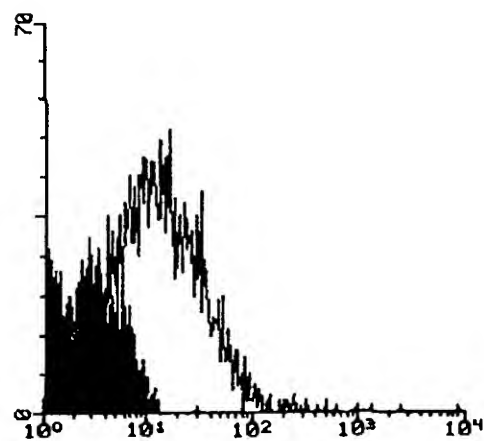
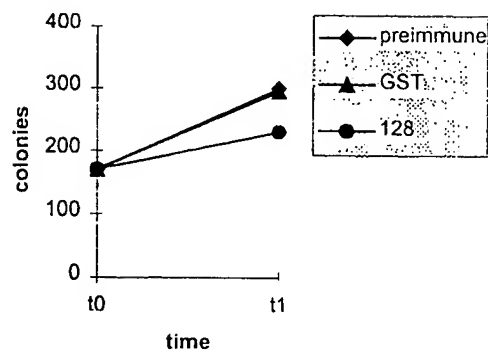
**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

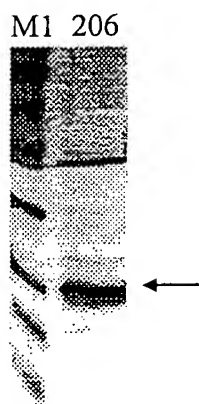
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

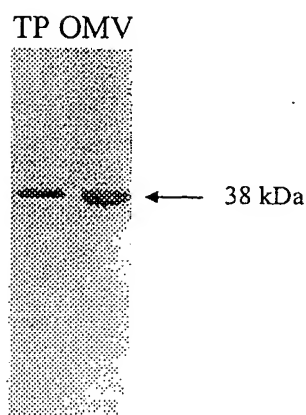
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

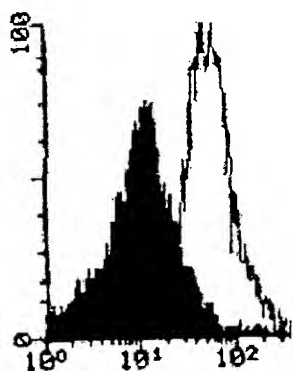
A) PURIFICATION



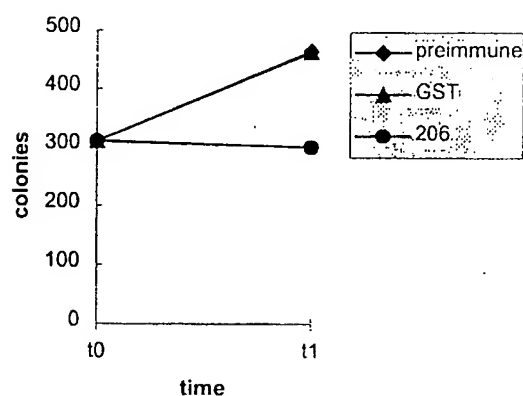
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

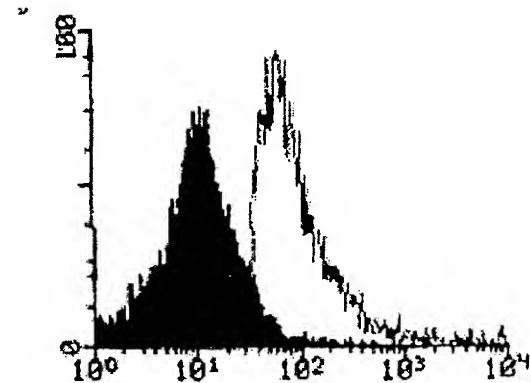
287 (78 kDa)

Fig. 8

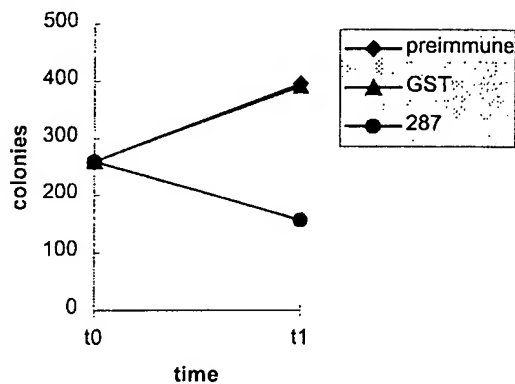
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

D) ELISA assay : positive

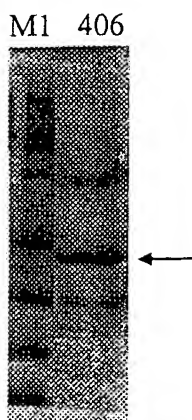
287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

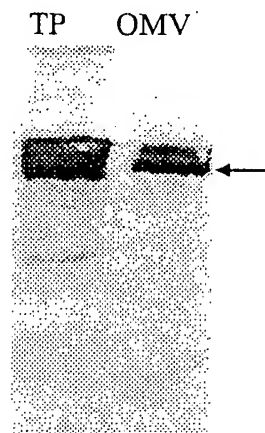
406 (33 kDa)

Fig. 9

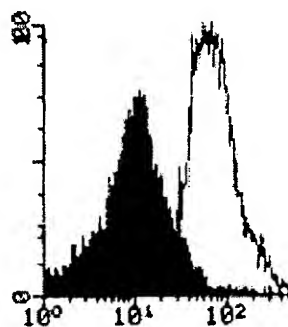
A) PURIFICATION



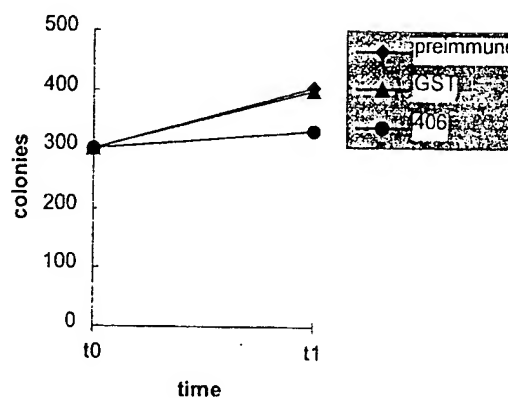
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

9/30

919

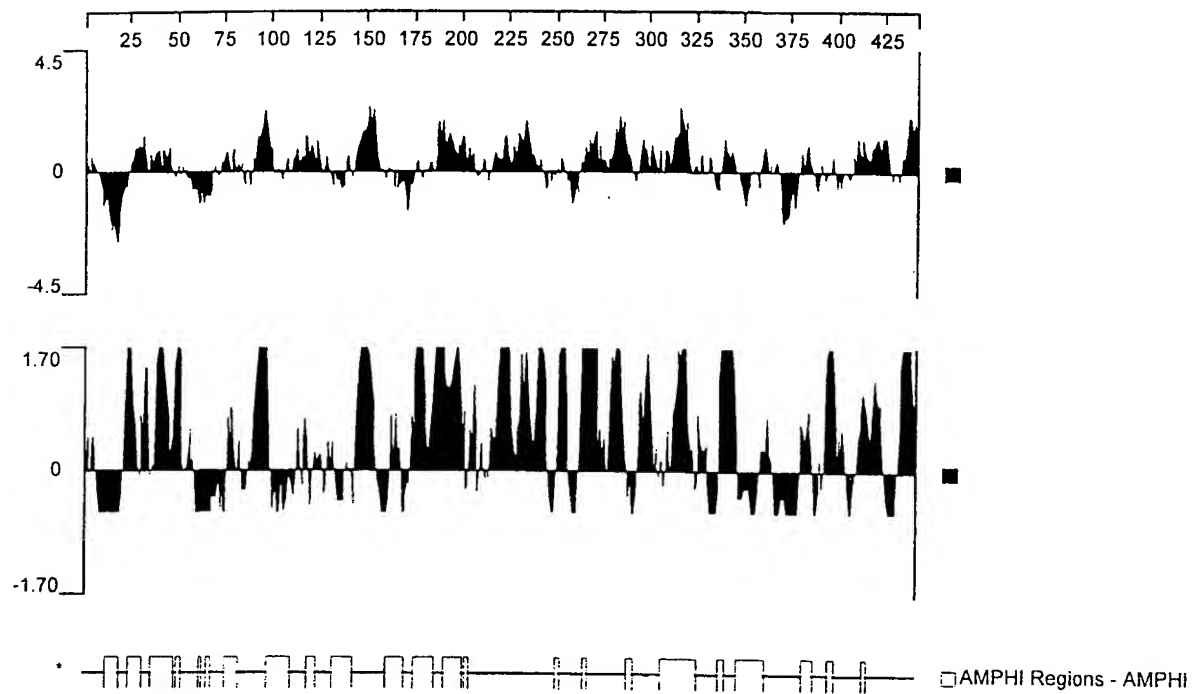
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

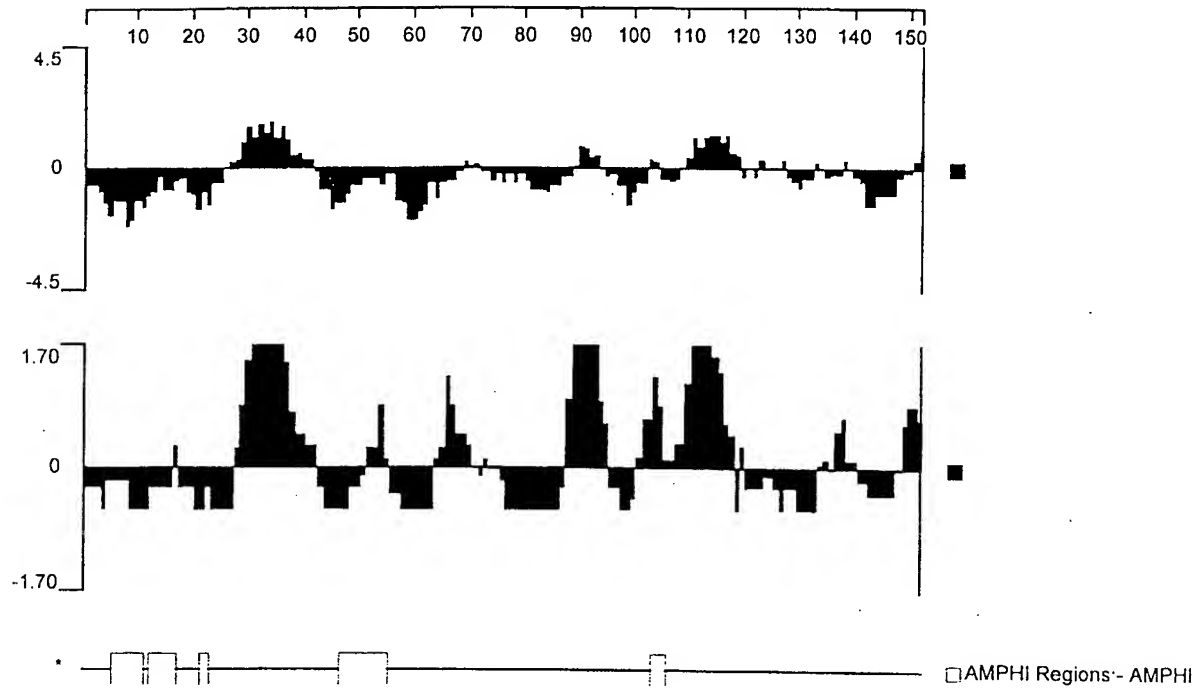
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

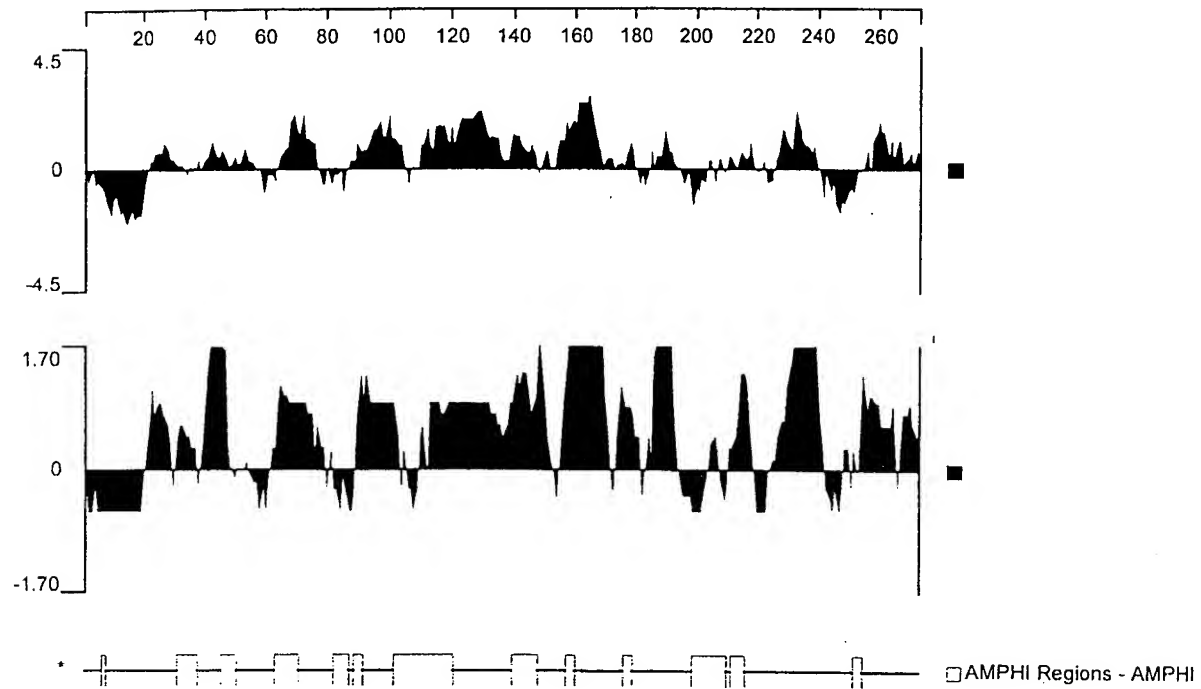
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

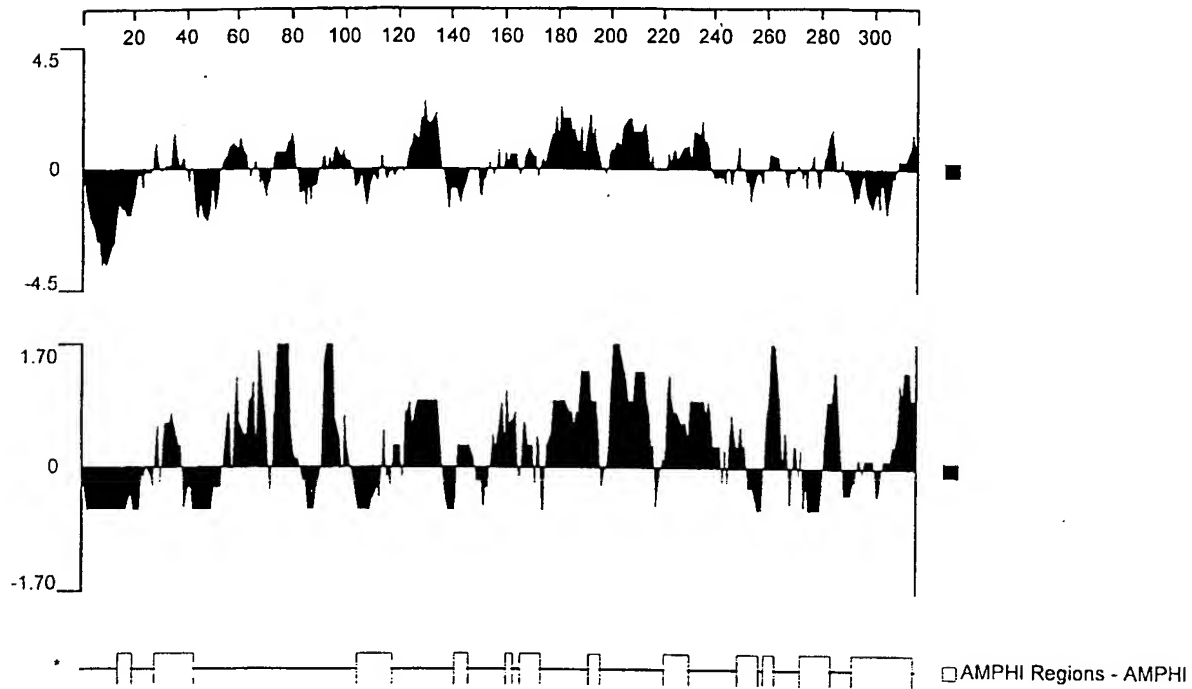
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

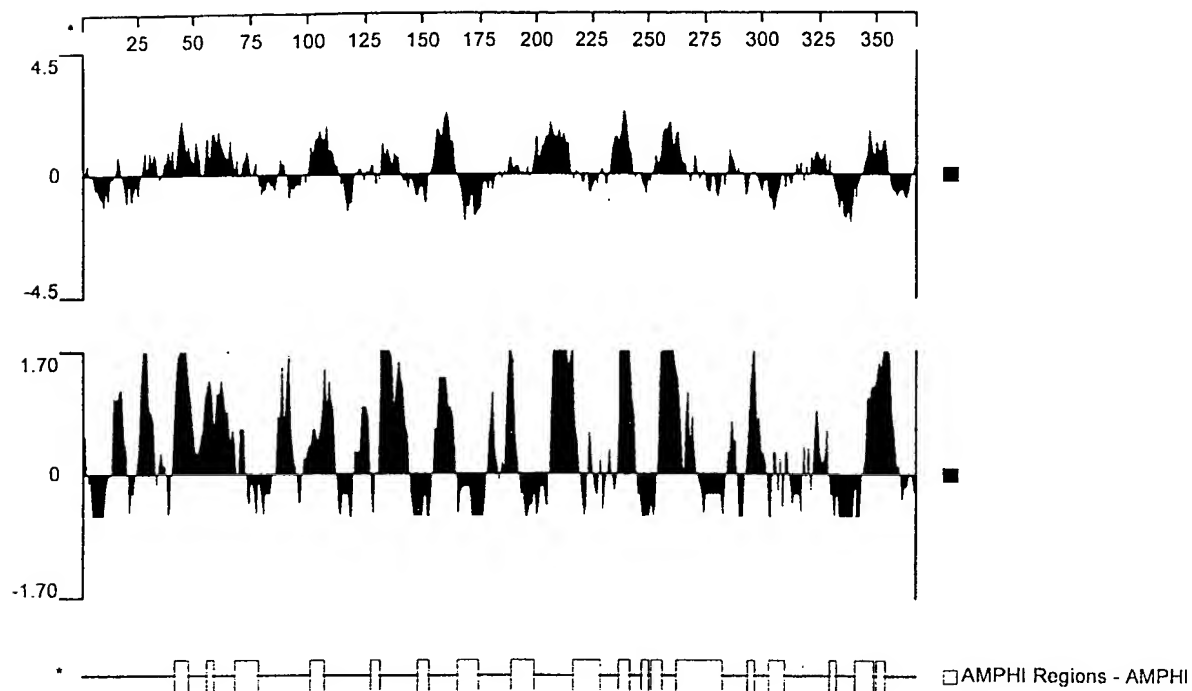
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

14/30

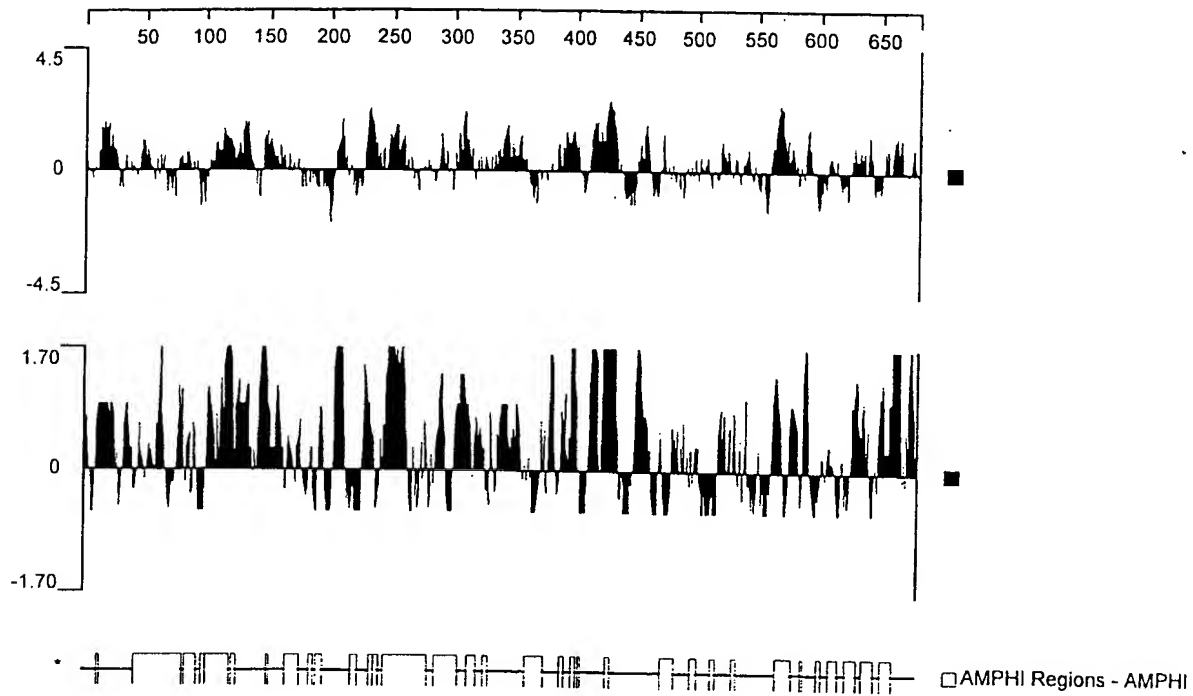
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

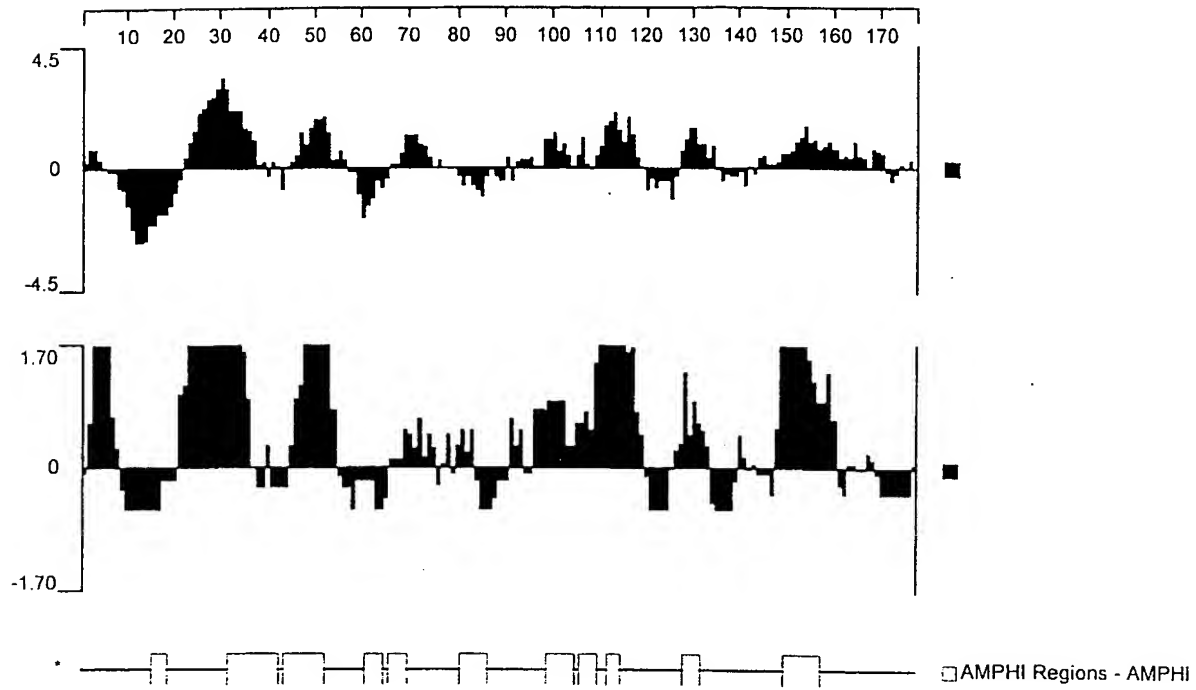
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

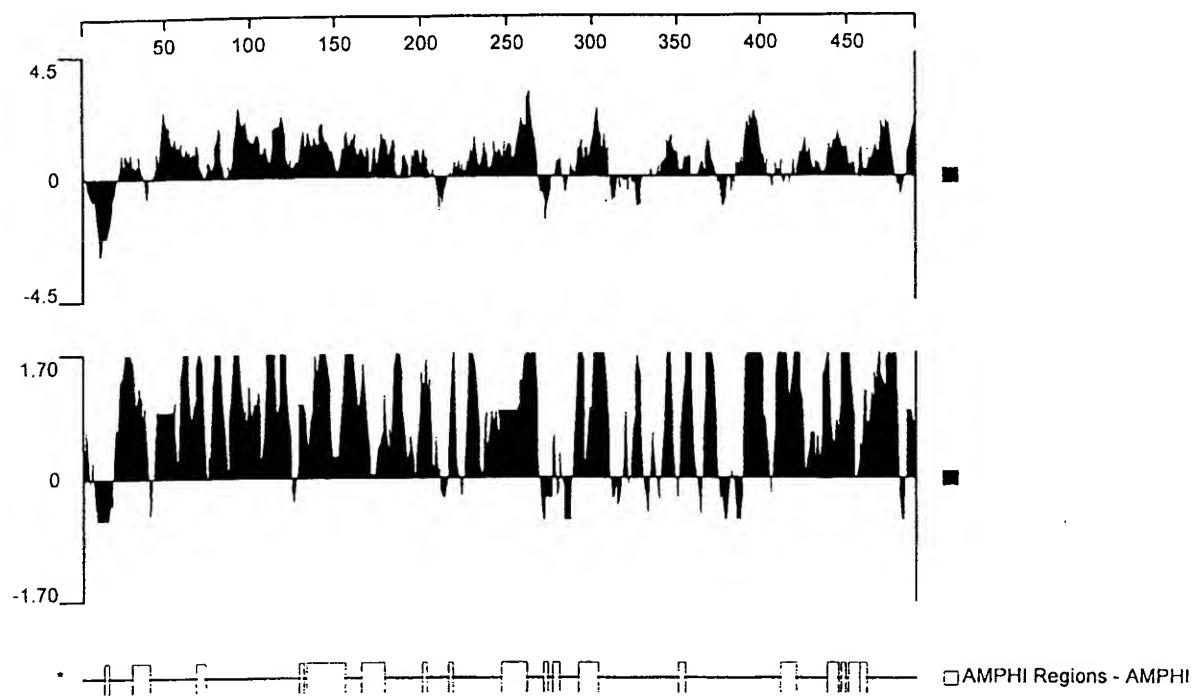
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

17/30

406

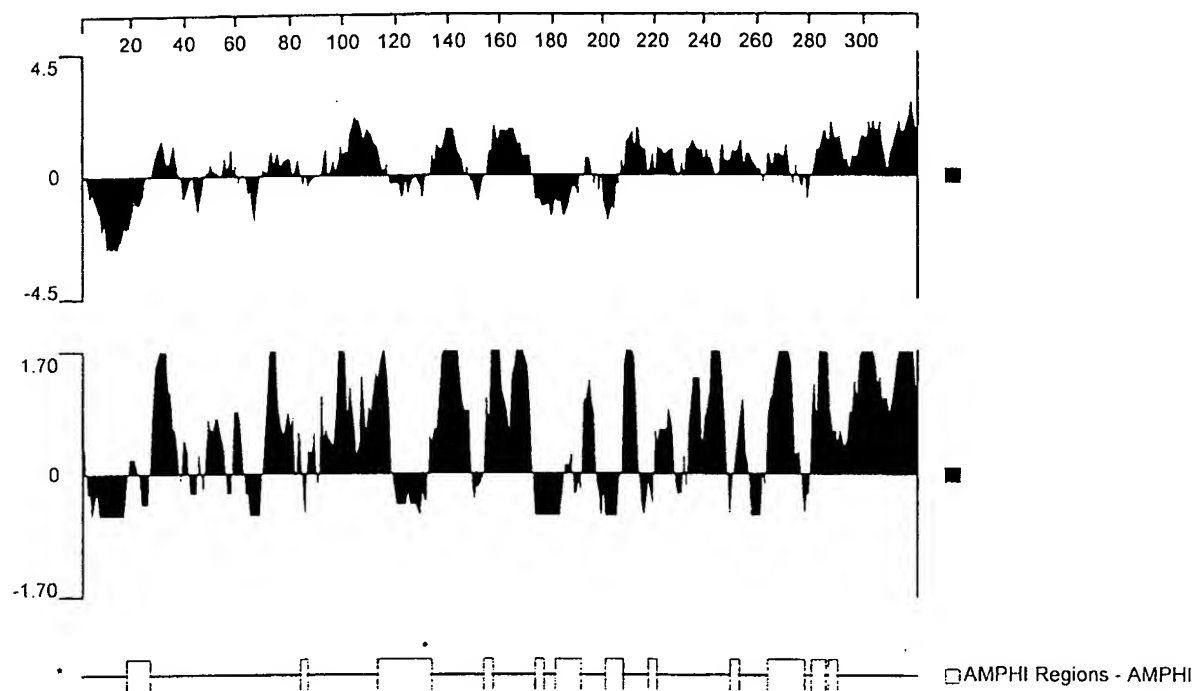
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

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z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

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gnmzq09	121	YQILDSVTTVSAKARLVDSRNGKVLWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq31	121	YQILDSVTTVSAKARLVDSRNGKVLWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
fa1090	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq32	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq33	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq01	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq05	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq08	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq02	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq03	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq04	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq07	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq10	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq11	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq13	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq15	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq16	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq17	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq19	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq21	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq22	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq23	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq24	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq25	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq27	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq28	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq29	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
z2491	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq14	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq18	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT
gnmzq26	121	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLLGALVSAVVNQIANSLT

gnmzq09	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq31	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
fa1090	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq32	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq33	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq01	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq05	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq08	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq02	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq03	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq04	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq07	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq10	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq11	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq13	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq15	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq16	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq17	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq19	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq21	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq22	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq23	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq24	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq25	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq27	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq28	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq29	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
z2491	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq14	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq18	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*
gnmzq26	181	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Fig. 20B

BEST AVAILABLE COPY³⁰

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVE.....KETE
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVE.....KETE
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVE.....KETE
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVE.....KETE
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVE.....KETE
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVVE.....KETE

287_14 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNDMPQNAADT
z2491 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNDMPQNAADT
287_9 61 VSGAPQADT...QDATAGKGGQDMAAVSAENTGNNGAAATDNPKNEDEGAQNDMPQNAADT
fa1090 61 AGGAPQADT...QDATAGKGGQDMAAVSAENTGNNGAAATDNPKNEDEGAQNDMPQNAADT

287_14 110 DSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_2 110 DSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_21 110 DSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
z2491 110 DSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_9 119 DSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
fa1090 117 DSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTA

287_14 170 AQTNOAENNOTAGSQNPASSTNPSTNSGGDFGRNTNNGNSVVIDGPSQNTLTHCKGDS
287_2 170 AQTNOAENNOTAGSQNPASSTNPSTNSGGDFGRNTNNGNSVVIDGPSQNTLTHCKGDS
287_21 170 AQTNOAENNOTAGSQNPASSTNPSTNSGGDFGRNTNNGNSVVIDGPSQNTLTHCKGDS
z2491 170 AQTNOAENNOTAGSQNPASSTNPSTNSGGDFGRNTNNGNSVVIDGPSQNTLTHCKGDS
287_9 178 DQANQAGNNQAGSSDPIPAENPAPANGGSGNFRVDLNGVVIDGPSQNTLTHCKGDS
fa1090 117 .ESANQAGNNQAGSSDPIPAENPAPANGGSGNFRVDLNGVVIDGPSQNTLTHCKGDS

287_14 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSVMKGINOYII
287_2 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSVMKGINOYII
287_21 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSVMKGINOYII
z2491 230 CSGNNFLDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSVMKGINOYII
287_9 238 CDRD.FLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSVMKGINOYII
fa1090 176 CDRD.FLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSVMKGINOYII

287_14 290 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNOADTLVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNOADTLVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNOADTLVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNOADTLVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSASSARFRSARSRRSLPAEMPLIPVNOADTLVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPT.....RSARSRRSLPAEMPLIPVNOADTLVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSYGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSYGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSYGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSYGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSYGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSYGRFAA

287_14 408 KVDGSGSKSVDGIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_2 408 KVDGSGSKSVDGIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_21 404 KVDGSGSKSVDGIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDGSGSKSVDGIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDGSGSKSVDGIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDGSGSKSVDGIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

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FIG. 21B

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z2491_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv26_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv22_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
fa1090_519     1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv32_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv11_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv28_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv96_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv02_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv03_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv04_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv05_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv01_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv07_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv12_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv18_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv19_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv21_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv27_519      1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv20_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv06_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv29_519ass    1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS

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z2491_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv26_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv22_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
fa1090_519     61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv32_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv11_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv28_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv96_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv02_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv03_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv04_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv05_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv01_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv07_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv12_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv18_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv19_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv21_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv27_519      61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv20_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv06_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv29_519ass    61 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG

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z2491_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519     121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519      121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass    121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

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FIG. 22A

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z2491_519      181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519     181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519       181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass    181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519      241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass    241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519     241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass    241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519       241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass    241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass    241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass    241 LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519      301 ISAGMKIIDSSKTAK*
zv26_519       301 ISAGMKIIDSSKTAK*
zv22_519ass    301 ISAGMKIIDSSKTAK*
fa1090_519     301 ISAGMKIIDSSKTAK*
zv32_519       301 ISAGMKIIDSSKTAK*
zv11_519       301 ISAGMKIIDSSKTAK*
zv28_519       301 ISAGMKIIDSSKTAK*
zv96_519       301 ISAGMKIIDSSKTAK*
zv02_519       301 ISAGMKIIDSSKTAK*
zv03_519       301 ISAGMKIIDSSKTAK*
zv04_519       301 ISAGMKIIDSSKTAK*
zv05_519       301 ISAGMKIIDSSKTAK*
zv01_519       301 ISAGMKIIDSSKTAK*
zv07_519       301 ISAGMKIIDSSKTAK*
zv12_519       301 ISAGMKIIDSSKTAK*
zv18_519       301 ISAGMKIIDSSKTAK*
zv19_519       301 ISAGMKIIDSSKTAK*
zv21_519ass    301 ISAGMKIIDSSKTAK*
zv27_519       301 ISAGMKIIDSSKTAK*
zv20_519ass    301 ISAGMKIIDSSKTAK*
zv06_519ass    301 ISAGMKIIDSSKTAK*
zv29_519ass    301 ISAGMKIIDSSKTAK*

```

Fig. 22B

Fig. 23A

fa1090	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm33asbc	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm32asbc	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm23asbc	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm27bc	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm09	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm10	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm24	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm25	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm14	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm04	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm11asbc	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm08n	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm96	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm01	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm02	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm03	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm07	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm12	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm18	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm19	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm20	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm21	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm06	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm17	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm13	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm05	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
z2491	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm22	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm26	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm28	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm29asbc	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm16	181	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm15	181	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL
zm31asbc	181	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAAIKGRFEGSRFLPYHTRNQINGGAL

Fig. 23B

Fig. 23C

BEST AVAILABLE COPY

fa1090	361	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	MKEFGYVWQLLPNGMKPEYRP*
zm27bc	421	MKEFGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D